

Result No.	Query			DB	ID	Description
	score	Match	Length			
1	2246	99.6	417	20	W98146	Human TRAIN-R. Hol
2	2241	99.4	423	20	W85724	Novel protein (Clo
3	2239	99.3	417	19	W70386	Amino acid sequenc
4	2230	98.9	423	19	W70387	Amino acid sequenc
5	2221	98.5	423	20	W93581	Human hAPO4-alpha
6	1563.5	69.3	416	20	W93579	Mouse mAPO4-alpha
7	1544.5	68.5	328	20	Y06400	Human NTR-5 recept
8	977	43.3	214	20	Y06522	Mouse STRFEL (Tan
9	977	43.3	214	20	W98145	Mouse TRAIN-R (lon
10	977	43.3	214	20	W93580	Mouse mAPO4-alpha
11	869	38.5	210	20	Y22223	Human TNFR superfa
12	854	37.9	150	20	W98148	TRAIN-R short. sol

PR 12-SEP-1997; 97US-0058631.
 XX (BIOU) BIOGEN INC.
 PA Hesslon C, Tschopp J;
 PI WPI; 1999-229238/19.
 XX DR N-PSDB; X24978.
 XX PT New cysteine-rich tumor necrosis factor receptor
 XX PS Claim 2; Page 26; 30pp; English.
 XX The present sequence is a novel human cysteine-rich tumor
 CC necrosis factor receptor family member termed TRAIN-R that is
 CC expressed at low levels in every tissue and cell line tested thus
 CC far, with higher expression detected in heart, prostate, ovary,
 CC testis, peripheral blood lymphocytes, thyroid and adrenal gland.
 CC Cell death can be induced by administering an agent capable of
 CC inhibiting the binding of TRAIN-R to its ligand. A claimed method
 CC of treating, or reducing, the advancement, severity or effects of
 CC an immunological disease in a mammal comprises administering a
 CC pharmaceutical composition which comprises a TRAIN-R blocking agent,
 CC e.g. soluble TRAIN-R. TRAIN-R can be fused to an immunoglobulin to
 CC produce a fusion protein which may be targeted to various sites.
 CC It can be used in binding assays, and to identify antagonists and
 CC agonists. Anti-TRAIN-R antibodies can be used to reduce the
 CC severity of an immune response or to treat cancer. TRAIN-R
 CC blocking agents can also be used to reduce the severity or effects
 CC of an immunological disease (all claimed).
 XX Sequence 417 AA;

Query Match 99.6%; Score 2246; DB 20; Length 417;
 Best Local Similarity 99.3%; Pred. No. 1.1e-199;
 Matches 414; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MALKVLEQEKTFLLVLLGLYSCKVTCTGDCROQEFDRDRSGNVCPCNQCQPGMELSK 60
 DB 1 malkvleqektftllvllglyskvtctesgdcrgqefdrsgnvcpcnqcpgmelsk 60

QY 61 ECGFGYGEDAQVTCRLHREKEDWGQKPCLDCAVNNRFKANCATSATDAICGDCPLG 120
 DB 61 ecgfygedaqvctrlhrfkedwgqkpcldcavnnrfkancatsatdaicgdcplg 120

QY 121 FYRKTILVGFQDMCEVPCGDPGPPPEPHCASKVNLVKIASTASPRDTALAAVICSALAT 180
 DB 121 fyrktlvgfdmcevcpgdppppphcaskvnlvkiaastasprdtalaavicsalat 180

QY 181 VLLALLILCVYCKRQFMKKPSWSLRSDIQYNGSELSCLDRLPQLHEYAHRACCCRRD 240
 DB 181 vllallilcvyckrfmekkpswslrsdqiyngselscldrlpqlheyahraccqrrd 240

QY 241 SVTCGVPVRLPSMCCEEACSPNPATLGCQVHSAASLQARNAGPAGEMVPTFFGSLTQSI 300
 DB 241 svtcgvpvrlpsmcceaacspnpatlgcgvhsaaslaqarnagpagemvptffgsltsqi 300

QY 301 CGEFSADWPLMQNPMGDDNLSFCDSPYELTGEDIHSLNPELESSTSLDSSODLVGGAV 360
 DB 301 cgefsadwplmqnmgddnlsfcdsypelgtgedihslnpelesstldssodlvggav 360

QY 361 PVQSHENFTAAATDLRYNNLTVESASTQDALTWRSQDQESGAITHPATOTSILQEA 417
 DB 361 pvqshenftaatdlrynnltvesastqdaltnrsqldqesgavthpatqtsilqea 417

RESULT 2
 W85724
 ID W85724 standard; Protein: 423 AA.
 XX
 AC W85724;
 XX

DT 27-SEP-1999 (first entry)
 XX Novel protein (Clone AX92_3).
 XX Polynucleotide; protein; nutrition; cytokine; cell proliferation;
 KW cell differentiation; immunostimulation; immunosuppression;
 KW haematopoiesis regulation; tissue growth; activin; inhibin;
 KW chemotaxis; chemokinesis; haemostasis; thrombolysis; receptor;
 KW ligand; anti-inflammatory; tumour suppression; gene therapy.
 XX Homo sapiens.
 OS
 XX W09920644-A1.
 PN
 XX 29-APR-1999.
 PD
 XX 16-OCT-1998; 98WO-US22034.
 PF
 XX 18-OCT-1997; 97US-0955557.
 PR
 XX (GEMY) GENETICS INST INC.
 PA
 XX Agostino MJ, Bowman MR, Evans C, Jacobs K, Lavallie ER;
 PI McCoy JM, Merberg D, Racie LA, Spaulding V, Treacy M;
 XX WPI; 1999-288272/24.
 DR N-PSDB; X08689.
 DR
 XX New polynucleotides encoding secreted human proteins
 PT
 XX Claim 32; Page 117-118; 136pp; English.
 PS
 XX The new human secreted proteins are encoded by polynucleotides
 CC obtained from human placenta, adult testes, fetal kidney, fetal
 CC brain, adult brain, adult brain and adult blood cDNA libraries.
 CC The polynucleotides and proteins are predicted to have biological
 CC activities which would make them suitable for treating, preventing or
 CC ameliorating medical conditions in humans and animals. Suggested
 CC activities include nutritional activity, cytokine and cell
 CC proliferation/differentiation activity, immune stimulating (e.g. as
 CC vaccines) or suppressing activity, haematopoiesis regulating
 CC activity, tissue growth activity, activin/inhibin activity,
 CC chemotactic/chemokinetic activity, haemostatic and thrombolytic
 CC activity, receptor/ligand activity, anti-inflammatory activity,
 CC cadherin/tumour invasion suppressor activity, and tumour inhibition
 CC activity. The polynucleotides are also stated to be useful for gene
 CC therapy. The sequences identified by a secretory leader
 CC sequence motif in the polynucleotide and it is thought that the
 CC encoded proteins have biological activity by virtue of their secreted
 CC nature. This polypeptide was encoded by a clone designated AX92_3
 CC (See X08689).
 XX Sequence 423 AA;

Query Match 99.4%; Score 2241; DB 20; Length 423;
 Best Local Similarity 99.8%; Pred. No. 3.2e-199;
 Matches 414; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MALKVLEQEKTFLLVLLGLYSCKVTCTGDCROQEFDRDRSGNVCPCNQCQPGMELSK 60
 DB 1 malkvleqektftllvllglyskvtctgdcrgqefdrsgnvcpcnqcpgmelsk 60

QY 61 ECGFGYGEDAQVTCRLHREKEDWGQKPCLDCAVNNRFKANCATSATDAICGDCPLG 120
 DB 61 ecgfygedaqvctrlhrfkedwgqkpcldcavnnrfkancatsatdaicgdcplg 120

QY 121 FYRKTILVGFQDMCEVPCGDPGPPPEPHCASKVNLVKIASTASPRDTALAAVICSALAT 180
 DB 121 fyrktlvgfdmcevcpgdppppphcaskvnlvkiaastasprdtalaavicsalat 180

QY 181 VLLALLILCVYCKRQFMKKPSWSLRSDIQYNGSELSCLDRLPQLHEYAHRACCCRRD 240
 DB 181 vllallilcvyckrfmekkpswslrsdqiyngselscldrlpqlheyahraccqrrd 240

Db 101 vllallllivlyckrqfmeckpwsrlsqdiqngselscldrpqhlayhraccqcrd 240
Qy 241 SVQTCGPVRLLPSCCEACSPNATLCCGVHSAASLQARNAGPAGEMVPTFFGSLTQSI 300
Db 241 svqtcgvrllpsmcceacspnatlpgcvhsaaslaqarnagpagemvptffgsltqsi 300
Qy 301 CGEFSDAWPLMONGMGNISFCDSYPELTGEDTHSLNPELESSTLSDNSQDLVGGAV 360
Db 301 cgefsdawplmqnpgmgdnisfcdsyplagedihslnpelesstlidsnssqdlvggav 360
Qy 361 PVQSHSENFTATDLRYNNLTVESASTQDALTMRSQDLQESGALIHHPATQTSLSQ 415
Db 361 pvqshsenftaatdlsrynntlivesastqdaltrmsqldqesgalihpatqtslsq 415
RESULT 3
W70386
ID W70386 standard; Protein; 417 AA.
XX
AC W70386;
XX
DT 02-DEC-1998 (first entry)
XX
DE Amino acid sequence of human alpha-OAF065.
XX
KW Human; alpha-OAF065; stroma cell; antibody; inflammatory;
KW cytokine-mediated disease; rheumatism; ulcerative colitis.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 223
FT /note= "encoded by AGA"
FT Misc-difference 224
FT /note= "encoded by CCT"
XX
FN WO9838304-A1.
XX
PD 03-SEP-1998.
XX
PF 26-FEB-1998; 98WO-JP00799.
XX
PR 27-FEB-1997; 97JP-0043143.
XX
PA (ONOY) ONO PHARM CO LTD.
XX
PI Fukushima D, Konishi M, Tada H;
XX
DR WPI; 1998-481205/41.
DR N-PSDB; V33361.
XX
PT Membrane polypeptide expressed by human stroma cells, and antibodies
PT recognising it - for treatment of inflammatory and other
PT cytokine-mediated diseases.
XX
PS Claim 1; Pages 28-30; 54pp; Japanese.
XX
CC This is the amino acid sequence of the human alpha-OAF065, used in
CC the method of the invention. The process involves the use of peptides
CC expressed by stroma cells, and its antibodies are used for in the
CC prevention and treatment of inflammatory and other cytokine-mediated
CC diseases such as rheumatism, ulcerative colitis.
XX
SQ Sequence 417 AA;
Query Match 99.3%; Score 2239; DB 19; Length 417;
Best Local Similarity 99.5%; Pred. NO. 4.8e-199;
Matches 415; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 MALKVLLSQEKTFFTLVLLGYLSCKVTCETDCRQEFDRBSGNCVPCNCGGPMELSK 60
Db 1 malkvllsqektffllvllgylsckvtcetdcrqefdrbsgncvpcncgpgmeisk 60

Qy 61 ECGFGYGEDAQCVTCLRHREKEDMGFOCKPCLCDCAVNVRFQKANCATSDAICGDCUPG 120
Db 61 ecgfygedaqcvctclrhrfkedwgfckpcldcavnvrfqkancatsdaicgdcupg 120
Qy 121 FYRKTGLVGFODMECVPCGDPPIPPYEPHCASKVNLVKIATASSPRDTALAAVICSALAT 180
Db 121 fyrktglvfgdmevcpcgdpippiyephcaskvnlvkiatassprdtalaavicsalat 180
Qy 181 VLLALLILCVLYCKROFMEKPSWLSRSDIQYNGSELSCLDRPOLHEYAHACCQCRD 240
Db 181 vllallilcvlyckrqfmeckpwsrlsqdiqngselscldrpqhlayhraccqcrd 240
Qy 241 SVQTCGPVRLLPSCCEACSPNATLCCGVHSAASLQARNAGPAGEMVPTFFGSLTQSI 300
Db 241 svqtcgvrllpsmcceacspnatlpgcvhsaaslaqarnagpagemvptffgsltqsi 300
Qy 301 CGEFSDAWPLMONGMGNISFCDSYPELTGEDTHSLNPELESSTLSDNSQDLVGGAV 360
Db 301 cgefsdawplmqnpgmgdnisfcdsyplagedihslnpelesstlidsnssqdlvggav 360
Qy 361 PVQSHSENFTATDLRYNNLTVESASTQDALTMRSQDLQESGALIHHPATQTSLSQEA 417
Db 361 pvqshsenftaatdlsrynntlivesastqdaltrmsqldqesgalihpatqtslsqea 417
RESULT 4
W70387
ID W70387 standard; Protein; 423 AA.
XX
AC W70387;
XX
DT 02-DEC-1998 (first entry)
XX
DE Amino acid sequence of human beta-OAF065.
XX
KW Human; beta-OAF065; stroma cell; antibody; inflammatory;
KW cytokine-mediated disease; rheumatism; ulcerative colitis.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 223
FT /note= "encoded by AGA"
FT Misc-difference 224
FT /note= "encoded by CCT"
XX
FN WO9838304-A1.
XX
PD 03-SEP-1998.
XX
PF 26-FEB-1998; 98WO-JP00799.
XX
PR 27-FEB-1997; 97JP-0043143.
XX
PA (ONOY) ONO PHARM CO LTD.
XX
PI Fukushima D, Konishi M, Tada H;
XX
DR WPI; 1998-481205/41.
DR N-PSDB; V33362.
XX
PT Membrane polypeptide expressed by human stroma cells, and antibodies
PT recognising it - for treatment of inflammatory and other
PT cytokine-mediated diseases.
XX
PS Disclosure; Pages 37-49; 54pp; Japanese.
XX
CC This is the amino acid sequence of the human beta-OAF065, used in
CC the method of the invention. The process involves the use of peptides
CC expressed by stroma cells, and its antibodies are used for in the
CC prevention and treatment of inflammatory and other cytokine-mediated
CC diseases such as rheumatism, ulcerative colitis.

KW APO6; APO8; TNRL-1; TNRL-3; diagnosis; treatment; therapy; disease;
 KW cytoplasmic domain; immunogen; antibody preparation; breast carcinoma;
 KW apoptosis; mouse; map04-alpha.

OS Mus sp.

XX WO9911791-A2.

PN 11-MAR-1999.

PD 04-SEP-1998; 98WO-US18393.

PF 05-SEP-1997; 97US-0924634.

PR (UNIW) UNIV WASHINGTON.

XX Chaudhary PM;

PI WPI; 1999-205191/17.

XX N-PSDB; X23413.

DR New Tumor Necrosis Factor family receptor polypeptides and ligands -
 XX useful for diagnosis and treatment of prostate cancer and
 XX developmental or gestational abnormalities

PS Claim I; Fig 7A; 156pp; English.

XX This invention describes isolated Tumor Necrosis Factor (TNF) family
 CC receptor polypeptides: APO4, APO6, APO8 and APO9 or their active
 CC fragments, and isolated TNF related ligands 1 and 3 (TNRL1 and TNRL3) or
 CC their active fragments. APO4 is useful for diagnosing prostate cancer
 CC by determining levels of APO4 in an individual. Prostate cancer can also
 CC be treated using APO4 selective binding agents linked to a therapeutic
 CC moiety. APO4 polypeptides are also useful for identifying selective
 CC binding agents, useful in diagnosis/treatment of disease by binding of
 CC agents to the polypeptide/active fragment which is extracellular, or
 CC expressed on the cell surface. The binding is preferably performed in
 CC vivo. APO4 polypeptides/active fragments are also useful for screening
 CC for agonists and antagonists by binding and observing the change in APO4
 CC activity. Effective pharmacological agents useful in diagnosis or
 CC treatment of disease are also identified using APO4 polypeptides/active
 CC fragments and APO4 signal transducer molecules that specifically interact
 CC with a cytoplasmic domain of APO4 and detecting a change in level of APO4
 CC activity. The method is performed in vivo or in vitro. APO polypeptides
 CC are all useful as immunogens for preparing antibodies. APO4 is also
 CC useful for diagnosis/treatment of developmental or gestational
 CC abnormalities. APO8 was transfected to human breast carcinoma cell line
 CC MCF-7, and induced apoptosis.

XX Sequence 416 AA;

Query Match 69.3%; Score 1563.5; DB 20; Length 416;
 Best Local Similarity 70.4%; Pred. No. 1.6e-136;
 Matches 295; Conservative 34; Mismatches 85; Indels 5; Gaps 3;

QY 1 MALKVLEGEKFTFTLLVLLGSKVTCETGCRQOEPRDSGNCVPCNQCQPGMELSK 60
 Db 1 malkvlpbrtvlfaailfllhckvscetgdcrgqefkdrsgncvclkcqpgmelsk 60
 QY 61 ECGFGYGEDAQCVTCRLHFRKEDWGQCKPCLDCAVNRFRKANCATSDAICGDCLEPG 120
 Db 61 ecgfygedaqcvpcrphrfkdwgfkckpcadcalvnrfrancshsdavcgdcclpg 120
 QY 121 FYRKTKLVGFQDMECVPCGDPPEPHCASKVNLVKIATSSPRDPTALAAVICSALAT 180
 Db 121 fyrtklvfgdmecvpcgdppephcaskvnlvkiatssvprdtalaavicsalat 180
 QY 181 VLLALITLCVYCKRQFMKKPSWSLRSQDIQVNGSELCLDRPOLHEVAHRACCCRRD 240
 Db 181 vllallilvcyckrfrmekpswslrsqdiqngselcscfqprrlhcacccqyhrd 240
 QY 241 SVOTCGFVRLPLSMCCEACSPNPATLGCVGVHSAASLQARNAGPAGEMVPTFFGSLTQSI 300

Db 241 sapmygpvhlpisclceearavlgclrspttlqernpasvgnntmpaffgsvsrsi 300
 QY 301 CGEFDADWPLMONGDNISFCDSYPELTGEDIHSLNPELESSTSLDSNSQDLVGGAV 360
 Db 301 caefsdawplmqnplggds-sicdsypeltdetnslnpenestaslssggqdlagta- 358
 QY 361 PVQSHSENFATADLSRYNN--TLVESASTQDALTMRSQLDQESGAIHHPATQTSLOEA 417
 Db 359 -alesngvsestdsprhgdgtvweqtlaqdaqrtpsaggwedrenlnlampaifqda 416

RESULT 7

Y06400

ID Y06400 standard; Protein; 328 AA.

XX AC Y06400;

XX 20-SEP-1999 (first entry)

DE Human NTR-5 receptor.

XX NTR-5; human; receptor; signal transduction; bone; muscle;

KW diagnosis; therapy.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Peptide 1..29

FT Protein /note= "signal peptide"

FT Domain /note= "mature protein"

FT Domain /note= "extracellular domain"

FT Domain /note= "transmembrane domain"

FT Domain /note= "intracellular domain"

XX WO9933967-A2.

XX 08-JUL-1999.

XX 28-DEC-1998; 98WO-US27688.

XX 29-DEC-1997; 97US-0068925.

XX (REGE-) REGENERON PHARM INC.

XX Valenzuela DM;

XX WPI; 1999-419102/35.

XX N-PSDB; X59346.

XX New mammalian receptor NTR-5 polypeptides

XX Claim 7; Page 21-22; 27pp; English.

CC The present sequence represents a novel human receptor, designated
 CC NTR-5, that shows homology to osteoprotegerin and to tumour necrosis
 CC factor receptor. The sequence was predicted from an isolated cDNA
 CC clone (see X59346). Homology to osteoprotegerin suggests that NTR-5
 CC is involved in the regulation of bone mass, and may be useful for
 CC regulating development, proliferation and death of osteoblast or
 CC osteoclast cells or for regulating muscle metabolism, and that it
 CC may be implicated in muscle diseases or disorders. A host-vector
 CC system for production of NTR-5 is claimed. NTR-5 polypeptides can
 CC be used as immunogens and in screening assays to identify NTR-5
 CC ligands, agonists and antagonists. Polypeptides comprising the
 CC extracellular domain of NTR-5 fused to an immunoglobulin constant
 CC region, especially to a human immunoglobulin gamma-1 fc region,
 CC are claimed. The invention also provides for diagnostic and
 CC therapeutic methods based on the interaction of NTR-5 and agents

RESULT 11
Y22223
ID Y22223 standard; Protein; 210 AA.
XX
XX Y22223;
AC
DT 16-SEP-1999 (first entry)
XX
XX Human TNFR superfamily soluble receptor protein sequence.
DE
XX
XX TNFL1; human; TNFR superfamily; tumour necrosis factor ligand; TNF;
KW tumour necrosis factor receptor; TNFR superfamily; cell proliferation;
KW cell differentiation; cytokine production; immunoglobulin; hyperplasia;
KW apoptosis inducer; activated T cell; autoimmune disease; inhibitor;
KW myasthenia gravis; insulin-dependent diabetes mellitus; endotoxin shock;
KW rheumatoid arthritis; multiple sclerosis; systemic lupus erythematosus;
KW tumour; proliferative disorder; neoplasia; dysplasia; immunocompetence;
KW lymphoid organogenesis; bacterial resistance; contact hypersensitivity;
KW delayed type sensitivity; therapy.
XX
XX Homo sapiens.
OS
XX
XX WO9933980-A2.
PN
XX
XX 08-JUL-1999.
PD
XX
XX 22-DEC-1998; 98WO-0527474.
PF
XX
XX 16-DEC-1998; 98US-0212270.
PR
XX
XX 30-DEC-1997; 97US-0068959.
PR
XX
XX (CHIR) CHIRON CORP.
PA
XX
XX Kassam A, Lamson G, Pot D, Tribouley C;
PI
XX
XX WPI; 1999-405508/34.
DR
XX
XX N-PSDB; X84622.
DR
XX
XX New tumour necrosis factor ligands, useful for induction of cell
PT death and/or proliferation of cells
PT
XX
XX Claim 13; Page 62; 69pp; English.
PS
XX
XX This sequence represents a tumour necrosis factor receptor (TNFR)
CC superfamily soluble protein of the invention. The invention also relates
CC to tumour necrosis factor (TNF) ligand (TNFL) family proteins. The TNFL
CC proteins play regulatory roles in cell proliferation and/or
CC differentiation, e.g. they can induce production of cytokines,
CC immunoglobulins, etc. A variety of diseases can be treated by modulating
CC the activity of TNFL proteins, e.g. they can induce apoptosis of
CC activated T cells but rescue resting T cell from apoptosis. TNFL
CC polypeptides can therefore be used to treat autoimmune diseases, such as
CC myasthenia gravis, insulin-dependent diabetes mellitus, rheumatoid
CC arthritis, multiple sclerosis, and systemic lupus erythematosus. TNFL
CC proteins also have tumour stimulating properties, so tumours can be
CC treated by inhibiting the expression or activity of TNFL. Other
CC proliferative disorders, such as neoplasias, dysplasias, and hyperplasia
CC can also be treated using TNFL inhibitors. The TNFL polypeptides and
CC polynucleotides can also be used to enhance or decrease TNF activity,
CC thus providing therapeutic benefits such as induction of cell death,
CC lymphoid organogenesis, or host bacterial resistance, and inhibition of
CC endotoxin shock, contact hypersensitivity, delayed type sensitivity or
CC immunocompetence of a transplant recipient. TNF and its receptors play a
CC major role in host defence and immunosurveillance. As such, there is a
CC need to identify new members of TNFR families. This invention provides
CC this need.
XX
XX Sequence 210 AA;
SQ

Matches 154; Conservative 11; Mismatches 19; Indels 0; Gaps 0;
QY 1 MALKVLEQEKTFTLLVLLGLYSCKVCTGTGCRQOEFDRSGNCVPCNQCGMELSK 60
DB 1 malkvlpplrvtlfaailfllhlaackvsctgdcrcqefkdrsgncvclckqcpmmelsk 60
QY 61 ECGFYGEDAQCVTCRLHFKEDWGFKCKPCLDCAVNRFOKANGSATSATSDAICGDLPG 120
DB 61 ecgfyggedaqcvpcrphrfkcdwgfkckpcadcalvnrfrqancshdscavcgdlpg 120
QY 121 FYRKTLLVGFQDMECVPCGDPDPPEPHCASKVNLVKIATASSTPRDTALAAVICALAT 180
DB 121 fyrtkllvgfdmecnecvpcgdpdppephctskvnlvkistvasprdtavaavicalat 180
QY 181 VLLA 184
DB 181 vlla 184
RESULT 12
W98148
ID W98148 standard; Peptide; 150 AA.
XX
AC W98148;
XX
DT 05-JUL-1999 (first entry)
XX
DE TRAIN-R short, soluble form.
XX
KW TRAIN-R; receptor; human; tumour necrosis factor receptor;
KW agonist; antagonist; cancer; immunological disease; therapy;
KW cytostatic.
XX
XX Homo sapiens.
OS
XX
XX WO9913078-A1.
PN
XX
XX 18-MAR-1999.
PD
XX
XX 11-SEP-1998; 98WO-0519030.
PF
XX
XX 06-MAY-1998; 98US-0084422.
PR
XX
XX 12-SEP-1997; 97US-0058631.
PR
XX
XX (BIOJ) BIOGEN INC.
PA
XX
XX Hesslon C, Tschopp J;
PI
XX
XX WPI; 1999-229238/19.
DR
XX
XX New cysteine-rich tumor necrosis factor receptor
PT
XX
XX Disclosure; Page 28; 30pp; English.
PS
XX
XX The present sequence comprises the putative short, secreted soluble
CC form of a novel human cysteine-rich tumour necrosis factor receptor
CC family member termed TRAIN-R. The sequence was produced from a
CC 30-amino acid peptide (see W98147) encoded by a cloned exon
CC sequence (see X24979) and by comparison to the murine TRAIN-R
CC short form (see W98144). The human soluble TRAIN-R protein is
CC expected to inhibit signalling by full-length human TRAIN-R (see
CC W98146). Human TRAIN-R is expressed at low levels in every tissue
CC and cell line tested thus far, with higher expression detected in
CC heart, prostate, ovary, testis, peripheral blood lymphocytes,
CC thymoid and adrenal gland. Cell death can be induced by
CC administering an agent capable of inhibiting the binding of TRAIN-R
CC to its ligand. A claimed method of treating, or reducing, the
CC advancement, severity or effects of an immunological disease in a
CC mammal comprises administering a pharmaceutical composition which
CC comprises a TRAIN-R blocking agent, e.g. soluble TRAIN-R. TRAIN-R
CC can be fused to an immunoglobulin to produce a fusion protein which
CC may be targeted to various sites. It can be used in binding assays,
CC and to identify antagonists and agonists. Anti-TRAIN-R antibodies.

Query Match 38.5%; Score 869; DB 20; Length 210;
Best Local Similarity 83.7%; Pred. No. 1.1e-72;

CC can be used to reduce the severity of an immune response or to treat
CC cancer. TRAIN-R blocking agents can also be used to reduce the
CC severity or effects of an immunological disease (all claimed).
XX
SQ Sequence 150 AA;

Query Match 37.9%; Score 854; DB 20; Length 150;
Best Local Similarity 99.3%; Pred. No. 1.7e-71;
Matches 148; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MALKVLLVLEKTFLLVLLGLVLSKVTCTGDCRQQRDRSGNVCPCNCGGPMELSK 60
|||||
Db 1 malkvillegektffllvllglvlskvtctesgdcqrqqrdrsgncvpcncgcpgmelsk 60
|||||
Qy 61 ECGFGYGDAQCVCRLHREFKEDWGFKCKPCLDCAVVNRFOKANCATSDAICGDCPLG 120
|||||
Db 61 ecgfygdaqcvcrtlhrfkdwgfkckpckldcavvnrfqkancatsdaicgdcplg 120
|||||
Qy 121 FYRKTLYGVFQDMECVPCGDPPEPHC 149
|||||
Db 121 fyrrtklvgfdmecnvpcgdppepyephc 149
|||||

RESULT 13
Y06399
ID Y06399 standard; Protein; 160 AA.
AC Y06399;
XX
XX Y06399;

DT 20-SEP-1999 (first entry)
DE Mouse NTR-5 receptor.
XX
XX NTR-5: mouse; receptor; signal transduction; bone; muscle;
KW diagnosis; therapy.
KW
XX

OS Mus musculus.
XX
XX WO9933967-A2.
PN
XX
PD 08-JUL-1999.
XX
XX 28-DEC-1998; 98WO-US27688.
PF
XX
XX 29-DEC-1997; 97US-0068925.
PR
XX
XX (REGE-) REGENERON PHARM INC.
PA

PI Valenzuela DM;
XX
XX WPI; 1999-419102/35.
DR
XX
XX N-PSDB; X59345.
XX

PT New mammalian receptor NTR-5 polypeptides
XX
XX
PS Example 1; Page 19; 27pp; English.

CC The present sequence represents a novel murine receptor, designated
CC NTR-5, that shows homology to osteoprotegerin and to tumour necrosis
CC factor receptor. The sequence was predicted from isolated cDNA
CC clones (see X59345). Human NTR-5 has also been identified (see
CC X06400). Homology to osteoprotegerin suggests that NTR-5 is
CC involved in the regulation of bone mass, and may be useful for
CC regulating development, proliferation and death of osteoblast or
CC osteoclast cells or for regulating muscle metabolism, and that it
CC may be implicated in muscle diseases or disorders. A host-vector
CC system for production of NTR-5 is claimed. NTR-5 polypeptides can
CC be used as immunogens and in screening assays to identify NTR-5
CC ligands, agonists and antagonists. The invention also provides for
CC diagnostic and therapeutic methods based on the interaction of
CC NTR-5 and agents that initiate signal transduction through binding
CC to NTR-5.

XX
SQ Sequence 160 AA;
Query Match 34.7%; Score 783; DB 20; Length 160;
Best Local Similarity 91.6%; Pred. No. 7e-65;
Matches 141; Conservative 4; Mismatches 9; Indels 0; Gaps 0;
Qy 55 GMEISKEGFGYGDAQCVCRLHREFKEDWGFKCKPCLDCAVVNRFOKANCATSDAIC 114
|||||
Db 1 gmeiskegfygdaqcvcprphrfkdwgfkckpcadcaivnrfqancshcsdavic 60
|||||
Qy 115 GDCLPFGFYRKTLYGVFQDMECVPCGDPPEPHCASKVNLVKIATASSPRDTALAAVI 174
|||||
Db 61 gdcplpgfyrrtklvgfdmecnvpcgdppepyephctskvnlvkiatassprdtalaavi 120
|||||
Qy 175 CSALATVLLALLILCVIYCKRQFMFKKPSWSLRS 208
|||||
Db 121 csalatvllallilcvlyckrgfmekpckpsklps 154
|||||

RESULT 14
Y06523
ID Y06523 standard; Protein; 150 AA.
XX
XX Y06523;
XX
XX 08-OCT-1999 (first entry)
DT
XX
XX Mouse STRIFE2 (Tango 127b) TNF receptor.

DE STRIFE2; Tango 127b; mouse; tumour necrosis factor receptor;
KW sepsis; circulatory collapse; toxic shock; infection;
KW immune disease; autoimmune disease; alcohol-induced hepatitis;
KW inflammation; graft versus host pathology; cancer; tumour;
KW cerebral malaria; multiple sclerosis; diagnosis; therapy.
XX
XX Mus musculus.

Key Location/Qualifiers
FT Peptide 1..29 /note= "signal peptide"
FT Protein 30..150 /note= "mature protein"
FT Domain 34..72 /note= "cysteine-rich domain"
FT Domain 75..114 /note= "cysteine-rich domain"
XX
XX WO9937818-A1.
PN
XX
XX 29-JUL-1999.
PD
XX
XX 27-JAN-1999; 99WO-US01679.
PF
XX
XX 27-JAN-1998; 98US-0014195.
PR
XX
XX (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.

PI Busfield SJ;
XX
XX WPI; 1999-458707/38.
DR
XX
XX N-PSDB; X87395.

PT New STRIFE1 and STRIFEII polypeptides, proteins and nucleic acid
PT molecules useful for modulating TNFR associated disorders
XX
XX Claim 26; Fig 2; 119pp; English.
CC The present sequence represents mouse STRIFE2 (also called Tango
CC 127b or T127b), a novel member of the tumour necrosis factor
CC receptor (TNFR) superfamily. 2 Splice forms of murine STRIFE have
CC been identified, one that is predicted to be membrane-bound

CC (STRIFE1, see Y06522) and one that is secreted (STRIFE2). STRIFE
CC was identified as a TNFR homologue by a computer-based search of
CC EST databases. The invention provides STRIFE1 and STRIFE2
CC polynucleotides and polypeptides, fusion proteins, antigenic
CC peptides and antibodies. It also provides expression vectors,
CC host cells and transgenic animals, as well as diagnostic, screening
CC and therapeutic methods. STRIFE I and STRIFE II may play a role in
CC mediating inflammatory, immune and host defense functions and may
CC play a role in various neoplastic disease states. They may be
CC useful as targets for developing novel diagnostic and therapeutic
CC agents for TNF- and TNFR-associated disorders such as sepsis
CC syndrome, circulatory collapse and shock resulting from bacterial
CC infection, acute and chronic parasitic or infectious processes,
CC acute and chronic immune and autoimmune pathologies, alcohol-induced
CC hepatitis, chronic inflammatory pathologies, vascular inflammatory
CC pathologies, graft-versus-host pathology, malignant pathologies
CC involving TNF-secreting tumors, cerebral malaria and multiple
CC sclerosis.
XX
SQ Sequence 150 AA;

Query Match 32.2%; Score 725; DB 20; Length 150;
Best Local Similarity 82.6%; Pred. No. 1.5e-59;
Matches 123; Conservative 9; Mismatches 17; Indels 0; Gaps 0;

QY 1 MALKVLEQEKTFETLLVLLGYLSCKVTCTGTGCRQEFDRSGNCVPCNQCQPGHLSK 60
DB 1 malkvplhrtvlfafllhllackvscetgdcrgqefkdrsgncvllckqcgpgmelsk 60

QY 61 ECGFGYGEDAQCCTRLHREFKDWGFKCKPCLDCAVVRFRKANGSATSDAICGDLCPG 120
DB 61 ecfgfygedaqcvcprhrfkedwgfgkckpcadcalvnfrqancshsdtavcgdcplg 120

QY 121 FYRKTklvgfQDMECVPCGDPpppppEPhc 149
DB 121 fyrktklvgfQDMECVPCGDPpppppEPhc 149

RESULT 15
Y22224
ID Y22224 standard; Protein; 150 AA.
AC Y22224;
DT 16-SEP-1999 (first entry)
XX Mouse TNFR superfamily soluble receptor protein sequence.
DE
XX TNFL1; human; TNFR superfamily; tumour necrosis factor ligand; TNF;
KW tumour necrosis factor receptor; TNFR superfamily; cell proliferation;
KW cell differentiation; cytokine production; immunoglobulin; hyperplasia;
KW apoptosis inducer; activated T cell; autoimmune disease; inhibitor;
KW myasthenia gravis; insulin-dependent diabetes mellitus; endotoxin shock;
KW rheumatoid arthritis; multiple sclerosis; systemic lupus erythematosus;
KW tumour; proliferative disorder; neoplasia; dysplasia; immunocompetence;
KW lymphoid organogenesis; bacterial resistance; contact hypersensitivity;
KW delayed type sensitivity; therapy.
XX
OS Mus sp.
XX
PN WO9933980-A2.
XX
PD 08-JUL-1999.
XX
PF 22-DEC-1998; 98WO-0527474.
XX
PR 16-DEC-1998; 98US-0212270.
PR 30-DEC-1997; 97US-0068959.
XX
PA (CHIR) CHIRON CORP.
XX Kassam A, Lamson G, Pot D, Tribouley C;

XX WPI; 1999-405508/34.
DR N-PSDB; X84623.
XX New tumour necrosis factor ligands, useful for induction of cell
PT death and/or proliferation of cells
XX
PS Claim 13; Page 62-63; 69pp; English.
XX
CC This sequence represents a tumour necrosis factor receptor (TNFR)
CC superfamily soluble protein of the invention. The invention also relates
CC to tumour necrosis factor (TNF) ligand (TNFL) family proteins. The TNFL
CC proteins play regulatory roles in cell proliferation and/or
CC differentiation, e.g. they can induce production of cytokines,
CC immunoglobulins, etc. A variety of diseases can be treated by modulating
CC the activity of TNFL proteins, e.g. they can induce apoptosis of
CC activated T cells but rescue resting T cell from apoptosis. TNFL
CC polypeptides can therefore be used to treat autoimmune diseases, such as
CC myasthenia gravis, insulin-dependent diabetes mellitus, rheumatoid
CC arthritis, multiple sclerosis, and systemic lupus erythematosus. TNFL
CC proteins also have tumour stimulating properties, so tumours can be
CC treated by inhibiting the expression or activity of TNFL. Other
CC proliferative disorders, such as neoplasias, dysplasias, and hyperplasia
CC can also be treated using TNFL inhibitors. The TNFL polypeptides and
CC polynucleotides can also be used to enhance or decrease TNF activity,
CC thus providing therapeutic benefits such as induction of cell death,
CC lymphoid organogenesis, or host bacterial resistance, and inhibition of
CC endotoxin shock, contact hypersensitivity, delayed type sensitivity or
CC immunocompetence of a transplant recipient. TNF and its receptors play a
CC major role in host defence and immunosurveillance. As such, there is a
CC need to identify new members of TNFR families. This invention provides
CC this need.
XX
SQ Sequence 150 AA;

Query Match 32.2%; Score 725; DB 20; Length 150;
Best Local Similarity 82.6%; Pred. No. 1.5e-59;
Matches 123; Conservative 9; Mismatches 17; Indels 0; Gaps 0;

QY 1 MALKVLEQEKTFETLLVLLGYLSCKVTCTGTGCRQEFDRSGNCVPCNQCQPGHLSK 60
DB 1 malkvplhrtvlfafllhllackvscetgdcrgqefkdrsgncvllckqcgpgmelsk 60

QY 61 ECGFGYGEDAQCCTRLHREFKDWGFKCKPCLDCAVVRFRKANGSATSDAICGDLCPG 120
DB 61 ecfgfygedaqcvcprhrfkedwgfgkckpcadcalvnfrqancshsdtavcgdcplg 120

QY 121 FYRKTklvgfQDMECVPCGDPpppppEPhc 149
DB 121 fyrktklvgfQDMECVPCGDPpppppEPhc 149

Search completed: February 16, 2001, 21:06:00
Job time: 155 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 16, 2001, 21:04:15 : Search time 31.47 Seconds
(without alignments)
899.732 Million cell updates/sec

Title: US-09-380-276A-4
Perfect score: 2255
Sequence: 1 MALKVLEQETFTLLVLL.....LDQSGAIHPATQSLQEA 417

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 195891 seqs, 67900655 residues

Total number of hits satisfying chosen parameters: 195891

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_66:*
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	157	7.0	454	1 GOMST1	tumor necrosis fac
2	157	7.0	454	2 I57826	tumor necrosis fac
3	147	6.5	416	1 JN0006	nerve growth facto
4	147	6.5	1797	2 A55677	laminin beta-2 cha
5	146.5	6.5	1801	1 MMRTS	tumor necrosis fac
6	145.5	6.5	435	2 I54182	OX40 antigen precu
7	145	6.4	271	2 S12783	gene ox40 protein
8	144	6.4	272	2 I48700	transcription fact
9	144	6.4	1104	2 I38869	tumor necrosis fac
10	141.5	6.3	461	1 GQRT11	nerve growth facto
11	140	6.2	425	1 A26431	laminin beta-1 cha
12	134	5.9	1786	1 MMS91	von Willebrand fac
13	133.5	5.9	2813	1 VWHU	thrombospondin 1 p
14	132.5	5.9	1170	2 A40558	B-cell activation
15	132	5.9	277	2 A60771	laminin beta-2 cha
16	129.5	5.7	1798	2 S33869	t2 protein - myxom
17	129	5.7	326	1 GGVZML	thrombospondin 1 p
18	128.5	5.7	1170	1 TSHUP1	dominant autoantig
19	127	5.6	1650	2 S53457	hypothetical prote
20	127	5.6	1827	2 T34288	gp330 protein prec
21	127	5.6	4660	2 T42737	serine proteinase
22	125.5	5.6	1548	2 S34593	laminin B2t chain
23	124.5	5.5	1111	2 B44018	laminin B2t chain
24	124.5	5.5	1193	2 A44018	laminin alpha-1 ch
25	124.5	5.5	3712	2 S18253	G2R protein - vari
26	124	5.5	349	2 D72175	furin (EC 3.4.21.7
27	123	5.5	837	2 S43656	furin (EC 3.4.21.7
28	122	5.4	1299	2 T43231	gene G4R protein -
29	121	5.4	349	2 D36858	

30	121	5.4	1192	2 S69000	laminin gamma 2 ch
31	121	5.4	1964	2 JC9059	notch4 - mouse
32	120.5	5.3	493	2 TC5486	membrane glycoprot
33	120.5	5.3	965	2 S62935	hypothetical prote
34	120	5.3	256	2 B32393	T-cell antigen 4-1
35	120	5.3	348	2 T28623	hypothetical prote
36	119	5.3	1680	2 A43434	furin (EC 3.4.21.7
37	119	5.3	1786	1 MMHUB1	laminin beta-1 cha
38	118.5	5.3	863	1 S51789	VLDL receptor prec
39	117.5	5.2	1251	2 A57293	latent transformin
40	117.5	5.2	3075	2 S14458	laminin alpha-1 ch
41	117	5.2	255	2 I38426	4-1BB - human
42	117	5.2	255	2 JT0752	lymphocyte activat
43	116	5.2	1106	2 T13938	gene shuttle craft
44	116	5.1	1790	1 MMFFB1	laminin beta-1 cha
45	115	5.1	1296	2 T16859	hypothetical prote

ALIGNMENTS

RESULT 1

QOMST1

tumor necrosis factor receptor 1 precursor - mouse

N:Alternate names: tumor necrosis factor receptor, 55K

C:Species: Mus musculus (house mouse)

C:Date: 30-Jun-1992 #sequence-revision 30-Jun-1992 #text-change 22-Jun-1999

C:Accession: A38634; B40254; S16677; S19021; I54532

R:Lewis, M.; Tartaglia, L.A.; Lee, A.; Bennett, G.L.; Rice, G.C.; Wong, G.H.W.; Chen, Proc. Natl. Acad. Sci. U.S.A. 88, 2830-2834, 1991

A:Title: Cloning and expression of cDNAs for two distinct murine tumor necrosis facto

A:Reference number: A38634; MUID:91187885

A:Accession: A38634

A:Molecule type: mRNA

A:Residues: 1-454 <LEW>

A:Cross-references: GB:M60468; NID:g199825; PIDN:AAA39751.1; PID:g199826

R:Goodwin, R.G.; Anderson, D.; Jerzy, R.; Davis, T.; Brannan, C.I.; Copeland, N.G.; J Mol. Cell. Biol. 11, 3020-3026, 1991

A:Title: Molecular cloning and expression of the type 1 and type 2 murine receptors f

A:Reference number: A40254; MUID:91246168

A:Accession: B40254

A:Molecule type: mRNA

A:Residues: 1-454 <G02>

A:Cross-references: GB:M60468; NID:g199825; PIDN:AAA39751.1; PID:g199826

R:Barrett, K.; Taylor-Fishwick, D.A.; Cope, A.P.; Kissoneghis, A.M.; Gray, P.W.; Fel Eur. J. Immunol. 21, 1649-1656, 1991

A:Title: Cloning, expression and cross-linking analysis of the murine p55 tumor necro

A:Reference number: S16677; MUID:91285014

A:Accession: S16677

A:Molecule type: mRNA

A:Residues: 1-454 <BAR>

A:Cross-references: EMBL:X59238; NID:g53578; PIDN:CAA41922.1; PID:g53579

R:Rothe, J.G.; Brockhaus, M.; Gentz, R.; Lesslauer, W. Immunogenetics 34, 338-340, 1991

A:Title: Molecular cloning and expression of the mouse Tnf receptor type b.

A:Reference number: S19021; MUID:92039815

A:Accession: S19021

A:Molecule type: mRNA

A:Residues: 1-454 <ROT>

A:Cross-references: EMBL:X57796; NID:g54848; PIDN:CAA40936.1; PID:g54849

R:Bebo, B.F. Immunogenetics 39, 450-451, 1994

A:Title: Nucleotide sequence of the TNF type I receptor from a mouse endothelioma cel

A:Reference number: I54532; MUID:94245292

A:Accession: I54532

A>Status: translated from GB/EMBL/DBDJ

A:Molecule type: mRNA

A:Residues: 1-454 <RES>

A:Cross-references: GB:L236349; NID:g430732; PIDN:AAA59361.1; PID:g430733

C:Comment: This protein is one of two distantly related receptors for both TNF-alpha

C:Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology

C:Keywords: duplication; glycoprotein; receptor; transmembrane protein

F:1-29/Domain: signal sequence #status predicted <SIG>

F:30-454/Product: tumor necrosis factor receptor type 1 #status predicted <MAT>
 F:30-212/Domain: extracellular #status predicted <EXT>
 F:44-82/Domain: NGF receptor repeat homology <NG1>
 F:84-126/Domain: NGF receptor repeat homology <NG2>
 F:127-167/Domain: NGF receptor repeat homology <NG3>
 F:168-204/Domain: NGF receptor repeat homology <NG4>
 F:213-235/Domain: transmembrane #status predicted <MEM>
 F:236-454/Domain: intracellular #status predicted <INT>
 F:54,151,202/Binding site: carbohydrate (Asn) #status predicted

Query Match 7.0%; Score 157; DB 1; Length 454;
 Best Local Similarity 21.0%; Pred. No. 0.00018;
 Matches 76; Conservative 42; Mismatches 140; Indels 104; Gaps 19;

QY 34 CROQEFDRSGNCVPCNQCQGMELSKGFGYGEDAQCVTCRLHRFKEDWGF-QKCKPC 92
 Db 44 CPQGVVHSHKNNISICTCKHKTGTYLVSDCP-SFGRDVTVCRECEKGTFTTASQNYLROCLSC 102
 QY 93 LDC-AVYNRFQKANCATSDAICG-----DCLPGFYRKTKL----- 127
 Db 103 KTCRKEMSOVEISPCQADKDTVCCKENQFQRYLSETHFQCVCDCPCFNGTVTIPCKETQ 162
 QY 128 -----VGF--QDMBCVPCGDPPIPPYEPHCASKVNLVKIA-----STASSPRDTALAAV 173
 Db 163 NTVCNCHAGFFLRESECVPCS-----HCKKNECMKLCPLPPPLANVTNPQDSGTAVL 214
 QY 174 ICSALATVLLALLILCVYCKRQFMKPSWLSRSDIOYNGSELSCLDPRPOLHEVAHRA 233
 Db 215 L---PLVILLGLLGFIF--SLMCRYPRW-----RPEVYSII--- 248
 QY 234 CQCRRDSV---QTCG-PVRLPSMCCCEACSPNATLGCQVHSAASLQARN----- 281
 Db 249 ---C-RDPVPVKEKAGKPLTAPSPAFSTSGFNP-TLGFSTPGFSSPVSTPISPIFG 303
 QY 282 -----AGPAGEMVPTFGS--LTQSIG-----EFSDAWPLMNQPMGGDNISFCDSYPEL 329
 Db 304 PSNWHMPVPSEVVPVTPQADPLLYESLCSVPAPTSVQKWEDSAHPQPDNADLAILYAVV 363
 QY 330 TG 331
 Db 364 DG 365

RESULT 2
 I57826
 tumor necrosis factor receptor - mouse
 C:Species: Mus musculus (house mouse)
 C>Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 23-Jul-1999
 C:Accession: I57826
 R:Rothe, J.G.; Bluetmann, H.; Gents, R.; Lesslauer, W.; Steinmetz, M.
 Mol. Immunol. 30, 165-176, 1993
 A:Title: Genomic organization and promoter function of the murine tumor necrosis factor
 A:Reference number: I57826; MUID:93156721
 A:Accession: I57826
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-454 <RES>
 A:Cross-references: GB:M76556; NID:9202100; PIDN:AAA40465.1; PID:9202102
 C:Genetics:
 A:Gene: TNFR-2
 A:Introns: 13/3; 65/1; 108/1; 158/1; 184/2; 210/1; 248/1; 257/3; 353/1
 C:Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology
 C:Keywords: cytokine receptor
 F:44-82/Domain: NGF receptor repeat homology <NGF>

Query Match 7.0%; Score 157; DB 2; Length 454;
 Best Local Similarity 21.0%; Pred. No. 0.00018;
 Matches 76; Conservative 42; Mismatches 140; Indels 104; Gaps 19;

QY 34 CROQEFDRSGNCVPCNQCQGMELSKGFGYGEDAQCVTCRLHRFKEDWGF-QKCKPC 92
 Db 44 CPQGVVHSHKNNISICTCKHKTGTYLVSDCP-SFGRDVTVCRECEKGTFTTASQNYLROCLSC 102
 QY 93 LDC-AVYNRFQKANCATSDAICG-----DCLPGFYRKTKL----- 127
 Db 103 KTCRKEMSOVEISPCQADKDTVCCKENQFQRYLSETHFQCVCDCPCFNGTVTIPCKETQ 162
 QY 128 -----VGF--QDMBCVPCGDPPIPPYEPHCASKVNLVKIA-----STASSPRDTALAAV 173
 Db 163 NTVCNCHAGFFLRESECVPCS-----HCKKNECMKLCPLPPPLANVTNPQDSGTAVL 214
 QY 174 ICSALATVLLALLILCVYCKRQFMKPSWLSRSDIOYNGSELSCLDPRPOLHEVAHRA 233
 Db 215 L---PLVILLGLLGFIF--SLMCRYPRW-----RPEVYSII--- 248
 QY 234 CQCRRDSV---QTCG-PVRLPSMCCCEACSPNATLGCQVHSAASLQARN----- 281
 Db 249 ---C-RDPVPVKEKAGKPLTAPSPAFSTSGFNP-TLGFSTPGFSSPVSTPISPIFG 303
 QY 282 -----AGPAGEMVPTFGS--LTQSIG-----EFSDAWPLMNQPMGGDNISFCDSYPEL 329
 Db 304 PSNWHMPVPSEVVPVTPQADPLLYESLCSVPAPTSVQKWEDSAHPQPDNADLAILYAVV 363
 QY 330 TG 331
 Db 364 DG 365

RESULT 3
 JN0006
 nerve growth factor receptor, low affinity precursor - chicken
 N:Alternate names: NGF receptor
 C:Species: Gallus gallus (Chicken)
 C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 C:Accession: JN0006; A60504
 R:Large, T.H.; Weskamp, G.; Heldér, J.C.; Radeke, M.J.; Misko, T.P.; Shooter, E.M.; R
 Neuron 2, 1123-1134, 1989
 A:Title: Structure and developmental expression of the nerve growth factor receptor 1
 A:Reference number: JN0006; MUID:90166579
 A:Accession: JN0006
 A:Molecule type: mRNA
 A:Residues: 1-416 <LAR>
 A:Experimental source: embryonic chick brain
 R:Heuer, J.G.; Fatemie-Nainie, S.; Wheeler, E.F.; Bothwell, M.
 Dev. Biol. 137, 287-304, 1990
 A:Title: Structure and developmental expression of the chicken NGF receptor.
 A:Reference number: A60504; MUID:90152140
 A:Accession: A60504
 A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 21-35,'Y',37-172,'K',174-275,'S',277-395,'R',397-416 <HEU>
 C:Comment: This receptor is found on sensory and sympathetic neurons, on neuroblastom
 C:Comment: The cysteine-rich region of the extracellular domain may form part or all
 C:Comment: This protein is thought to form a high-affinity receptor when it associate
 C:Superfamily: nerve growth factor receptor; NGF receptor repeat homology
 C:Keywords: duplication; glycoprotein; heterodimer; monomer; phosphoprotein; receptor
 F:1-20/Domain: signal sequence #status predicted <SIG>
 F:21-416/Product: nerve growth factor receptor #status predicted <EXT>
 F:21-239/Domain: extracellular #status predicted <EXT>
 F:24-57/Domain: NGF receptor repeat homology <NG1>
 F:59-100/Domain: NGF receptor repeat homology <NG2>
 F:101-139/Domain: NGF receptor repeat homology <NG3>
 F:141-181/Domain: NGF receptor repeat homology <NG4>
 F:189-237/Region: serine/threonine-rich
 F:240-261/Domain: transmembrane #status predicted <MEM>
 F:262-416/Domain: intracellular #status predicted <INT>
 F:52/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 6.5%; Score 147; DB 1; Length 416;
 Best Local Similarity 29.9%; Pred. No. 0.00093;
 Matches 56; Conservative 17; Mismatches 82; Indels 32; Gaps 10;

QY 20 LGYLSCKVTCETGD-----CROQEFDRD-SGNCVPCNQCQGMELSKGFGY-----G 67

Db 82 VGLHSMAPCVESDDAVRCAYGYFQDELSGSKCEKCSIC-----EVGFLMPFPCRDS 133
Qy 68 EDAQCVCRLHREFKDWGKFORCKPCLDCAVV--NRFORANGSATSDAICGDLPGFYRKT 125
Db 134 QTVCEEGPEGTFSDEANF--VDPCLPTCEENEVWVWKECTATSDACRDLHPRWTHHT 191
Qy 126 -KLGVFODMECVPCDPPPPYEPHCAKSNVLKIASTASSP---RDTA--LAAAVICSALA 179
Db 192 PSLAGSDSPE--PITRDFNTEGMATTLADIVTTVMGSSQPVVSRGTADNLIPVYCSILA 249
Qy 180 TVLLALL 186
Db 250 AVVWGLV 256

RESULT 4
A55677
laminin beta-2 chain precursor (version 1) - human
C:Species: Homo sapiens (man)
C:Date: 03-Mar-1995 #sequence_revision 03-Mar-1995 #text_change 17-Mar-1999
C:Accession: A55677
R:Wexler, U.M.; Gerecke, D.R.; Durkin, M.E.; Kurtz, K.S.; Mattei, M.G.; Champliaud, M.F.;
Genomics 24, 243-252, 1994
A:Title: Human beta2 chain of laminin (formerly S chain): cDNA cloning, chromosomal loca
A:Reference number: A55677; MUID:95213013
A:Accession: A55677
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-1797 <NEW>
A:Cross-references: GB:X79683

C:Genetics:
A:Gene: GDB:LAMB2
A:Cross-references: GDB:L32363; OMIM:150325
A:Map position: 3p21.3-3p21.2
C:Superfamily: laminin beta-1 chain; laminin-type EGF-like homology
C:Keywords: basement membrane; extracellular matrix; glycoprotein; heterotrimer
F:1-32/Domain: signal sequence #status predicted <SIG>
F:33-1797/Product: laminin beta-2 chain #status predicted <MAT>
F:283-344/Domain: laminin-type EGF-like homology <LE01>
F:347-407/Domain: laminin-type EGF-like homology <LE02>
F:410-467/Domain: laminin-type EGF-like homology <LE03>
F:470-519/Domain: laminin-type EGF-like homology <LE04>
F:522-552/Domain: laminin-type EGF-like homology #status atypical <LE05>
F:783-828/Domain: laminin-type EGF-like homology <LE06>
F:831-874/Domain: laminin-type EGF-like homology <LE07>
F:877-924/Domain: laminin-type EGF-like homology <LE08>
F:927-982/Domain: laminin-type EGF-like homology <LE09>
F:985-1034/Domain: laminin-type EGF-like homology <LE10>
F:1037-1091/Domain: laminin-type EGF-like homology <LE11>
F:1094-1139/Domain: laminin-type EGF-like homology <LE12>
F:1142-1186/Domain: laminin-type EGF-like homology <LE13>

Query Match 6.5%; Score 147; DB 2; Length 1797;
Best Local Similarity 22.4%; Pred. No. 0.0046;
Matches 88; Conservative 35; Mismatches 144; Indels 136; Gaps 24;
Qy 17 LVLLGLYSCKVTCETGDCRQQRDRSGNVC-----PCNQCQPGMSEKCEGFGYK- 67
Db 775 LIYNGALPCQ--CNPQGSLSSECNPHGQCICKPGVVGRRCTCAPY-----YGRGP 825

Qy 68 -----EDAQCVCRLHRF-----KEDWGFKCKRCPCL----- 93
Db 826 TGCQACQCSPRGALSSLCERTSGQCL-CRTGAFGLRCDACQGWGFPFCRCPVCNGHAD 884
Qy 94 DCVVNRFOKA--NC-SATSDAICGDCLPGFYRKYKLVGFQDMCEVPCGDDPP-PPYEPHC 149
Db 885 EC---NTHTGACLGCRDLTGGEHCERCITAGFHGDPRLP--YGAQCRPCPCPEGPGSRHF 939
Qy 150 ASKVNVLKVIATSPPTALAAVICSALATVLLALLILCVLYCKRQFME-KKP----- 202
Db 940 AT-----SCHQDEYSQOIVCHCRAGY---TGLRCEACAPGQFGDPSRPGACQLC 985

Qy 203 --SWSLRSDIO-----YNGSELSCLE-----DRPOLHEYA-----HRACQCRRDS 241
Db 986 ECSGNIDPMDPDACDPHPGQCQLRCLHTEGPHCAHSKGFHGQAAARQSCHRCTNLLGTN 1045
Qy 242 VQTC-----GPVRLPSM--CCCEACSPN--PATLGGCGVHSAASLAQARNAGP- 284
Db 1046 PQQCPSPDQCHDFSSGQCPLPNVQALAVDRCAPFNWLTSGHGCQPCACLPSSREGPT 1105
Qy 285 ----AGEMVP--TFFGSLTQSGEFSDAWPLMQ 312
Db 1106 CNEFTGQCHPGAGFGGRTCSQCQLHWDGDPGLQ 1138

RESULT 5
MURTS
laminin beta-2 chain precursor - rat
N:Alternate names: laminin chain B3; S-laminin
C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 10-Dec-1999
C:Accession: S03539
R:Hunter, D.D.; Shah, V.; Merlie, J.P.; Sanes, J.R.
Nature 338, 229-234, 1989
A:Title: A laminin-like adhesive protein concentrated in the synaptic cleft of the ne
A:Reference number: S03539; MUID:89159410
A:Accession: S03539
A:Molecule type: mRNA
A:Residues: 1-1801 <HUN>
A:Cross-references: EMBL:X16563; NID:957250; PIDN:CAA34561.1; PID:957251
C:Complex: Laminins are trimers of an alpha-type, a beta-type, and a gamma-type lamin
C:Function:
A:Description: interact with cells and with other basement membrane proteins to promo
C:Superfamily: laminin beta-1 chain; laminin-type EGF-like homology
C:Keywords: basement membrane; calcium binding; cell binding; coiled coil; extracellu
F:1-35/Domain: signal sequence #status predicted <SIG>
F:36-1801/Product: laminin beta-2 chain #status predicted <MAT>
F:36-285/Domain: VI <DOM6>
F:286-555/Domain: V <DOM5>
F:286-347/Domain: laminin-type EGF-like homology <LE01>
F:350-410/Domain: laminin-type EGF-like homology <LE02>
F:413-470/Domain: laminin-type EGF-like homology <LE03>
F:473-522/Domain: laminin-type EGF-like homology <LE04>
F:525-555/Domain: laminin-type EGF-like homology #status atypical <LE05>
F:556-784/Domain: IV <DOM4>
F:786-831/Domain: laminin-type EGF-like homology <LE06>
F:788-1196/Domain: III <DOM3>
F:834-877/Domain: laminin-type EGF-like homology <LE07>
F:880-927/Domain: laminin-type EGF-like homology <LE08>
F:930-986/Domain: laminin-type EGF-like homology <LE09>
F:989-1038/Domain: laminin-type EGF-like homology <LE10>
F:1041-1095/Domain: laminin-type EGF-like homology <LE11>
F:1098-1143/Domain: laminin-type EGF-like homology <LE12>
F:1146-1190/Domain: laminin-type EGF-like homology <LE13>
F:1197-1412/Domain: II <DOM2>
F:1197-1412/Region: heptad repeats
F:1413-1445/Domain: alpha <ALP>
F:1446-1801/Domain: heptad repeats
F:1446-1801/Domain: I <DOM1>
F:45-50/Disulfide bonds: #status predicted
F:251,371,1088,1252,1311,1351,1502/Binding site: carbohydrate (Asn) (covalent) #statu
F:1193,1196,1800/Disulfide bonds: interchain #status predicted

Query Match 6.5%; Score 146.5; DB 1; Length 1801;
Best Local Similarity 22.9%; Pred. No. 0.005;
Matches 99; Conservative 33; Mismatches 146; Indels 155; Gaps 27;
Qy 17 LVLLGLYSCKVTCETGDCRQQRDRSGNVCPCNQCQPGMSEKCEK-----GFG--- 65
Db 778 LIYNGALPCQ--CDPQGSLSSECNPHGQC-----RCKPGV-VGRRCDACATGYGFGPAG 830
Qy 66 -----YGEDAQCVTCRLHRF-----KEDWGFKCKPCLDCAVNRNF 101

Db 831 CQACQSPDGAISALCEGTSGOCL-ORTGAFGLRCDHCQRGOWFPNCRPC-----VCNG 884
 QY 102 QKANCATSDAI-----CGDCLGCFYKTKL-VGFODMECVCPGDDP-PPYEPH 148
 Db 885 RADECDHTGACGLGCRDYTGGEHCERCIAGFDHPLPYGGQ---CRPCPEGPGSQRH 941
 QY 149 CASKVNLVXIASTPASSPRTALAAVTSALATVLLALLILCVYCKRQFME-KKPSWSLR 207
 Db 942 FAT-----SCHRDGYSQIIVCHCRAGY---TGLRCEACAPGHEGDSKPGGRQC 987
 QY 208 -----SDIOQ-----YNGSELSCLD-----RPQLHEYA-----HRACQOCRR 239
 Db 988 LCSCSNIDPTDPTGACDPHTGQCLRLHHTGPHGCHGCKPGEFHGQAARQSCHRCTCNLLG 1047
 QY 240 DSVQTC-----GPNRLLP---SMCCEACSPN-PATLCGCVHSAASLAARNA 282
 Db 1048 TDPQPCSTDLCHCDPSTGQCPCPLHVQGLSCDR-CAPFNWFTSGRGQPCACHPFSRAR 1106
 QY 283 GP-----AGEMVPTFFGSLTQSGEGFSDAWPLMQ-----NPMGGD----- 318
 Db 1107 GPTCNEFTGOCHCHAG-----FGGRTSECQELHWGDFGLQCRACDCDPRGIDKPCQHR 1160
 QY 319 NISFCDSPYELTG 331
 Db 1161 STGHCSRCRPGVSG 1173

RESULT 6
 I54182
 tumor necrosis factor receptor 2-related protein - human
 C:Species: Homo sapiens (man)
 C:Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 17-Mar-2000
 C:Accession: I54182
 R:Baens, M.; Chaffanet, M.; Cassiman, J.J.; Van den Berghe, H.; Marynen, P.
 Genomics 16, 214-218, 1993
 A:Title: Construction and evaluation of a hncDNA library of human 12p transcribed sequen
 A:Reference number: I54182; MUID:93252381
 A:Accession: I54182
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-435 <RES>
 A:Cross-references: GDB:L04270; NID:9339761; PIDN:AAA36757.1; PID:9339762
 A:Gene: GDB:LTBR
 A:Map position: 12p13.3-12p13.1
 C:Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology

Query Match 6.5%; Score 145.5; DB 2; Length 435;
 Best Local Similarity 21.4%; Pred. No. 0.0013;
 Matches 73; Conservative 41; Mismatches 108; Indels 119; Gaps 19;

QY 16 LVLVLLGYLSCK-----VTCETGDCRQRP---FRDRSGNVCPCNCGPGMELSKCEGFG 65
 Db 18 VLGLGLLAASQPAVPPYASENQTRDQKEYEYEPQHRIC---CSRCPPTGYVSACR--S 73
 QY 66 YGEDAQCVTRLHRFRFEDWGF-----QKCRPC-----LDCAVNRRQKANCATSATDAIC- 114
 Db 74 RIRDTVCATCAENSYNEHWNLYTICQLCRPCDPVMGLEIAPCTSKRKTQCRQCPGMFCA 133
 QY 115 -----GDCLPGFYRKTK-LVGFDMECVPC-----GDPpppyEPH--CAS 151
 Db 134 AWALECTHCELLSDCPGPTGTAELKDEVGKNNHCVCCKAGHFQNTSPSARCQPHRTCN 193
 QY 152 KVNLVKIA-----STASSPRD-----TALAIVCSALATVLLALLILCVIY---- 192
 Db 194 Q-GLVEAAPAGTAQSDTCKNPLEPLPPMMSGTMLMLAVLLPLAFFLLATVFCIWKSHP 252
 QY 193 --CKR--QFMKKP-----SNLSRSQDIQYNGSELSCLDRLPOLHEYAHRACCOCR 238
 Db 253 SLCKRLGSLLRKRRQGGPNPVAGSW-----EPPRAHPYF----- 287

QY 239 RDSVQTCGPVRLLPSCMCCEACSPNATLGCQGVHSAASLQA 279
 Db 288 PDLVQPLLPi-----SGDVSVPSTGLPAPVLEA 316

RESULT 7
 I52783
 OX40 antigen precursor - rat
 N:Alternate names: nerve growth factor receptor homolog
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 05-Nov-1999
 C:Accession: S12783; S08036
 R:Maliet, S.; Fossum, S.; Barclay, A.N.
 EMBO J. 9, 1063-1068, 1990
 A:Title: Characterization of the MRC OX40 antigen of activated CD4 positive T lymphoc
 A:Reference number: S12783; MUID:90214614
 A:Accession: S12783
 A:Molecule type: mRNA
 A:Residues: 1-271 <MAL>
 A:Cross-references: EMBL:X17037; NID:g57830; PIDN:CAA34897.1; PID:g57831
 C:Superfamily: CD27 antigen; NGF receptor repeat homology
 C:Keywords: growth factor receptor; transmembrane protein
 F:1-19/Domain: signal sequence #status predicted <Sig>
 F:20-271/Product: OX40 antigen #status predicted <MAT>
 F:211-235/Domain: transmembrane #status predicted <TMM>

Query Match 6.4%; Score 145; DB 2; Length 271;
 Best Local Similarity 28.6%; Pred. No. 0.00083;
 Matches 54; Conservative 23; Mismatches 76; Indels 36; Gaps 12;

QY 9 QEKTFFTLLVLLGLYSCKVTCTGTGDCRQEFRRDR--SGN-CVPCNCGPGMELSKCEGFG 65
 Db 6 QQPTAFLLLGLSLGVIVKLN-----VKDTYPSGHKC--CRECQPHGMVSR--D 52
 QY 66 YGEDAQCVTRLHRFRFEDWGFQKRCPLDCAVVRNRFQ-KANCATSATDAICGDCPLGPFYRK 124
 Db 53 HTRDVTCHPCPCPGFYNEAVNYDTCKQCTQCNHRSGSELKQNTPTEDTVC-QCRPGTQPR 111
 QY 125 TKLVGFQDMCEVPCGDPpppyEP-----HCASKVNLV-----KIATASSPRDTALAIVC- 175
 Db 112 QDSSHLKGLVDCVPC--PPGHFSPGSGNQACKPWTNCTLSKQIRHPASNSLDT-----VCE 164
 QY 176 --SALATVL 182
 Db 165 DRSLLATLL 173

RESULT 8
 I48700
 gene OX40 protein - mouse
 N:Alternate names: OX40 antigen
 C:Species: Mus musculus (House mouse)
 C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 11-Jan-2000
 C:Accession: I48700; I48334; S34377
 R:Calderhead, D.M.; Buhlmann, J.E.; van den Eertwegh, A.J.; Claassen, E.; Noelle, R.J.
 J. Immunol. 151, 5261-5271, 1993
 A:Title: Cloning of mouse OX40: a T cell activation marker that may mediate T-B cell
 A:Reference number: I48700; MUID:94044750
 A:Accession: I48700
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-272 <RES>
 A:Cross-references: EMBL:Z21674; NID:g312827; PIDN:CAA79772.1; PID:g312828
 R:Birdeland, M.L.; Copeland, N.G.; Gilbert, D.J.; Jenkins, N.A.; Barclay, A.N.
 Eur. J. Immunol. 25, 926-930, 1995
 A:Title: Gene structure and chromosomal localization of the mouse homologue of rat OX
 A:Reference number: I48334; MUID:95255413
 A:Accession: I48334
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-14, 'G', 16-272 <RE2>
 A:Cross-references: EMBL:X85214; NID:g732818; PIDN:CAA59476.1; PID:g732819

•

RESULT 13
vwvu
von Willebrand factor precursor - human
C:Species: Homo sapiens (man)
C:Date: 04-Dec-1986 #sequence_revision 30-Jun-1993 #text_change 22-Jun-1999
C:Accession: A34480; S03377; A37139; S23676; A25298; A25469; A25366; S23618;
R:Mancuso, D.J.; Tuley, E.A.; Westfield, L.A.; Worrall, N.K.; Shelton-Inloes, B.B.; Sora
S23645; A94

```

F:34-386/Domain: type D repeat 1 <DD1>
F:387-745/Domain: type B repeat 2 <DD2>
F:698-700/Region: cell attachment (R-G-D) motif
F:764-2813/Product: von Willebrand factor #status predicted <WA2>
F:784-865/Domain: D' <DD0>
F:788-833,2216-2261/Region: duplication
F:826-853,2400-2515,2544-2662/Region: duplication
F:842-1130,1934-2203/Region: duplication
F:866-1241/Domain: type D repeat 3 <DD3>
F:1275-1443/Domain: von Willebrand factor type A repeat homology <VWA1>
F:1496-1654/Domain: von Willebrand factor type A repeat homology <VWA2>
F:1689-1854/Domain: von Willebrand factor type A repeat homology <VWA3>
F:1947-2295/Domain: type D repeat 4 <DD4>
F:2296-2330/Domain: type B repeat 1 <VB1>
F:2340-2365/Domain: type B repeat 2 <VB2>
F:2375-2399/Domain: type B repeat 3 <VB3>
F:2430-2497/Domain: von Willebrand factor type C repeat homology <VWC1>
F:2507-2509/Region: cell attachment (R-G-D) motif
F:2581-2647/Domain: von Willebrand factor type C repeat homology <VWC2>
F:857,1231,1515,1574,2223,2290,2357,2400,2546,2585,2790/Binding site: carbohydrate (A)
F:1147/Binding site: carbohydrate (Asn) (covalent) #status atypical
F:1248,1255,1256,1468,1477,1487,1679,2298/Binding site: carbohydrate (Thr) (covalent)
F:1263,1486/Binding site: carbohydrate (Ser) (covalent) #status experimental

Query Match 5.9%; Score 133.5; DB 1; Length 2813;
Best Local Similarity 21.4%; Pred. No. 0.078;
Matches 78; Conservative 38; Mismatches 107; Indels 141; Gaps 19;

QY 44 GNCVP---CNCQCGPMELSKCEGFGYGEDAQCVCRLHRFREDWGFQCKPCCLDCAVNR 100
Db 2246 GSCVPEACTQC-----IGEDGV-----QHQFLEAW-VPDHPQCICICTLUG 2286

QY 101 FOKANCSA---TSDA-ICGDCPLGPFYRKTCLVGFQDMEC-----VPCGDGPPPPPEPHCAS 151
Db 2287 -RKVNCTTQCPPTAKAPTCLGCEVARLRNADQCPEVCVCDPLDP---VPHCR 2342

QY 152 KVNLVIASTASPRDTALAAVICSALATVLLALLILCVYCKRQFMKPKSWSLRSDI 211
Db 2343 -----GLQPTLTNPGE-----CRPNF----- 2358

QY 212 QYNGSELCLDRPQLHEYAHRAACCCRRDSVOTGPGVRLLPNM-----CCEE---ACSPNP 264
Db 2359 -----TCACRKE-----ECKRVSPPSCPPHR-LPTLRKTQCCDEYECACNVN 2400

QY 265 ATLCGCVHSAASLQARNAGPAGEMVPTFFGSLTQTCGEFSDAWPL----- 310
Db 2401 STVSCPLGYLASTATNDGC-----CTTTCLDPKVCVHRSTIYPVGQFWEBCGDVCTCT 2454

QY 311 -MGNPMGGDNISPCDSYP-----ELTGEDIHSLNPELESSTSLDSNSQ 353
Db 2455 DMEDAVNGLRVAQCSQKPCDCSDSCRSFGTYVHHEGCCRCCLPSACEVVTGSPRGDSQSSW 2514

QY 354 DLVG 357
Db 2515 KSVG 2518

RESULT 14
A40558
Thrombospondin 1 precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 05-Jun-1992 #sequence_revision 05-Jun-1992 #text_change 20-Aug-1999
C:Accession: A40558; A37905; B42587; S68787
R:Lawler, J.; Duquette, M.; Ferro, P.; Copeland, N.G.; Gilbert, D.J.; Jenkins, N.A.
Genomics 11, 587-600, 1991
A:title: Characterization of the murine thrombospondin gene.
A:Reference number: A40558; MUID:92128941
A:Accession: A40558
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1170 <LAW>
A:Cross-references: GB:M62449; GB:M62450; GB:M62451; GB:M62452; GB:M62453; GB:M62454;

```

M62465; GB:M62466; GB:M62467; GB:M62468; GB:M62469; GB:M62470; NID:G511867; PIDN:AAA5061
R:Bornstein, P.; Alfai, D.; Devaravala, S.; Framson, P.; Li, P.
J. Biol. Chem. 265, 16691-16698, 1990
A:Title: Characterization of the mouse thrombospondin gene and evaluation of the role of
A:Reference number: A37905; MUID:90375546
A:Accession: A37905
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-490 <BOR>
A:Cross-references: GB:J05605; GB:J05606; NID:G201991; PIDN:AAA40431.1; PID:G554390
R:Laherty, C.D.; O'Rourke, K.; Wolf, F.W.; Katz, R.; Seldin, M.F.; Dixit, V.M.
J. Biol. Chem. 267, 3274-3281, 1992
A:Title: Characterization of mouse thrombospondin 2 sequence and expression during cell
A:Reference number: A42587; MUID:92147683
A:Accession: B42587
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-1152, 'P', 1154-1170 <LAH>
A:Cross-references: GB:M87276
A:Note: sequence extracted from NCBI backbone (NCBIP:81501)
R:Chen, H.; Aeschlimann, D.; Nowlen, J.; Mosher, D.F.
FEBS Lett. 387, 36-41, 1996
A:Title: Expression and initial characterization of recombinant mouse thrombospondin 1 a
A:Reference number: S68787; MUID:96234006
A:Accession: S68787
A:Molecule type: protein
A:Residues: 19-26, 'X', 28-37 <CHE>
C:Complex: homotrimer, disulfide linked
C:Superfamily: thrombospondin 1; EGF homology; thrombospondin type 1 repeat homology; v
C:Keywords: calcium binding; glycoprotein; homotrimer
F:1-18/Domain: signal sequence #status predicted <SIG>
F:19-1170/Product: thrombospondin 1 #status predicted <MAT>
F:317-375/Domain: von Willebrand factor type C repeat homology <VWC>
F:378-429/Domain: thrombospondin type 1 repeat homology <THR1>
F:434-490/Domain: thrombospondin type 1 repeat homology <THR2>
F:491-547/Domain: thrombospondin type 1 repeat homology <THR3>
F:551-586/Domain: EGF homology <EGF>
F:248,360,708,1067/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 5.9%; Score 132.5; DB 2; Length 1170;
Best Local Similarity 21.0%; Pred. No. 0.036;
Matches 88; Conservative 39; Mismatches 141; Indels 151; Gaps 25;

Qy 26 KVTCTGCRQOEFDRSGNCVPCNQCGPG-----MELSKCEGFGY----- 66
Db 350 KVSCLPIMCSNATVPD--GEC--CPRCWPSDSADGNSFWSEWTSCATCGNGIQGRS 405
Qy 67 -----GEDAQCVTCRLH-----RFKEDMGFKCKPCLDCA-----VNNRFOKAN-- 105
Db 406 CDSLNNRCEGSSVQRTCHIQCDKRRFKQDGGWHSWSPSSCVTCGDGVITRIRLCNSP 465
Qy 106 -----CSATSDAICGDCPLGPFYRKTKL 127
Db 466 SPQMGKPCGEARETKACKKDACPINGWGWSPWDCISVT-----CGG---GVQRRSRL 518
Qy 128 VGFQDMECVPCDPPPPY-EPHCASKVNLVKIATSPASPRDTALAAVICSALATVLLALL 186
Db 519 -----CNNPTFPQGRKDCVDVTENQVCNKQDCPIDCLSNP-CFAGAK----- 561
Qy 187 ILCVITYKRRQFMKKPSNLSRSDIQYNGSELSCILDRPOLHE-----YAHRAACQCRD 240
Db 562 --CTSY-----PDGSWKCGACPGYSGNGIQCKDQVDECKEVPDPCFNHNGEHRCKNTD 612
Qy 241 SVQTC--GPVRLLP-----MCCEACSP-NPATLG---CGVHSAASLQARNAGP 284
Db 613 PCYNCLPCPPRFTGSGQFGRGVHEAMANKQCKPRNRPCTDGTDCNKAACNYLGHYSDP 672
Qy 285 --AGEWVPTFFGSLTQSGEFS--DAMPLMONPMGGDNISF-----CDSYPELTGED 333
Db 673 MYRCECKPGYAGN--GIICGEDTDLGDP--NENLYCVANATYHCKKDKCNPLNPSGQED 728

RESULT 15
A60771
B:cell activation protein CD40 precursor - human
N:Alternate names: B-cell surface antigen Bp50
C:Species: Homo sapiens (man)
C:Date: 03-Jun-1993 #sequence_revision 03-Feb-1994 #text_change 21-Jul-2000
C:Accession: S04460; A60771
R:Stamenkovic, I.; Clark, E.A.; Seed, B.
EMBO J. 8, 1403-1410, 1989
A:Title: A B-lymphocyte activation molecule related to the nerve growth factor recept
A:Reference number: S04460; MUID:89356608
A:Accession: S04460
A:Molecule type: mRNA
A:Residues: 1-277 <STA>
A:Cross-references: EMBL:X60592; NID:G29850; PIDN:CAA43045.1; PID:G29851
R:Braesch-Andersen, S.; Paulie, S.; Koho, H.; Nika, H.; Aspenstrom, P.; Perlmann, P.
J. Immunol. 142, 562-567, 1989
A:Title: Biochemical characteristics and partial amino acid sequence of the receptor-
A:Reference number: A60771; MUID:89093941
A:Accession: A60771
A:Molecule type: protein
A:Residues: 21-50 <BRA>
A:Experimental source: Burkitt lymphoma cell line Raji
C:Genetics:
A:Gene: GDB:CD40
A:Cross-references: GDB:215268; OMIM:109535
A:Map position: 20q12-20q13.2
C:Superfamily: CD27 antigen; NGF receptor repeat homology
C:Keywords: B-cell; glycoprotein; phosphoprotein; surface antigen; transmembrane prot
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-277/Product: B-cell activation protein CD40 #status experimental <MAT>
F:21-193/Domain: extracellular #status predicted <EXT>
F:194-215/Domain: transmembrane #status predicted <TM>
F:216-277/Domain: intracellular #status predicted <CYT>
F:153,180/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 5.9%; Score 132; DB 2; Length 277;
Best Local Similarity 24.6%; Pred. No. 0.0081;
Matches 52; Conservative 27; Mismatches 78; Indels 54; Gaps 11;

Qy 34 CRQOEFDRSGNCVPCNQCGPMELSKCEGFGYGEDAQCVTCRLHFRKEDWG-----F 86
Db 26 CREKOYLINS-QC--CSLCQPGQKLVSDC--TEFTETELCPGGESEFLDTWNRETHCHQH 80
Qy 87 QKCKPCLDCAVNVRFQKANCATSDAIC-----GDCLPGFYRKTKL 127
Db 81 KYCDPNLGL----RVQKGTSET-DTICTCEGWHCTSEACESCVLHRSCSPGFGVKQIA 135
Qy 128 VGFQDMECVPC-----GDPPPPYE-----PHCASKVNLVKIAT-----ASSPRDTALAA 172
Db 136 TGVSDTICEPCVPGVFFSNVSSAFKCHPWTSCETKDLVVQOAGTNKTDVCCGPDRLRAL 195
Qy 173 VICSALATVLLALLILCVITYKRRQFMKKPS 203
Db 196 VWPIIFGLIFALLLVLFVFKK---VAKKPT 223

Search completed: February 16, 2001, 21:06:39
Job time: 144 sec

THIS PAGE BLANK (USPTO)

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	157	7.0	454	1	TNR1_MOUSE	P25118 mus musculus
2	147	6.5	416	1	NGPR_CHICK	P18519 gallus galli
3	146.5	6.5	1801	1	LMB2_RAT	P15800 rattus norv
4	145.5	6.5	435	1	TNR2_HUMAN	P36941 homo sapien
5	145	6.4	271	1	OX40_RAT	P15725 rattus norv
6	144	6.4	272	1	OX40_MOUSE	P47741 mus musculu
7	144	6.4	1104	1	NFX1_HUMAN	Q12986 homo sapien
8	141.5	6.3	461	1	TNR1_RAT	P22934 rattus norv
9	140	6.2	425	1	NGPR_RAT	P07174 rattus norv
10	136.5	6.1	1798	1	LMB2_HUMAN	P55268 homo sapien
11	134.5	6.0	415	1	TNR3_MOUSE	P50284 mus musculu
12	134	5.9	1786	1	LMB1_MOUSE	P02469 mus musculu
13	133.5	5.9	1799	1	LMB2_MOUSE	Q61292 mus musculu
14	133.5	5.9	2813	1	VWF_HUMAN	P04275 homo sapien
15	132.5	5.9	1170	1	TSPL_MOUSE	P35441 mus musculu
16	132	5.9	277	1	CD40_HUMAN	P25942 homo sapien
17	129	5.7	326	1	VIZ2_MTXVL	P29825 myxoma viru
18	128.5	5.7	1170	1	TSPL_HUMAN	P07996 homo sapien
19	127	5.6	4660	1	LRP2_RAT	P98158 rattus norv
20	126.5	5.6	471	1	TNR1_BOVIN	O19131 bos taurus
21	125.5	5.6	1173	1	TSPL_XENLA	P35448 xenopus lae
22	124.5	5.5	3712	1	LMA_DROME	Q00174 drosophila
23	121	5.4	349	1	VC22_VARV	P34015 variola vir
24	121	5.4	1192	1	LMG2_MOUSE	Q61092 mus musculu
25	121	5.4	1964	1	NTC4_MOUSE	P31695 mus musculu
26	120.5	5.3	965	1	YNC3_YEAST	P53971 saccharomyc
27	120.5	5.3	2813	1	VWF_CANFA	Q28295 canis famil
28	120	5.3	256	1	41BB_MOUSE	P20334 mus musculu
29	119.5	5.3	1193	1	LMG2_HUMAN	Q13753 homo sapien
30	119	5.3	1680	1	FUR2_DROME	P30432 drosophila
31	119	5.3	1786	1	LMB1_HUMAN	P07942 homo sapien
32	118.5	5.3	863	1	LDVR_CHICK	P98165 gallus galli
33	118	5.2	1592	1	SOBL_CHICK	Q98930 g sortilin-

"Genomic organization and promoter function of the murine tumor necrosis factor receptor beta gene."

RL Mol. Immunol. 30:165-175(1993).

-1- FUNCTION: RECEPTOR FOR TNF-ALPHA. THE ADAPTOR MOLECULE FADD RECRUITS CASPASE-8 TO THE ACTIVATED RECEPTOR. THE RESULTING AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC) PERFORMS CASPASE-8 PROTEOLYTIC ACTIVATION WHICH INITIATES THE SUBSEQUENT CASCADE OF CASPASES (ASPARTATE-SPECIFIC CYSTEINE PROTEASES) MEDIATING APOPTOSIS (BY SIMILARITY).

-1- SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFR1 LEADS TO

HOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS

PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY

WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING

PROTEINS SUCH AS TRAFs, RIP AND POSSIBLY FADD, ARE RECRUITED TO

TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX

ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND

NF-KAPPA B SIGNALING (BY SIMILARITY).

-1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

-1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.

-1- SIMILARITY: CONTAINS 1 DEATH DOMAIN.

This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

DR EMBL; M60468; AAA39751.1; -

DR EMBL; M59377; AAA40464.1; -

DR EMBL; X59238; CAA41922.1; -

DR EMBL; X57796; CAA40936.1; -

DR EMBL; L26349; AAA59361.1; -

DR EMBL; W76656; AAA40465.1; -

DR EMBL; M88067; AAA40465.1; JOINED.

DR EMBL; M76655; AAA40465.1; JOINED.

DR PIR; A38634; GQMST1.

DR PIR; S16677; S16677.

DR PIR; S19021; S19021.

DR HSSP; P19438; LEXT.

DR MGD; MGI:1314884; TNFRSF1A.

DR INTERPRO; IPR000488; -

DR INTERPRO; IPR001368; -

DR PFAM; PF00020; TNFR_c6; 4.

DR PFAM; PF00531; death; 1.

DR PROSITE; PS00652; TNFR_NGFR_1; 3.

DR PROSITE; PS00650; TNFR_NGFR_2; 3.

DR PROSITE; PS50017; DEATH_DOMAIN; 1.

KW Receptor; Transmembrane; Glycoprotein; Repeat; Signal; Apoptosis.

FT SIGNAL 1 21

FT CHAIN 22 454

FT DOMAIN 22 212 TUMOR NECROSIS FACTOR RECEPTOR 1.

FT TRANSMEM 213 235 EXTRACELLULAR (POTENTIAL).

FT DOMAIN 236 454 POTENTIAL.

FT DOMAIN 43 196 CYTOPLASMIC (POTENTIAL).

FT REPEAT 43 82 4 X TNFR-CYS.

FT REPEAT 83 125 TNFR-CYS 1.

FT REPEAT 126 166 TNFR-CYS 2.

FT REPEAT 167 196 TNFR-CYS 3.

FT DOMAIN 339 349 TNFR-CYS 4.

FT DOMAIN 356 441 N-SMASE ACTIVATION DOMAIN (NSD).

FT DISULFID 44 58 DEATH DOMAIN.

FT DISULFID 59 72 BY SIMILARITY.

FT DISULFID 62 81 BY SIMILARITY.

FT DISULFID 84 99 BY SIMILARITY.

FT DISULFID 102 117 BY SIMILARITY.

FT DISULFID 105 125 BY SIMILARITY.

FT DISULFID 127 143 BY SIMILARITY.

FT DISULFID 146 158 BY SIMILARITY.

FT DISULFID 149 166 BY SIMILARITY.

FT DISULFID 168 179 BY SIMILARITY.

FT DISULFID 182 191 BY SIMILARITY.

FT DISULFID 182 191 BY SIMILARITY.

FT DISULFID 182 191 BY SIMILARITY.

FT DISULFID 182 191 BY SIMILARITY.

FT DISULFID 182 191 BY SIMILARITY.

FT DISULFID 182 191 BY SIMILARITY.

FT DISULFID 182 191 BY SIMILARITY.

FT DISULFID 182 191 BY SIMILARITY.

FT DISULFID 182 191 BY SIMILARITY.

FT DISULFID 185 195 BY SIMILARITY.
FT CARBOHYD 54 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 151 151 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 202 202 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 334 334 R -> G (IN REF. 6).
SQ SEQUENCE 454 AA; 50129 MW; 0710C2E8C3C2B6D9 CRC64;

Query Match 7.0%; Score 157; DB 1; Length 454;

Best Local Similarity 21.0%; Pred. No. 4.5e-05;

Matches 76; Conservative 42; Mismatches 140; Indels 104; Gaps 19;

QY 34 CRQEFDRSGNCVPCNQCQPGMELSKGEGFGYGDAQCQVTCRLHFRKEDWGF-QKCKPC 92

Db 44 CPOGKYVHSHKNNISICCTKCHKGTLYLSDCP-SPGRDTCRECEKGTFTASQNYLROCLSC 102

QY 93 LDC-AVNVRFQKANCATSATDAICG-----DCLPGFYRKTKL----- 127

Db 103 KTCRKEMSQVEISPCQADKDTVCCKENQFQRYLSETHFQCVCDCSPCFNGTVTIPCKETQ 162

QY 128 -----VGF--QDMCEVCPGDPPEPHCASKVNLVKIA-----STASSPRDTALAAV 173

Db 163 NTVNCNCHAGFFFLRESECVFCS-----HCKNECMKLCCLPPPLANVTNPQDSGTAVL 214

QY 174 ICSALATVLLALILCVYCKQFMKPKPSWLSRSDIQVNGSELSCLDRLPQLHEYAHRA 233

Db 215 L---PLVILLGLCLLSFIFI--SLMCRYPRW-----RPEVYSII--- 248

QY 234 CCOCRRDSV-----QTCG-PVRLLPSCMCBEACSPNATLCCGVHSAASLQARN----- 281

Db 249 ---C-RDPVPVKEEKAGKPLTPAPSPAFSPTSGFNP-TLGFSTPGFSSPVSTPISPIFG 303

QY 282 -----AGPAGEVMPTEFGS--LTQSIGC-----EFSDAWPLMONGMGNISPCDSYPEL 329

Db 304 PSNWHFMPVSEVVPVTPQAGDPLLYESLCVSPAPTSVQKWNDSAHPRPDNADLAILYAVV 363

QY 330 TG 331

Db 364 DG 365

RESULT 2

NGFR_CHICK

ID NGFR_CHICK STANDARD; PRT: 416 AA.

AC P18519;

DT 01-NOV-1990 (Rel. 16, Created)

DT 01-NOV-1990 (Rel. 16, Last sequence update)

DT 01-OCT-2000 (Rel. 40, Last annotation update)

DE LOW-AFFINITY NERVE GROWTH FACTOR RECEPTOR PRECURSOR (NGF RECEPTOR)

GN NGFR.

OS Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;

OC Gallus.

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE-BRAIN;

RX MEDLINE-90166579; PubMed-2560385;

RA Large T.H., Weskamp G., Helder J.C., Radeke M.J., Misko T.P.,

RA Shooter E.M., Reichardt L.F.;

RT "Structure and developmental expression of the nerve growth factor

receptor in the chicken central nervous system.";

RL Neuron 2:1123-1134(1989).

RP [2]

RN SEQUENCE OF 21-416 FROM N.A.

RX MEDLINE-90152140; PubMed-2154393;

RA Heuer J.G., Fatemie-Nainie S., Wheeler E.F., Bothwell M.;

RT "Structure and developmental expression of the chicken NGF receptor.";

RL Dev. Biol. 137:287-304(1990).

CC -1- FUNCTION: LOW AFFINITY RECEPTOR WHICH CAN BIND TO NGF, BDNF,

CC NT-3, AND NT-4.

CC -1- SUBUNIT: NGF RECEPTOR CAN FORM A HOMODIMER THROUGH DISULFIDE

```

CC CC BOND FORMATION.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- PTM: N- AND O-GLYCOSYLATED AND IS PHOSPHORYLATED ON SERINE.
CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
CC -1- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
DR PIR; JN0006; JN0006.
DR PIR; A60504; A60504.
DR HSSP; P07174; INGR.
DR INTERPRO; IPR000488; -.
DR INTERPRO; IPR001368; -.
DR PFAM; PF00020; TNFR_C6; 4.
DR PFAM; PF00331; death; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; 3.
DR PROSITE; PS00652; TNFR_NGFR_2; 3.
DR PROSITE; PS00050; TNFR_NGFR_2; 1.
DR PROSITE; PS0017; DEATH_DOMAIN; 1.
KW Receptor; Neurogenesis; Transmembrane; Glycoprotein; Repeat;
KW Phosphorylation; Signal.
FT SIGNAL 1 19
FT CHAIN 20 416
FT CHAIN 20 416
FT DOMAIN 29 239
FT TRANSMEM 240 261
FT DOMAIN 262 416
FT DOMAIN 23 181
FT REPEAT 23 57
FT REPEAT 58 100
FT REPEAT 101 140
FT REPEAT 141 181
FT REPEAT 182 236
FT DOMAIN 188 236
FT DOMAIN 333 410
FT DISULFID 24 35
FT DISULFID 36 49
FT DISULFID 39 56
FT DISULFID 59 75
FT DISULFID 78 91
FT DISULFID 81 99
FT DISULFID 101 114
FT DISULFID 117 130
FT DISULFID 120 138
FT DISULFID 141 156
FT DISULFID 159 172
FT DISULFID 162 180
FT CARBOHYD 52 52
FT CONFLICT 36 36
FT CONFLICT 173 173
FT CONFLICT 276 276
FT CONFLICT 396 396
SQ SEQUENCE 416 AA; 44654 MW; 6BCEAAB54F4D2D56 CRC64;

Query Match
Best Local Similarity 6.5%; Score 147; DB 1; Length 416;
Matches 56; Conservative 17; Mismatches 82; Indels 32; Gaps 10;

QY 20 LGLSKVTCETGD-----CROQEFDR-SGNCVPCNOCQPGMELSKGFGY-----G 67
Db 82 VGLHMSAPCVESDDAVCRCAVGYQDELGSGCKECSIC-----EVGGLMFPFCRDS 133
QY 68 EDAQCVCRLHRFKEDWGFQKCPCLDCAV--NRFQKANCATSATGDCGLPGFYRKT 125
Db 134 QTVCECEPGEFTSDEANF--VDPCLPCTICEENVMVKECTATSDAECRLHPRWTTHT 191
QY 126 -KLVGQDMECVPCGDPDPPEPHCAKSNLVKIASTASP---RDTA--LAAVICSALA 179
Db 192 PSLAGSDSE--PITRDPNTEGMATTLADIYTVWGSSQPVVSRGTADNLIPVCSILA 249
QY 180 TVLLALL 186
Db 250 AVVGLV 256

RESULT 3
LMB2_RAT

```

```

ID AC LMB2_RAT STANDARD; PRT; 1801 AA.
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE LAMININ BETA-2 CHAIN PRECURSOR (S-LAMININ) (LAMININ CHAIN B3).
DS LAMB2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RX MEDLINE=89159410; PubMed=2922051;
RA Hunter D.D., Shah V., Merlie J.P., Sanes J.R.;
RT "A laminin-like adhesive protein concentrated in the synaptic cleft
of the neuromuscular junction.";
RL Nature 338:229-234(1989).
CC -1- FUNCTION: BINDING TO CELLS VIA A HIGH AFFINITY RECEPTOR, LAMININ
IS THOUGHT TO MEDIATE THE ATTACHMENT, MIGRATION, & ORGANIZATION OF
CELLS INTO TISSUES DURING EMBRYONIC DEVELOPMENT BY INTERACTING
WITH OTHER EXTRACELLULAR MATRIX COMPONENTS.
CC -1- SUBUNIT: LAMININ IS A COMPLEX GLYCOPROTEIN, CONSISTING OF THREE
DIFFERENT POLYPEPTIDE CHAINS (ALPHA, BETA, GAMMA), WHICH ARE BOUND
TO EACH OTHER BY DISULFIDE BONDS INTO A CROSS-SHAPED MOLECULE
COMPRISING ONE LONG & THREE SHORT ARMS WITH GLOBULES AT EACH END.
CC THE BETA-2 CHAIN IS A SUBUNIT OF LAMININ-3 (S-LAMININ), LAMININ-4
(S-MEROSIN), AND LAMININ-7 (KS-LAMININ).
CC -1- SUBCELLULAR LOCATION: EXTRACELLULAR.
CC -1- TISSUE SPECIFICITY: FOUND IN THE BASEMENT MEMBRANES (MAJOR
COMPONENT). S-LAMININ IS CONCENTRATED IN THE SYNAPTIC
CLEFT OF THE NEUROMUSCULAR JUNCTION.
CC -1- DOMAIN: THE ALPHA-HELICAL DOMAINS I AND II ARE THOUGHT TO INTERACT
WITH OTHER LAMININ CHAINS TO FORM A COILED COIL STRUCTURE.
CC -1- DOMAIN: DOMAINS VI AND IV ARE GLOBULAR.
CC -1- SIMILARITY: CONTAINS 1 LAMININ N-TERMINAL DOMAIN (DOMAIN VI).
CC -1- SIMILARITY: CONTAINS 12.5 LAMININ EGF-LIKE DOMAINS.
CC -1- SIMILARITY: CONTAINS 1 LAMININ DOMAIN IV.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X16563; CAA34561.1; -.
DR PIR; S03539; MMRTS.
DR HSSP; P02468; 1KLO.
DR INTERPRO; IPR000561; -.
DR INTERPRO; IPR001886; -.
DR INTERPRO; IPR002049; -.
DR PFAM; PF00053; laminin_EGF; 13.
DR PFAM; PF00055; laminin_Nterm; 1.
DR PRINTS; PR00011; EGF_LAMININ.
DR PROSITE; PS00022; EGF_1; 10.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01248; LAMININ_TYPE_EGF; 12.
DR Glycoprotein; Basement membrane; Extracellular matrix; Coiled coil;
KW Laminin EGF-like domain; Cell adhesion; Repeat; Signal.
FT SIGNAL 1 35
FT CHAIN 36 1801
FT DOMAIN 36 283
FT DOMAIN 286 555
FT DOMAIN 286 349
FT DOMAIN 350 412
FT DOMAIN 413 472
FT DOMAIN 473 524
FT DOMAIN 525 555
FT DOMAIN 556 785
FT DOMAIN 786 1192
FT DOMAIN 8 X LAMININ EGF-LIKE REPEATS (DOMAIN
V).
FT LAMININ BETA-2 CHAIN.
FT LAMININ N-TERMINAL (DOMAIN VI).
FT 4.5 X LAMININ EGF-LIKE REPEATS (DOMAIN
V).
FT LAMININ EGF-LIKE 1.
FT LAMININ EGF-LIKE 2.
FT LAMININ EGF-LIKE 3.
FT LAMININ EGF-LIKE 4.
FT LAMININ EGF-LIKE 5 (INCOMPLETE).
FT LAMININ DOMAIN IV.
FT 8 X LAMININ EGF-LIKE REPEATS (DOMAIN

```


modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announcement/> or send an email to license@isb-sib.ch).

```
CC EMBL; L04270; AAA36757.1; -.
CC HSSP; P25942; ICDF.
CC MIN; 600979; -.
CC INTERPRO; IPR001368; -.
CC PFAM; PF00020; TNFR_C6; 4.
CC PROSITE; PS00652; TNFR_NGFR_1; 2.
CC PROSITE; PS00050; TNFR_NGFR_2; 3.
KW Receptor; Transmembrane; Glycoprotein; Repeat; Signal.
FT SIGNAL 1 30
FT CHAIN 31 435
FT DOMAIN 31 227
FT TRANSMEM 228 248
FT DOMAIN 249 435
FT DOMAIN 42 211
FT REPEAT 42 81
FT REPEAT 82 124
FT REPEAT 125 168
FT REPEAT 169 211
FT DISULFID 43 58
FT DISULFID 59 72
FT DISULFID 62 80
FT DISULFID 83 98
FT DISULFID 101 116
FT DISULFID 104 124
FT DISULFID 126 132
FT DISULFID 139 148
FT DISULFID 142 167
FT DISULFID 170 185
FT CARBOHYD 40 40
FT CARBOHYD 177 177
SQ SEQUENCE 435 AA; 46709 MW; 624626E6022F656F CRC64;

Query Match 6.5%; Score 145.5; DB 1; Length 435;
Best Local Similarity 21.4%; Pred. No. 0.00034;
Matches 73; Conservative 41; Mismatches 108; Indels 119; Gaps 19;

QY 16 LVLVLLGLYSCK-----VTCETGDCROE---FDRSGNVCVPCNOCGPGLMELSKCEGFG 65
Db 18 VLGLFGLLAASQOAPVYPYASENCTCRDQKEYEYEQHRC--CSRCPGGTVYSAKC--S 73

QY 66 YGEDAQCVTCRLHFRKEDWGF---QKCKPC-----LDCAVNRFOKANCATSATDAIC- 114
Db 74 RIOTVCATCAENSYNEHWNLTICQLCRPCDPVGMGLEEIAPTCKRTQCRQCPGMFCA 133

QY 115 -----GDCLPQGYRKT-K-LVGQDMCVPC-----GDPPIPPYEPH--CAS 151
Db 134 AWALECTHCELLSDCPCTEAEKLDKDEVGKGNHCVPCKAGHFQNTSSPSARCQPHPTRCEN 193

QY 152 KVNVLKIA-----STASSPRD-----TALAANVCISALATVLLALLILCVIY---- 192
Db 194 Q-GLVEAPGTAQSDTTCKNLEPLPPMESTGMLMLVLLPLAFELLATVFCIWKSHG 252

QY 193 ---CKR--QFMKKKP-----SWLSRSDIQYNGSELSCLDRLPOLHEVAHRACCCQR 238
Db 253 SLCKRLGSLKRRQGGEGPNPVAGSW-----EPPKAHPYF----- 287

QY 239 RDSVQTCGVRLPLPMSMCEAEACSPNPATLGGCVHSAASLQA 279
Db 288 PDLVQPLLEPI-----SGDVSPVSTGLPAAPVLEA 316

RESULT 5
OX40_RAT
ID OX40_RAT STANDARD; PRT; 271 AA.
AC P15725;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)

DE OX40L RECEPTOR PRECURSOR (OX40 ANTIGEN) (MRC OX40).
GN TNFRSF4 OR TXGPIL OR OX40.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN [1]
RN SEQUENCE FROM N.A.
RC TISSUE-T-CELL;
RX MEDLINE=90214614; PubMed=2157591;
RA Mallett S., Fossum S., Barclay A.N.;
RT "Characterization of the MRC OX40 antigen of activated CD4 positive T
RL Lymphocytes -- a molecule related to nerve growth factor receptor.";
CC -!- FUNCTION: RECEPTOR FOR THE OX40L/GP34 CYTOKINE.
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -!- TISSUE SPECIFICITY: ACTIVATED T-CELLS.
CC -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announcement/
CC or send an email to license@isb-sib.ch).
```

RESULT 6
OX40_MOUSE

```

CC -1- SUBCELLULAR LOCATION: NUCLEAR.
CC -1- INDUCTION: BY INTERFERON-GAMMA.
CC -1- SIMILARITY: TO D.MELANOGASTER SHUTTLE CRAFT PROTEIN (STC) AND
CC YEAST YNL023C.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collabor
CC between the Swiss Institute of Bioinformatics and the EMBL outstac
CC the European Bioinformatics Institute. There are no restrictions on
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commer
CC entities requires a license agreement (See http://www.isb-sib.ch/anno
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; U15306; AAA69517.1; -.
CC DR HSP; P02876; 2WGC.
CC DR INTERPRO: IPR000967; -.
CC DR INTERPRO: IPR001374; -.
CC DR PFAM; PF01424; R3H; 1.
CC DR PFAM; PF01422; zf-NF-X1; 8.
CC DR KW Transcription regulation; Repressor; DNA-binding; Nuclear protein;
CC Repeat.
CC KW Repeat.
CC FT 424 876 7 X APPROXIMATE REPEATS, CYS-RICH.
CC FT REPEAT 424 463 1.
CC FT REPEAT 480 517 2.
CC FT REPEAT 541 580 3.
CC FT REPEAT 606 647 4.
CC FT REPEAT 695 734 5.
CC FT REPEAT 806 842 6.
CC FT REPEAT 836 876 7.
CC FT REPEAT 1104 AA; 123149 MW; 36FEC4292F78130C CRC64;
CC SQ SEQUENCE

```

FT	REPEAT	000	047	4.
FT	REPEAT	695	734	5.
FT	REPEAT	806	842	6.
FT	REPEAT	836	876	7.
SQ	SEQUENCE	1104	AA: 123149	MM: 36FEC4292F78130C CRC64;

SEQUENCE	1104 AMY	122449 AMY	30LE4429221/012305 GRC67
Query Match		6.4%	Score 144; DB 1; Length 1104;
Best Local Similarity		18.8%	
Matches 110; Conservative		59; Mismatches 181; Indels 236; Gaps	

QY 180 TVLLALLILCV-ITYKROFMEKPSWLSRSDIQYNGSELCLDRPQLHEYAHRAACQCR 238
 Db 220 LGICLFFICISLLC-----RYPQW-----RRVYSII-----C- 248
 QY 239 RDSVQTCGPVNR-----LLPSMCCCEACSPNPA---TLGCGV-----HSAASLQA 279
 Db 249 RDS-----APVKEVEGEGIVTKLTPASI--PAFSPNPGFNPTLGFSTPRFSPVSTPI 302
 QY 280 RNA-GPAG-----EMVPT-----FEGSL 296
 Db 303 SPVFGSPNNHNFVPPVREVVTGADPLLYGSL 335
 RESULT 9
 NGFR_RAT STANDARD; PRT; 425 AA.
 AC P07174;
 DT 01-APR-1988 (Rel. 07, Created)
 DT 01-APR-1988 (Rel. 07, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE LOW-AFFINITY NERVE GROWTH FACTOR RECEPTOR PRECURSOR (NGF RECEPTOR)
 DE (GP80-LNGFR) (P75 ICD).
 GN NGFR.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87115859; PubMed=3027580;
 RA Radeke M.J., Misko T.P., Hsu C., Herzenberg L.A., Shooter E.M.;
 RT "Gene transfer and molecular cloning of the rat nerve growth factor
 RT receptor.";
 RL Nature 325:593-597(1987).
 RN [2]
 RP SEQUENCE OF 1-22 FROM N.A.
 RC TISSUE=LIVER;
 RX MEDLINE=93077038; PubMed=1446821;
 RA Metsis M., Timmusk T., Allikmets R., Saarma M., Persson H.;
 RT "Regulatory elements and transcriptional regulation by testosterone
 RT and retinoic acid of the rat nerve growth factor receptor promoter.";
 RL Gene 121:247-254(1992).
 RN [3]
 RP STRUCTURE BY NMR OF 334-418.
 RX MEDLINE=97449145; PubMed=9305641;
 RA Liepinsh E., Ilag L.L., Otting G., Ibanez C.F.;
 RT "NMR structure of the death domain of the p75 neurotrophin receptor.";
 RL EMBO J. 16:4999-5005(1997).
 CC -1- FUNCTION: LOW AFFINITY RECEPTOR WHICH CAN BIND TO NGF, BDNF,
 CC NT-3, AND NT-4.
 CC -1- SUBUNIT: NGF RECEPTOR CAN FORM A HOMODIMER THROUGH DISULFIDE
 CC BOND FORMATION.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- PTM: N- AND O-GLYCOSYLATED AND IS PHOSPHORYLATED ON SERINE.
 CC -1- SIMILARITY: CONTAINS A LEA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
 CC -1- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See [http://www.isb-sib.ch/](http://www.isb-sib.ch/announce/) or
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; X05137; CAA28793.1; -;
 DR EMBL; X61269; -; NOT_ANNOTATED_CDS.
 DR PIR; A26431; A26431.
 DR PDB; INGR; 29-JUL-97.
 DR INTERPRO; IPR000488; -;
 DR INTERPRO; IPR001368; -;
 DR PFAM; PF00020; TNFR_c6; 4.
 DR PFAM; PF00531; death; 1.

DR PROSITE; PS00652; TNFR_NGFR_1; 3.
 DR PROSITE; PS00500; TNFR_NGFR_2; 4.
 DR PROSITE; PS00117; DEATH_DOMAIN; 1.
 KW Receptor; Neurogenesis; Transmembrane; Glycoprotein; Repeat;
 KW Phosphorylation; Signal; 3D-structure.
 FT SIGNAL 1 29
 FT CHAIN 30 425 LOW-AFFINITY NERVE GROWTH FACTOR
 FT RECEPTOR.
 FT DOMAIN 30 251 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 252 273 POTENTIAL.
 FT DOMAIN 274 425 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 32 190 4 X TNFR-CYS.
 FT REPEAT 32 66 TNFR-CYS 1.
 FT REPEAT 67 108 TNFR-CYS 2.
 FT REPEAT 109 148 TNFR-CYS 3.
 FT REPEAT 149 190 TNFR-CYS 4.
 FT DOMAIN 198 249 SER/THR-RICH.
 FT DOMAIN 354 419 DEATH DOMAIN.
 FT DISULFID 33 44 BY SIMILARITY.
 FT DISULFID 45 58 BY SIMILARITY.
 FT DISULFID 48 65 BY SIMILARITY.
 FT DISULFID 68 84 BY SIMILARITY.
 FT DISULFID 87 100 BY SIMILARITY.
 FT DISULFID 90 108 BY SIMILARITY.
 FT DISULFID 110 123 BY SIMILARITY.
 FT DISULFID 126 139 BY SIMILARITY.
 FT DISULFID 139 147 BY SIMILARITY.
 FT DISULFID 150 165 BY SIMILARITY.
 FT DISULFID 168 181 BY SIMILARITY.
 FT DISULFID 171 189 BY SIMILARITY.
 FT CARBOHYD 61 61 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 71 71 N-LINKED (GLCNAC. .) (POTENTIAL).
 SQ SEQUENCE 425 AA; 45432 MW; B2EL52D94D3827F8 CRC64;
 Query Match 6.2%; Score 140; DB 1; Length 425;
 Best Local Similarity 20.8%; Pred. No. 0.00087;
 Matches 85; Conservative 52; Mismatches 172; Indels 100; Gaps 20;
 QY 16 LLVLLGLYLS--CAVTCETGDCRQOEFRDRSGNVCPCNQCPCGMEKSGCGFGVGEDAQCV 73
 Db 18 LLILVLGVSGGAKETCTSG-----LYTHSGEC--KACNLGEGVAQPCG---ANOTVCE 66
 QY 74 TCRHFRKED--WGFQKCKPCLDCAVVNVRFQKANCATSDAICGDCGLPGFYRKT----- 126
 Db 67 PCLDNVTFSDVVSATEPCPKTECLGL-QSMSAPCVCVEADAVC-RCAYGVYQDEETGHCE 124
 QY 127 -----LVGFQDMCEVPCGDPDPPEYEPHCASKVNLVKIATSPASPRDTALAIVC 175
 Db 125 ACSVCEVSGSLVFCQDKQNTVCECP---EGTYSDEANHV-----DPCLPCTVC 171
 QY 176 SALATVLLALLILCVLYCKRQFMKPKPSLSRSDIQYNGSELCLDRPQLHEYAHRAACC 235
 Db 172 EDTEROLRE---CTPWDAECEIEPGRWIPRSTPPEGSDSTAPSTQEPVPP----- 220
 QY 236 QCRSDSVQTCGPVRLLPSPCCCEACSPNATLGCVGHSASQAARNAGAPAGEMVPTFFGS 295
 Db 221 --EQD-----LVPSIVADNVTT---VMG-----SSQPVVTRGTDNLPIVYCSI 259
 QY 296 LTOSIGCEFS-----DAWPLMQNPMGGDNIISFCDSYPELGTEDITHSLNPELESSTLSDNS 351
 Db 260 LAAYVVLVAVYIAFKRWNSCKNQKQANSRPVNTQTPPECEKLS-----DSGISVDSQS 314
 QY 352 SQDLVGAVPVQSHSENFATDLSRYNNTLVESASTQDALTMRSDQ 400
 Db 315 LHD-----QOHTQ--TASQALAGDGNLYSSL-----PLTKREEVEK 350
 RESULT 10
 LMB2_HUMAN
 ID LMB2_HUMAN STANDARD; PRT; 1798 AA.
 AC P55268; Q16321;
 DT 01-OCT-1996 (Rel. 34, Created)

DT	01-OCT-1996 (Rel. 34, Last sequence update)	FT	283	346	V).
DE	01-OCT-2000 (Rel. 40, Last annotation update)	FT	347	409	LAMININ EGF-LIKE 1.
DE	LAMININ BETA-2 CHAIN PRECURSOR (S-LAMININ).	FT	410	469	LAMININ EGF-LIKE 2.
GN	LAMB2.	FT	470	521	LAMININ EGF-LIKE 3.
OS	Homo sapiens (Human).	FT	522	552	LAMININ EGF-LIKE 4.
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	FT	553	781	LAMININ EGF-LIKE 5 (INCOMPLETE).
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	FT	782	1190	LAMININ DOMAIN IV.
RN	[1]	FT			8 X LAMININ EGF-LIKE REPEATS (DOMAIN III).
RN	SEQUENCE FROM N.A.	FT			
RX	MEDLINE-95213013; PubMed=7698745;	FT	783	830	LAMININ EGF-LIKE 6.
RA	Wewer U.M., Gerecke D.R., Durkin M.E., Kurtz K.S., Mattei M.-G.,	FT	831	876	LAMININ EGF-LIKE 7.
RA	Champlaud M.F., Burgess R.E., Albrechtsen R.;	FT	877	926	LAMININ EGF-LIKE 8.
RA	"Human beta 2 chain of laminin (formerly S chain): cDNA cloning,	FT	927	985	LAMININ EGF-LIKE 9.
RT	chromosomal localization, and expression in carcinomas.";	FT	986	1037	LAMININ EGF-LIKE 10.
RL	Genomics 24:243-252(1994).	FT	1038	1094	LAMININ EGF-LIKE 11.
RN	[2]	FT	1095	1142	LAMININ EGF-LIKE 12.
RN	SEQUENCE FROM N.A.	FT	1143	1189	LAMININ EGF-LIKE 13.
RX	MEDLINE-95316263; PubMed=7795887;	FT	1190	1409	DOMAIN II.
RA	Iivanainen A., Vuolteenaho R., Sainio K., Eddy R., Shows T.B.,	FT	1410	1442	DOMAIN ALPHA.
RA	Sariola H., Tryggvason K.;	FT	1443	1798	DOMAIN I.
RT	"The human laminin beta 2 chain (S-laminin): structure, expression in	FT	1253	1319	COILED COIL (POTENTIAL).
RT	fetal tissues and chromosomal assignment of the LAMB2 gene.";	FT	1472	1526	COILED COIL (POTENTIAL).
RL	Matrix Biol. 14:489-497(1995).	FT	1577	1790	COILED COIL (POTENTIAL).
CC	-I- FUNCTION: BINDING TO CELLS VIA A HIGH AFFINITY RECEPTOR, LAMININ	FT	283	292	BY SIMILARITY.
CC	IS THOUGHT TO MEDIATE THE ATTACHMENT, MIGRATION, & ORGANIZATION OF	FT	285	310	BY SIMILARITY.
CC	CELLS INTO TISSUES DURING EMBRYONIC DEVELOPMENT BY INTERACTING	FT	312	321	BY SIMILARITY.
CC	WITH OTHER EXTRACELLULAR MATRIX COMPONENTS.	FT	324	344	BY SIMILARITY.
CC	-I- SUBUNIT: LAMININ IS A COMPLEX GLYCOPROTEIN, CONSISTING OF THREE	FT	347	356	BY SIMILARITY.
CC	DIFFERENT POLYPEPTIDE CHAINS (ALPHA, BETA, GAMMA), WHICH ARE BOUND	FT	349	374	BY SIMILARITY.
CC	TO EACH OTHER BY DISULFIDE BONDS INTO A CROSS-SHAPED MOLECULE	FT	377	386	BY SIMILARITY.
CC	COMPRISING ONE LONG & THREE SHORT ARMS WITH GLOBULES AT EACH END.	FT	389	407	BY SIMILARITY.
CC	THE BETA-2 CHAIN IS A SUBUNIT OF LAMININ-3 (S-LAMININ), LAMININ-4	FT	410	423	BY SIMILARITY.
CC	(S-MEROSIN), AND LAMININ-7 (KS-LAMININ).	FT	412	438	BY SIMILARITY.
CC	-I- SUBCELLULAR LOCATION: EXTRACELLULAR.	FT	440	449	BY SIMILARITY.
CC	-I- TISSUE SPECIFICITY: FOUND IN THE BASEMENT MEMBRANES (MAJOR	FT	452	467	BY SIMILARITY.
CC	COMPONENT). S-LAMININ IS CONCENTRATED IN THE SYNAPTIC	FT	470	484	BY SIMILARITY.
CC	CLEFT OF THE NEUROMUSCULAR JUNCTION.	FT	472	491	BY SIMILARITY.
CC	-I- DOMAIN: THE ALPHA-HELICAL DOMAINS I AND II ARE THOUGHT TO INTERACT	FT	493	502	BY SIMILARITY.
CC	WITH OTHER LAMININ CHAINS TO FORM A COILED COIL STRUCTURE.	FT	505	519	BY SIMILARITY.
CC	-I- DOMAIN: DOMAINS VI AND IV ARE GLOBULAR.	FT	783	795	BY SIMILARITY.
CC	-I- SIMILARITY: CONTAINS 1 LAMININ N-TERMINAL DOMAIN (DOMAIN VI).	FT	785	802	BY SIMILARITY.
CC	-I- SIMILARITY: CONTAINS 12.5 LAMININ EGF-LIKE DOMAINS.	FT	804	813	BY SIMILARITY.
CC	-I- SIMILARITY: CONTAINS 1 LAMININ DOMAIN IV.	FT	816	828	BY SIMILARITY.
CC	-----	FT	831	843	BY SIMILARITY.
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration	FT	833	850	BY SIMILARITY.
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -	FT	852	861	BY SIMILARITY.
CC	the European Bioinformatics Institute. There are no restrictions on its	FT	864	874	BY SIMILARITY.
CC	use by non-profit institutions as long as its content is in no way	FT	877	886	BY SIMILARITY.
CC	modified and this statement is not removed. Usage by and for commercial	FT	879	893	BY SIMILARITY.
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/	FT	896	905	BY SIMILARITY.
CC	or send an email to license@isb-sib.ch).	FT	908	924	BY SIMILARITY.
CC	-----	FT	927	943	BY SIMILARITY.
DR	EMBL; Z68155; CAA92279.1; -	FT	929	954	BY SIMILARITY.
DR	EMBL; Z68156; CAA92279.1; JOINED.	FT	956	965	BY SIMILARITY.
DR	EMBL; X79683; CAA36130.1; -	FT	968	983	BY SIMILARITY.
DR	EMBL; S77512; AAB34682.2; -	FT	986	1000	BY SIMILARITY.
DR	HSSP; P02468; 1KLO.	FT	1007	1019	BY SIMILARITY.
DR	MTM; 150325; -	FT	1010	1019	BY SIMILARITY.
DR	INTERPRO; IPR000561; -	FT	1022	1035	BY SIMILARITY.
DR	INTERPRO; IPR001886; -	FT	1095	1107	BY SIMILARITY.
DR	INTERPRO; IPR002049; -	FT	1097	1114	BY SIMILARITY.
DR	PFAM; PF00053; laminin_EGF_13.	FT	1116	1125	BY SIMILARITY.
DR	PFAM; PF00055; laminin_Nterm; 1.	FT	1128	1140	BY SIMILARITY.
DR	PRINTS; PR00011; EGFLAMIN.	FT	1143	1155	BY SIMILARITY.
DR	PROSITE; PS00022; EGF_1; 10.	FT	1145	1162	BY SIMILARITY.
DR	PROSITE; PS01186; EGF_2; 2.	FT	1164	1173	BY SIMILARITY.
DR	PROSITE; PS01248; LAMININ_Type_EGF; 12.	FT	1176	1187	BY SIMILARITY.
KW	Glycoprotein; Basement membrane; Extracellular matrix; Coiled coil;	FT	1190	1190	INTERCHAIN (PROBABLE).
KW	Laminin EGF-like domain; Cell adhesion; Repeat; Signal.	FT	1193	1193	INTERCHAIN (PROBABLE).
FT	SIGNAL 1 32 POTENTIAL.	FT	1797	1797	INTERCHAIN (PROBABLE).
FT	CHAIN 33 1798 LAMININ BETA-2 CHAIN.	FT	248	248	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	DOMAIN 33 280 LAMININ N-TERMINAL (DOMAIN VI).	FT	368	368	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	DOMAIN 281 552 4-5 X LAMININ EGF-LIKE REPEATS (DOMAIN	FT	1085	1085	N-LINKED (GLCNAC. . .) (POTENTIAL).

```

FT CARBOHYD 1249 1249 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 1308 1308 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 1348 1348 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 1499 1499 N-LINKED (GLCNAC...) (POTENTIAL).
FT CONFLICT 914 914 R -> G (IN REF. 2).
FT CONFLICT 1179 1179 G -> A (IN REF. 2).
SQ SEQUENCE 1798 AA; 196079 MW; 9555CF5B24850CB7 CRC64;

Query Match
Best Local Similarity 6.1%; Score 136.5; DB 1; Length 1798;
Matches 87; Conservative 39; Mismatches 136; Indels 167; Gaps 25;

QY 17 LVLLGYLSKVTGETGDCRQOEFRDSGNCV-----PCNQCGPMELSKCEGFGY- 67
D 17 LVLLGYLSKVTGETGDCRQOEFRDSGNCV-----PCNQCGPMELSKCEGFGY- 67
D 775 LIYNGALPCQ--CNQOGLSSECNPHGGQCLKPGVVGVRCDLCAPGY-----YGFPG 825
QY 68 -----EDAQCVTCRLHRF-----KEDWGFQCKPKCLDCAVVN 99
D 68 -----EDAQCVTCRLHRF-----KEDWGFQCKPKCLDCAVVN 99
D 826 TGCQACQCSHEGALSSICKETSQCL-CRTGAFGLRCDRCQRGWGFPPSCRPCV----- 878
QY 100 RFQKANCSDAI-----CGDCLPGFYRKTL-VGFQDMECVPCGD 140
D 100 RFQKANCSDAI-----CGDCLPGFYRKTL-VGFQDMECVPCGD 140
D 879 -----CNGHADCENTHTGACLRDHTGHEHCERCIAGFHRDPRUPYGGQ----CRPCPC 929
QY 141 PP-PPYEPHCASKNVLVKIATASPRDTALAAVIGSALATVLLALLILCVYCKRQFME 199
D 141 PP-PPYEPHCASKNVLVKIATASPRDTALAAVIGSALATVLLALLILCVYCKRQFME 199
D 930 PEGGSORHPAT-----SCHQDEYSQIVCHCRAGY---TCLRCEACAPGHFGD 975
QY 200 -KKP-----SWLSRSODIO-----YNGSELSCLD-----RPLHBYA----- 230
D 200 -KKP-----SWLSRSODIO-----YNGSELSCLD-----RPLHBYA----- 230
D 976 PSRPGRCQLCEGSGNIDPMDACDPHTQCCLRHHTEGPHCAHCKPGFHGQAARQSC 1035
QY 231 HRACCOCRRDSVOTC-----GPVRLLPSPM---CCEACSPN---PATLGGCGVHS 273
D 231 HRACCOCRRDSVOTC-----GPVRLLPSPM---CCEACSPN---PATLGGCGVHS 273
D 1036 HRTCNLLGTNPQCCSPDOCHDPSGQCPCLPNVGGPSCDR-CAPNFNWLTSGHGCGP 1094
QY 274 AASLQARNAGPAGEMVPTFFGSLTSQICGFSFSDAWPLQNPMDGNISFCDSYPELTGED 333
D 274 AASLQARNAGPAGEMVPTFFGSLTSQICGFSFSDAWPLQNPMDGNISFCDSYPELTGED 333
D 1095 CACHPSRARGPT-----CNEFTGOCHCRAG-FGGRTCSEC-----QE 1130
QY 334 IHSNLEPE 342
D 334 IHSNLEPE 342
D 1131 LHWGDPGLQ 1139

RESULT 11
TNRC_MOUSE STANDARD; PRT; 415 AA.
AC P50284;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE LYMPHOTOXIN-BETA RECEPTOR PRECURSOR.
GN LTBR OR TNFR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CVB; TISSUE=LUNG;
RX MEDLINE=96072804; PubMed=7594541;
RA Force W.R., Walter B.N., Hession C., Tizard R., Kozak C.A.,
RA Browning J.L., Ware C.F.;
RT "Mouse lymphotoxin-beta receptor. Molecular genetics, ligand binding,
RT and expression."
RL J. Immunol. 155:5280-5289 (1995).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=96163885; PubMed=8586432;
RA Nakanura T., Tashiro K., Nazarea M., Nakano T., Sasayama S.,
RA Honjo T.;
RT "The murine lymphotoxin-beta receptor cDNA: isolation by the signal

```

```

RT sequence trap and chromosomal mapping."
RL Genomics 30:312-319 (1995).
CC -1- FUNCTION: RECEPTOR FOR THE LYMPHOTOXIN-BETA. POSSIBLE FUNCTION IN
CC IMMUNE DEVELOPMENT.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL: U29173; AAA68964.1; -
CC EMBL: L38423; AAB00846.1; -
CC EMBL: U30798; AAA81334.1; -
CC HSSP: P25942; ICDF.
CC MGD: MGI:104875; LTBR.
CC INTERPRO: IPR001368; -
CC PFAM: PF00020; TNFR_G6; 3.
CC PROSITE: PS00652; TNFR_NGFR_1; 2.
CC PROSITE: PS00500; TNFR_NGFR_2; 3.
KW Receptor; Transmembrane; Glycoprotein; Repeat; Signal.
FT SIGNAL 1 30
FT CHAIN 31 415
FT DOMAIN 31 223
FT TRANSMEM 224 244
FT DOMAIN 245 415
FT DOMAIN 42 213
FT REPEAT 42 81
FT REPEAT 82 124
FT REPEAT 125 170
FT REPEAT 171 213
FT DISULFID 43 58
FT DISULFID 59 72
FT DISULFID 62 80
FT DISULFID 83 98
FT DISULFID 101 116
FT DISULFID 104 124
FT DISULFID 126 132
FT DISULFID 139 150
FT DISULFID 142 169
FT DISULFID 172 187
FT CARBOHYD 40 40
FT CARBOHYD 179 179
SQ SEQUENCE 415 AA; 44956 MW; 29B326A566AEF661 CRC64;

Query Match
Best Local Similarity 6.0%; Score 134.5; DB 1; Length 415;
Matches 46; Conservative 28; Mismatches 70; Indels 45; Gaps 8;

QY 47 VPCNQCGPMELSKCEGFGYGEDAQCVTCRLHFRKEDWG--FQCKPCDCAVYNRFQK-A 104
D 47 VPCNQCGPMELSKCEGFGYGEDAQCVTCRLHFRKEDWG--FQCKPCDCAVYNRFQK-A 104
D 57 VCCSRPPGFEVAVC--SRSDQTVCKTCPHNSYNEHNLSTCOLCRPCDIVLGEFEVA 114
QY 105 NCSATSDAICGDCDLPGF-----YKTKLVGFQ-----DMECVPC- 138
D 105 NCSATSDAICGDCDLPGF-----YKTKLVGFQ-----DMECVPC- 138
D 115 PCTSDRKAEC-RCQPGMSCVYLDNECVHCEERLVLCQPGTAEVTDMDTVNCPVK 173
QY 139 -----GDPPEPPEHCASKVNLVKIATASPRDTAL-----AAVICSALATVLLA 184
D 139 -----GDPPEPPEHCASKVNLVKIATASPRDTAL-----AAVICSALATVLLA 184
D 174 PGHFQNTSSPRACQPHTRCEIOGLVEAPGTSYSDTICKNPPPGAMLLALLLSLVLF 233
QY 185 LLILCVYC 193
D 185 LLILCVYC 193
D 234 LLFTTVLAC 242

RESULT 12
LMB1_MOUSE

```


FT	DOMAIN	556	782		LAMININ DOMAIN IV.
FT	DOMAIN	783	1191		8 X LAMININ EGF-LIKE REPEATS (DOMAIN III).
FT	DOMAIN	784	831		LAMININ EGF-LIKE 6.
FT	DOMAIN	832	877		LAMININ EGF-LIKE 7.
FT	DOMAIN	878	927		LAMININ EGF-LIKE 8.
FT	DOMAIN	928	986		LAMININ EGF-LIKE 9.
FT	DOMAIN	987	1038		LAMININ EGF-LIKE 10.
FT	DOMAIN	1039	1095		LAMININ EGF-LIKE 11.
FT	DOMAIN	1096	1143		LAMININ EGF-LIKE 12.
FT	DOMAIN	1144	1190		LAMININ EGF-LIKE 13.
FT	DOMAIN	1191	1410		DOMAIN II.
FT	DOMAIN	1411	1443		DOMAIN ALPHA.
FT	DOMAIN	1444	1799		DOMAIN I.
FT	DOMAIN	1257	1304		COILED COIL (POTENTIAL).
FT	DOMAIN	1473	1527		COILED COIL (POTENTIAL).
FT	DOMAIN	1577	1791		COILED COIL (POTENTIAL).
FT	DISULFID	286	295		BY SIMILARITY.
FT	DISULFID	288	313		BY SIMILARITY.
FT	DISULFID	315	324		BY SIMILARITY.
FT	DISULFID	327	347		BY SIMILARITY.
FT	DISULFID	350	359		BY SIMILARITY.
FT	DISULFID	352	377		BY SIMILARITY.
FT	DISULFID	380	389		BY SIMILARITY.
FT	DISULFID	392	410		BY SIMILARITY.
FT	DISULFID	413	426		BY SIMILARITY.
FT	DISULFID	415	441		BY SIMILARITY.
FT	DISULFID	443	452		BY SIMILARITY.
FT	DISULFID	455	470		BY SIMILARITY.
FT	DISULFID	473	487		BY SIMILARITY.
FT	DISULFID	475	494		BY SIMILARITY.
FT	DISULFID	496	505		BY SIMILARITY.
FT	DISULFID	508	522		BY SIMILARITY.
FT	DISULFID	784	796		BY SIMILARITY.
FT	DISULFID	786	803		BY SIMILARITY.
FT	DISULFID	805	814		BY SIMILARITY.
FT	DISULFID	817	829		BY SIMILARITY.
FT	DISULFID	832	844		BY SIMILARITY.
FT	DISULFID	834	851		BY SIMILARITY.
FT	DISULFID	853	862		BY SIMILARITY.
FT	DISULFID	865	875		BY SIMILARITY.
FT	DISULFID	878	887		BY SIMILARITY.
FT	DISULFID	880	894		BY SIMILARITY.
FT	DISULFID	897	906		BY SIMILARITY.
FT	DISULFID	909	925		BY SIMILARITY.
FT	DISULFID	928	944		BY SIMILARITY.
FT	DISULFID	930	955		BY SIMILARITY.
FT	DISULFID	957	966		BY SIMILARITY.
FT	DISULFID	969	984		BY SIMILARITY.
FT	DISULFID	987	1001		BY SIMILARITY.
FT	DISULFID	989	1008		BY SIMILARITY.
FT	DISULFID	1011	1020		BY SIMILARITY.
FT	DISULFID	1023	1036		BY SIMILARITY.
FT	DISULFID	1096	1108		BY SIMILARITY.
FT	DISULFID	1098	1115		BY SIMILARITY.
FT	DISULFID	1117	1126		BY SIMILARITY.
FT	DISULFID	1129	1141		BY SIMILARITY.
FT	DISULFID	1144	1156		BY SIMILARITY.
FT	DISULFID	1146	1163		BY SIMILARITY.
FT	DISULFID	1165	1174		BY SIMILARITY.
FT	DISULFID	1177	1188		BY SIMILARITY.
FT	DISULFID	1191	1191		INTERCHAIN (PROBABLE).
FT	DISULFID	1194	1194		INTERCHAIN (PROBABLE).
FT	DISULFID	1798	1798		INTERCHAIN (PROBABLE).
FT	CARBOHYD	251	251		N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	371	371		N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	1086	1086		N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	1250	1250		N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	1309	1309		N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	1349	1349		N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	1300	1500		N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	SEQUENCE	1799	196352		AA; 196352 MW; 1F28967A67AEDE33 CRC64;

Query Match
Best Local Similarity 5.9%; Score 133.5; DB 1; Length 1799;
Matches 92; Conservative 40; Mismatches 121; Indels 205; Gaps 27;

Qy	17	LVLLGYLSCKVTCTGDCRQOEFRDRSGNVCNQCNGFGLMELSKEC	-----GFG---	65
Db	776	LIYNGALPCQ--CDPQGSLSSECSPHGGQC-----RCKPGV-VGRRCDCVATGYVGFPGAG	828	
Qy	66	-----YGEDAQCVTCRLHRF-----	KEDWGFQKCKPCLDCAVNR	101
Db	829	COACOCSPDGALSALCEGTSQC-PCRFAGFLRCDHCGQGWGPNCRPCV	-----	879
Qy	102	OKANCATSDAI-----CGDCLPGFYRKTKL-VGFQDMBCVPCGDDP	142	
Db	880	---CNGRADECDTHTGACLCGRDYTGGEHCERCITAGHGDPRPYGGQ---CRPCPCPE	932	
Qy	143	-PPYEPHCASKVNLVIASTASPRDTALAAVICSALATVLLALLILCVICKRQFM---	198	
Db	933	GPSQRHEAT-----SCHRDGYSQIIVC-----HCRAGYTGRLR	965	
Qy	199	-----EKRP-----SWLSRSQDIQ-----YNGSELSCLD-----	RP 224	
Db	966	CEACAPGPGDPSPKPGRCQLCECSGNIDPMDPADCPHTGQCRLCHNTEGPHGCKP	1025	
Qy	225	QLH-EVAHRACOCRRDSVQTCGPVRLLPSCM-----CE-----	EA 259	
Db	1026	GFHGQAAQSCHRC-----TCNLIGTPRRCPSTDLCHCDPSTQCPCPLPHVQGLNCDH	1079	
Qy	260	CSPN--PATLGCYVHSAASLQARNAGP-----AGEMVPTFFGSLTQSICGEFS	305	
Db	1080	CAPNFWNTSGRCQPCACHPSPARGPTCNEFTGOCHCHAG-----FGGRTCSCEQELY	1133	
Qy	306	DAWPLMQ-----NPMGGD-----NISFCDYSYELTG	331	
Db	1134	WGDPGLQCRACDCDPRGIDKPKQCHRSTGHCSCRPGVSG	1171	

RESULT 14
VWF_HUMAN
ID VWF_HUMAN STANDARD; PRT; 2813 AA.
AC P04275;
DT 20-MAR-1987 (Rel. 04, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE VON WILLEBRAND FACTOR PRECURSOR (VWF).
GN F8VWF OR VWF.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-90062044; PubMed-2584182;
RA Mancuso D.J., Tuley E.A., Westfield L.A., Worrall N.K.,
RA Shelton-Inloes B.B., Sorace J.M., Alevis Y.G., Sadler J.E.;
RT "Structure of the gene for human von Willebrand factor.";
RL J. Biol. Chem. 264:19514-19527(1989).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE-87016349; PubMed-3489923;
RA Bonthron D., Orr E.C., Mitsock L.M., Ginsburg D., Handin R.I.,
RA Orkin S.H.;
RT "Nucleotide sequence of pre-pro-von Willebrand factor cDNA";
RL Nucleic Acids Res. 14:7125-7128(1986).
RN [3]
RP SEQUENCE OF 1-120 FROM N.A., AND SEQUENCE OF 23-56.
RC TISSUE=UMBILICAL VEIN ENDOTHELIAL CELLS;
RX MEDLINE-87213253; PubMed-3495266;
RA Shelton-Inloes B.B., Broze G.J. Jr., Miletiich J.P., Sadler J.E.;
RT "Evolution of human von Willebrand factor: cDNA sequence
polymorphisms, repeated domains, and relationship to von Willebrand
antigen II.";
RL Biochem. Biophys. Res. Commun. 144:657-665(1987).

RA [4] SEQUENCE OF 1-1400 FROM N.A.
RX MEDLINE=87004550; PubMed=3019665;
RA Verweij C.L., Diergaarde P.J., Hart M., Pannekoek H.;
RT "Full-length von Willebrand factor (vWF) cDNA encodes a highly
RT repetitive protein considerably larger than the mature vWF subunit.";
RL EMBO J. 5:1839-1847(1986).
RN [5]
RP ERRATUM.
RA Verweij C.L., Diergaarde P.J., Hart M., Pannekoek H.;
RL EMBO J. 5:3074-3074(1986).
RN [6]
RP SEQUENCE OF 764-2813.
RX MEDLINE=86269895; PubMed=3524673;
RA Titani K., Kumar S., Takio K., Ericsson L.H., Wade R.D., Ashida K.,
RA Walsh K.A., Choquet M.W., Sadler J.E., Fujikawa K.;
RT "Amino acid sequence of human von Willebrand factor.";
RL Biochemistry 25:3171-3184(1986).
RN [7]
RP SEQUENCE OF 781-1424 FROM N.A.
RX MEDLINE=86269894; PubMed=3488076;
RA Shelton-Inloes B.B., Titani K., Sadler J.E.;
RT "cDNA sequences for human von Willebrand factor reveal five types of
RT repeated domains and five possible protein sequence polymorphisms.";
RL Biochemistry 25:3164-3171(1986).
RN [8]
RP SEQUENCE OF 764-873 AND 1289-2813 FROM N.A.
RX MEDLINE=86016708; PubMed=2864688;
RA Sadler J.E., Shelton-Inloes B.B., Sorace J.M., Harlan J.M.,
RA Titani K., Davie E.W.;
RT "Cloning and characterization of two cDNAs coding for human von
RT Willebrand factor.";
RL Proc. Natl. Acad. Sci. U.S.A. 82:6394-6398(1985).
RN [9]
RP SEQUENCE OF 990-1947 FROM N.A.
RX MEDLINE=91105089; PubMed=1988024;
RA Mancuso D.J., Tuley E.A., Westfield L.A., Lester-Mancuso T.L.,
RA Le-Beau M.M., Sorace J.M., Sadler J.E.;
RT "Human von Willebrand factor gene and pseudogene: structural analysis
RT and differentiation by polymerase chain reaction.";
RL Biochemistry 30:253-269(1991).
RN [10]
RP SEQUENCE OF 2731-2813 FROM N.A.
RX MEDLINE=85269603; PubMed=3875078;
RA Verweij C.L., de Vries C.J.M., Distel B., van Zonneveld A.-J.,
RA Geurts van Kessel A., van Mourik J.A., Pannekoek H.;
RT "Construction of cDNA coding for human von Willebrand factor using
RT antibody probes for colony-screening and mapping of the chromosomal
RL gene.";
RL Nucleic Acids Res. 13:4699-4717(1985).
RN [11]
RP SEQUENCE OF 1-177 FROM N.A.
RX MEDLINE=88111704; PubMed=2828057;
RA Bonthron D., Orkin S.H.;
RT "The human von Willebrand factor gene. Structure of the 5' region.";
RL Eur. J. Biochem. 171:51-57(1988).
RN [12]
RP SEQUENCE OF 2621-2813 FROM N.A.
RX MEDLINE=85244588; PubMed=3874428;
RA Ginsburg D., Handin R.I., Bonthron D.T., Donlon T.A., Bruns G.A.P.,
RA Latt S.A., Orkin S.H.;
RT "Human von Willebrand factor (vWF): isolation of complementary DNA
RT (cDNA) clones and chromosomal localization.";
RL Science 228:1401-1406(1985).
RN [13]
RP SEQUENCE OF 2731-2813 FROM N.A.
RX MEDLINE=85201687; PubMed=3873280;
RA Lynch D.C., Zimmerman T.S., Collins C.J., Brown M., Morin M.J.,
RA Ling E.H., Livingston D.M.;
RT "Molecular cloning of cDNA for human von Willebrand factor:
RT authentication by a new method.";
RL Cell 41:49-56(1985).
RN [14]

RP REVISIONS.
RA Lynch D.C.;
RL Submitted (JUL-1991) to the EMBL/GenBank/DBJ databases.
RN [15]
RP SEQUENCE OF 2731-2813 FROM N.A.
RX MEDLINE=87260814; PubMed=3496594;
RA Collins C.J., Underdahl J.P., Levene R.B., Ravera C.P.,
RA Morin M.J., Dombalagian M.J., Ricca G., Livingston D.M.,
RA Lynch D.C.;
RT "Molecular cloning of the human gene for von Willebrand factor and
RT identification of the transcription initiation site.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:4393-4397(1987).
RN [16]
RP DISULFIDE BONDS.
RX MEDLINE=88163465; PubMed=3502076;
RA Marti T., Rosselet S.J., Titani K., Walsh K.A.;
RT "Identification of disulfide-bridged substructures within human von
RT Willebrand factor.";
RL Biochemistry 26:8099-8109(1987).
RN [17]
RP STRUCTURE OF CARBOHYDRATES.
RX MEDLINE=86274702; PubMed=3089784;
RA Samor B., Michalski J.C., Debray H., Mazurier C., Goudemand M.,
RA van Halbeek H., Villegenthart J.F.G., Montreuil J.;
RT "Primary structure of a new tetraantennary glycan of the N-
RT acetylactosaminic type isolated from human factor VIII/von
RT Willebrand factor.";
RL Eur. J. Biochem. 158:295-298(1986).
RN [18]
RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 1261-1468.
RX MEDLINE=98221174; PubMed=9553097;
RA Emsley J., Cruz M., Handin R., Liddington R.;
RT "Crystal structure of the von Willebrand factor A1 domain and
RT implications for the binding of platelet glycoprotein Ib.";
RL J. Biol. Chem. 273:10396-10401(1998).
RN [19]
RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF 1685-1873.
RX MEDLINE=97472999; PubMed=9331419;
RA Huijzinga E.G., Martijn van der Plas R., Kroon J., Sixma J.J., Gros P.;
RT "Crystal structure of the A3 domain of human von Willebrand factor:
RT implications for collagen binding.";
RL Structure 5:1147-1156(1997).
RN [20]
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 1686-1872.
RX MEDLINE=97460108; PubMed=9312128;
RA Bienkowska J., Cruz M., Atiemo A., Handin R., Liddington R.;
RT "The von Willebrand factor A3 domain does not contain a metal ion-
RT dependent adhesion site motif.";
RL J. Biol. Chem. 272:25162-25167(1997).
RN [21]
RP VARIANTS TRP-1597 AND ASP-1607.
RX MEDLINE=89264495; PubMed=2786201;
RA Ginsburg D., Konkle B.A., Gill J.C., Montgomery R.R.,
RA Bockenstedt P.L., Johnson T.A., Yang A.Y.;
RT "Molecular basis of human von Willebrand disease: analysis of
RT platelet von Willebrand factor mRNA.";
RL Proc. Natl. Acad. Sci. U.S.A. 86:3723-3727(1989).
RN [22]
RP VARIANT THR-1628.
RX MEDLINE=91196734; PubMed=1673047;
RA Iannuzzi M.C., Hidaka N., Boehnke M., Bruck M.E., Hanna W.T.,
RA Collins F.S., Ginsburg D.;
RT "Analysis of the relationship of von Willebrand disease (vWD) and
RT hereditary hemorrhagic telangiectasia and identification of a
RT potential type IIA vWD mutation (Ile865 to Thr).";
RL Am. J. Hum. Genet. 48:757-763(1991).
RN [23]
RP VARIANTS NORMANDY-2 AND NORMANDY-3.
RX MEDLINE=92001464; PubMed=1832934;
RA Gaucher C., Mercier B., Jorieux S., Oufkir D., Mazurier C.;
RT "Identification of two point mutations in the von Willebrand factor
RT gene of three families with the 'Normandy' variant of von Willebrand
RT disease.";

```
RL Br. J. Haematol. 78:506-514(1991).
RN [24]
RP VARIANT CYS-1308.
RX MEDLINE-92104315; PubMed-1761120;
RA Donner M., Andersson A.-M., Kristoffersson A.-C., Nilsson I.M.,
RA Dahlback B., Holmberg L.;
RT "An Arg545-->Cys545 substitution mutation of the von Willebrand
RT factor in type IIB von Willebrand's disease.";
RL Eur. J. Haematol. 47:342-345(1991).
RN [25]
RP VARIANTS TRP-1306; CYS-1308 AND PRO-1613.
RX MEDLINE-91185601; PubMed-2010538;
RA Randi A.M., Rabinowitz I., Mancuso D.J., Mannucci P.M., Sadler J.E.;
RT "Molecular basis of von Willebrand disease type IIB. Candidate
RT mutations cluster in one disulfide loop between proposed platelet
RT glycoprotein Ib binding sequences.";
RL J. Clin. Invest. 87:1220-1226(1991).
RN [26]
RP VARIANTS TRP-1306; CYS-1308; MET-1316; GLN-1341 AND HIS-1399.
RX MEDLINE-91185602; PubMed-1672694;
RA Cooney K.A., Nichols W.C., Bruck M.E., Bahou W.F., Shapiro A.D.,
Query Match 5.9%; Score 133.5; DB 1; Length 2813;
Best Local Similarity 21.4%; Pred. No. 0.023;
Matches 78; Conservative 38; Mismatches 107; Indels 141; Gaps 19;
QY 44 GNCVPT---CNCQCPGMELSKGCGFGYGAQCVTCRLHFKEDWGFKCKPCLDCAVVR 100
DB 2246 GSCVPEACTQC-----IGEDGV-----QHGFLEAW-VPDHPQICITCLSG 2286
QY 101 FKANGSA-----TSDA-ICGDCPLPGYRKTCLVGFODMEC---VPCGDPPIPPYEPHCAS 151
DB 2287 -RVNCTTQPCPTAKAPTGCGLCEVARLRQADQCCPEYECVCDPVSCDLLPP---VPHCR 2342
QY 152 KYNLVKIATSTASPRDTALAAVICSALATVLLALLILVIYCKRQPMKKPWSLSRQDI 211
DB 2343 -----GLQPTLNPGE-----CRPNP----- 2358
QY 212 QYNGSELCLDRPQLRHEAHACCCQRRDSVOTGVPVRLPSM-----CCCEE---ACSPNP 264
DB 2359 -----TCACRKE-----ECKRVSPSPCPHPR-LPTLRKTQCCDEYECACNCVN 2400
QY 265 ATLCGCVHSAASLQARNAGPAGWVTFPGSLTQSCGFESDAWPL----- 310
DB 2401 STVSCPLGLYLASTATNDCG-----CTTTTCLPKVCHVRSTIYPVQFWEEGCDVCTCT 2454
QY 311 -MNPNGDNIISFCDSP-----ELTGEDIHSLNPELESSTSLDSSNQ 353
DB 2455 DMEDAVNGLRVAOCOKPCEDSCRSRGFTVYLHEGECGRCLPSACEVVTGSPRGDSQSSW 2514
QY 354 DLVG 357
DB 2515 KSVG 2518
RESULT 15
TSPI_MOUSE STANDARD; PRT; 1170 AA.
AC P35441.
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE THROMBOSPONDIN 1 PRECURSOR.
GN THBS1 OR TSPI.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RX MEDLINE-92128941; PubMed-1774063;
RA Lawler J., Duquette M., Ferro P., Copeland N.G., Gilbert D.J.,
RA Jenkins N.A.;
RT "Characterization of the murine thrombospondin gene.";
```

KW Glycoprotein; Cell adhesion; Calcium-binding; Heparin-binding; Repeat; EGF-like domain; Signal.
FT SIGNAL 1 18
FT CHAIN 19 1170
FT DOMAIN 19 232
FT DOMAIN 316 373
FT DOMAIN 379 548
FT DOMAIN 549 690
FT DOMAIN 723 950
FT DOMAIN 951 1170
FT REPEAT 379 430
FT REPEAT 435 491
FT REPEAT 492 548
FT DOMAIN 549 587
FT DOMAIN 588 645
FT DOMAIN 646 690
FT REPEAT 723 758
FT REPEAT 759 781
FT REPEAT 818 840
FT REPEAT 841 878
FT REPEAT 879 914
FT REPEAT 915 950
FT SITE 926 928
FT DISULFID 270 270
FT DISULFID 274 274
FT DISULFID 551 562
FT DISULFID 556 572
FT DISULFID 575 586
FT DISULFID 592 608
FT DISULFID 599 617
FT DISULFID 620 644
FT DISULFID 650 663
FT DISULFID 657 675
FT DISULFID 678 689
FT CARBOHYD 248 248
FT CARBOHYD 360 360
FT CARBOHYD 708 708
FT CARBOHYD 1067 1067
FT CONFLICT 1025 1025
SQ SEQUENCE 1170 AA; 129646 MW; 0443E493615E7F06 CRC64;

Query Match 5.9%; Score 132.5; DB 1; Length 1170;
Best Local Similarity 21.0%; Pred. No. 0.01;
Matches 88; Conservative 39; Mismatches 141; Indels 151; Gaps 25;

QY 26 KVTCTGDCRQEFDRSGNCVPCNQCQPG-----MELSKGCGFY----- 66
DB 350 KVSCLPMPSCNATVPD--GEC--CPRCWPSSDADDGWSWSEWTSCTATCGNGIQGRS 405
QY 67 -----GEDACVTCRLH---REFEDWFGKCKPCLDCA-----VYVREFKAN-- 105
DB 406 CDSLNNRCGSSVQVTRTCHIQECDKRFKQDGGWSHSPWSSCVTCGDGVITRILCNPS 465
QY 106 -----CSATSDAICGCLPLGFYRKTCL 127
DB 466 SPQNGKPCGEARETRACKKADCPINGGWPSPWDICSVT-----CGG---GVQRESRL 518
QY 128 VGFQDMCEVCGDPPPY-EPHCASKYLVKVIATSSPRDTALAIVICSALATVLLALL 186
DB 519 -----CNPPTQFGKDCVGVTEQVNCNKQDCPIDGCLSNP-CFAGAK----- 561
QY 187 ILCVIYCKRFMEKPSLSRSDIOYNGSELSCLDRLPOLHE-----YAHRAACCOCRR-D 240
DB 562 --CYSY-----PDGSKWKGACPPGSGNGIQCKVDCEKVEVPDCAFNHNGEHRKNTD 612
QY 241 SVQTC--GPVRLFPS-----MCEEACSP-NPATLG---CGVHSAASLQARNAGP 284
DB 613 PGYNCLCPPRFTGSPFGRGVEHAMANKQVCKPRNCTDGTGTHDCNKNKACNYLGHYSDP 672
QY 285 --AGENVPTFGSLTQSGICEFS--DAPLMLQNPWGDNISF-----CDSYBELTGED 333

Db 673 MYRCECKPGVAGN--GIICGEDTDLDGWP-NENLVCVANATYHCKKDNCPNLPNSQGED 728

Search completed: February 16, 2001, 21:09:26
Job time: 231 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 16, 2001, 21:05:05 ; Search time 53.31 Seconds
(without alignments)
916.820 Million cell updates/sec

Title: US-09-380-276A-4
Perfect score: 2255
Sequence: 1 MALKVLLLEQEKFTFTLLVLL.....LDQESGAIHPATQTSIQEA 417

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues

Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: SPTREMBL_15:*
- 2: sp_archaea:*
- 3: sp_bacteria:*
- 4: sp_fungi:*
- 5: sp_human:*
- 6: sp_invertebrate:*
- 7: sp_mammal:*
- 8: sp_mhc:*
- 9: sp_organelle:*
- 10: sp_phage:*
- 11: sp_plant:*
- 12: sp_rodent:*
- 13: sp_virus:*
- 14: sp_vertebrate:*
- 15: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	2237	99.2	423	4 Q9NS68	Q9ns68 homo sapien
2	2221	98.5	423	4 Q9NZV2	Q9nzv2 homo sapien
3	1565.5	69.4	416	11 Q9JH6	Q9jh6 mus musculus
4	1563.5	69.3	416	11 Q9JL3	Q9jl3 mus musculus
5	1472.5	65.3	348	11 Q9QXW7	Q9qxw7 mus musculus
6	977	43.3	214	11 Q9JHF1	Q9jhf1 mus musculus
7	725	32.2	150	11 Q9JLL2	Q9jll2 mus musculus
8	197	8.7	448	11 Q9R187	Q9r187 mus musculus
9	191	8.5	448	4 Q9UNE0	Q9une0 homo sapien
10	191	8.5	448	4 Q9UND9	Q9und9 homo sapien
11	170.5	7.6	387	13 Q9PVD4	Q9pvd4 xenopus lae
12	144.5	6.4	430	6 Q9N092	Q9n092 macaca fasc
13	142	6.3	417	11 Q9Z0W1	Q9z0w1 mus musculus
14	142	6.3	426	4 O14865	O14865 homo sapien
15	137.5	6.1	186	12 Q72735	Q72735 cowpox viru
16	136	6.0	625	11 O35305	O35305 mus musculus
17	134.5	6.0	3396	5 Q9VM55	Q9vm55 drosophila
18	134	5.9	186	12 Q9YP87	Q9yp87 cowpox viru
19	134	5.9	277	4 O14866	O14866 homo sapien

20	134	5.9	348	12	O57277	monkeypox v
21	134	5.9	348	12	O57103	monkeypox v
22	134	5.9	348	12	O57108	monkeypox v
23	133.5	5.9	350	12	O57123	cowpox viru
24	133	5.9	543	5	Q9VJ05	Q9vj05 drosophila
25	133	5.9	620	5	Q9NKD8	Q9nk8 drosophila
26	132.5	5.9	3680	5	Q9VR08	Q9vr08 drosophila
27	131.5	5.8	349	12	O57291	monkeypox v
28	131.5	5.8	349	12	O57099	monkeypox v
29	131.5	5.8	349	12	O57100	monkeypox v
30	131.5	5.8	349	12	O57101	monkeypox v
31	131.5	5.8	349	12	O57102	monkeypox v
32	130	5.8	186	12	O9WJB4	Q9wj4 vaccinia vi
33	129.5	5.7	1254	13	Q9YHU2	Q9yhu2 brachydanio
34	128	5.7	347	12	O57115	cowpox viru
35	128	5.7	355	12	O85308	cowpox viru
36	128	5.7	401	13	Q9PRG7	Q9prg7 xenopus lae
37	127.5	5.7	349	12	O57111	variolela vir
38	127	5.6	1114	11	Q9JKW7	Q9jkw7 mus musculu
39	127	5.6	1650	11	Q9QVT6	Q9qvt6 rattus sp.
40	127	5.6	1792	13	O57484	Q57484 gallus gall
41	127	5.6	1827	5	O20535	Q20535 caenorhabdi
42	126.5	5.6	380	4	O00280	homo sapien
43	126.5	5.6	1394	5	Q9VS89	Q9vs89 drosophila
44	126	5.6	349	12	O57305	cowpox viru
45	126	5.6	350	12	O57116	cowpox viru

ALIGNMENTS

RESULT 1	
Q9NS68	
ID Q9NS68	PRELIMINARY: PRT: 423 AA.
AC Q9NS68	
DT 01-OCT-2000 (TREMBLrel. 15, Created)	
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)	
DE HTROY.	
DE 01-OCT-2000 (TREMBLrel. 15, Last annotation update)	
GN HTROY.	
OS Homo sapiens (Human).	
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
OX NCBI_TaxID=9606;	
RN [1]	
RP SEQUENCE FROM N.A.	
RA Kojima T., Morikawa Y., Copeland N.G., Gilbert D.J., Jenkins N.A.,	
RA Senba E., Kitamura T.;	
RT "TROY, a newly identified member of the tumor necrosis factor receptor	
RT superfamily, exhibits a homology with Edar and is expressed in	
RT embryonic skin and hair follicles";	
RL J. Biol. Chem. 275:20742-20747(2000).	
DR EMBL; AB040434; BAB03269.1; -;	
SQ SEQUENCE 423 AA; 46015 MW; B5891CEA9ED45361 CRC64;	

Query Match	99.2%; Score 2237; DB 4; Length 423;
Best Local Similarity	99.3%; Pred. No. 2.9e-199;
Matches 412; Conservative 2; Mismatches 1; Indels 0; Gaps 0;	
Qy 1 MALKVLLLEQEKFTFTLLVLLGYLSCKVTCETGDCRQOEFRDRSGNVCPCNQCQPGMELSK 60	
Db 1 MALKVLLLEQEKFTFTLLVLLGYLSCKVTCESGDCRQOEFRDRSGNVCPCNQCQPGMELSK 60	
Qy 61 ECGFGYGEDAQCVTCRLHFRKEDMGFKCKPCLDCAVNVRFQKANCATSATSDAICGDCPLG 120	
Db 61 ECGFGYGEDAQCVTCRLHFRKEDMGFKCKPCLDCAVNVRFQKANCATSATSDAICGDCPLG 120	
Qy 121 FYRKYKLVCFQDMECVPCGDPDPPEPHPCASKNLVKIATASSPPDPTALAAVICSALAT 180	
Db 121 FYRKYKLVCFQDMECVPCGDPDPPEPHPCASKNLVKIATASSPPDPTALAAVICSALAT 180	
Qy 181 VLLALLILCVIYCKRQFMKPKPSWLSRSDIQYNGSELSCLDPRPQLHAYHRAACQCRRD 240	

```
Db 181 VLLALLILCIYKROFMKPKSWLSRSDIQYNGSELSCFDRPQLHEYAHRAACCCRRD 240
Qy 241 SVOTCGPVRLLPSCMCCBEACSPNATLGGCVHSAASLQARNAGPAGEMVPTFFGSLTQSI 300
Db 241 SVOTCGPVRLLPSCMCCBEACSPNATLGGCVHSAASLQARNAGPAGEMVPTFFGSLTQSI 300
Qy 301 CGEFSDAWPLMQNPMGMDNISFCDSYPELTGEDIHSLNPELESSTLSDNSSQDLVGGAV 360
Db 301 CGEFSDAWPLMQNPMGMDNISFCDSYPELTGEDIHSLNPELESSTLSDNSSQDLVGGAV 360
Qy 361 PVQSHSENFTAATDLSRYNNLTVESASTQDALTMRSOLDQESGAIHPATQTSIQ 415
Db 361 PVQSHSENFTAATDLSRYNNLTVESASTQDALTMRSOLDQESGAIHPATQTSIQ 415

RESULT 2
Q9NZV2
ID Q9NZV2 PRELIMINARY; PRT; 423 AA.
AC Q9NZV2;
DT 01-OCT-2000 (TEMBLrel. 15, Created)
DT 01-OCT-2000 (TEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TEMBLrel. 15, Last annotation update)
DE TAJ-ALPHA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Eby M.T., Jasmin A., Kumar A., Sharma K., Chaudhary P.M.;
RT "TAJ, a Novel Member of the Tumor Necrosis Factor Receptor Family,
RT Activates the c-Jun N-terminal Kinase Pathway and Mediates Caspase-
RT Independent Cell Death."
RL J. Biol. Chem. 275:15336-15342(2000).
DR EMBL: AF167555; AAF1828.1; -.
SQ SEQUENCE 423 AA; 46071 MW; BB7C9917132A4B2F CRC64;
```

```
Query Match 98.5%; Score 2221; DB 4; Length 423;
Best Local Similarity 98.8%; Pred. No. 8.8e-198;
Matches 409; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MALKVLEQEKTFETLLVLLGYLSCKVTCTGDCRQOEFRDRSGNCVPCNQCGPMELSK 60
Db 1 MALKVLEQEKTFETLLVLLGYLSCKVTCTGDCRQOEFRDRSGNCVPCNQCGPMELSK 60
Qy 61 ECGFGYGEDAQCVTRLHREKEDWGFKCKPCLDCAVVRNFRKANCATSADAICGDCPLG 120
Db 61 ECGFGYGEDAQCVTRLHREKEDWGFKCKPCLDCAVVRNFRKANCATSADAICGDCPLG 120
Qy 121 FYRKTCLVGFQDMCEVPCGDPPEPPHPCASKVNLVKIASTASSPRDTALAAVICSALAT 180
Db 121 FYRKTCLVGFQDMCEVPCGDPPEPPHPCASKVNLVKIASTASSPRDTALAAVICSALAT 180
Qy 181 VLLALLILCIYKROFMKPKSWLSRSDIQYNGSELSCFDRPQLHEYAHRAACCCRRD 240
Db 181 VLLALLILCIYKROFMKPKSWLSRSDIQYNGSELSCFDRPQLHEYAHRAACCCRRD 240
Qy 241 SVOTCGPVRLLPSCMCCBEACSPNATLGGCVHSAASLQARNAGPAGEMVPTFFGSLTQSI 300
Db 241 SVOTCGPVRLLPSCMCCBEACSPNATLGGCVHSAASLQARNAGPAGEMVPTFFGSLTQSI 300
Qy 301 CGEFSDAWPLMQNPMGMDNISFCDSYPELTGEDIHSLNPELESSTLSDNSSQDLVGGAV 360
Db 301 CGEFSDAWPLMQNPMGMDNISFCDSYPELTGEDIHSLNPELESSTLSDNSSQDLVGGAV 360
Qy 361 PVQSHSENFTAATDLSRYNNLTVESASTQDALTMRSOLDQESGAIHPATQTSIQ 415
Db 361 PVQSHSENFTAATDLSRYNNLTVESASTQDALTMRSOLDQESGAIHPATQTSIQ 415

RESULT 3
```

```
Q9JHH6
ID Q9JHH6 PRELIMINARY; PRT; 416 AA.
AC Q9JHH6;
DT 01-OCT-2000 (TEMBLrel. 15, Created)
DT 01-OCT-2000 (TEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TEMBLrel. 15, Last annotation update)
DE TROY.
GN TROY.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Kojima T., Morikawa Y., Copeland N.G., Gilbert D.J., Jenkins N.A.,
RA Senba E., Kitamura T.;
RT "TROY, a newly identified member of the tumor necrosis factor receptor
RT superfamily, exhibits a homology with Edar and is expressed in
RT embryonic skin and hair follicles."
RL J. Biol. Chem. 275:20742-20747(2000).
DR EMBL: AB040432; BAB03267.1; -.
SQ SEQUENCE 416 AA; 45265 MW; 9BDC7C7A2D6A9C47 CRC64;

Query Match 69.4%; Score 1565.5; DB 11; Length 416;
Best Local Similarity 70.4%; Pred. No. 4.9e-137;
Matches 295; Conservative 35; Mismatches 84; Indels 5; Gaps 3;

Qy 1 MALKVLEQEKTFETLLVLLGYLSCKVTCTGDCRQOEFRDRSGNCVPCNQCGPMELSK 60
Db 1 MALKVLEQEKTFETLLVLLGYLSCKVTCTGDCRQOEFRDRSGNCVPCNQCGPMELSK 60
Qy 61 ECGFGYGEDAQCVTRLHREKEDWGFKCKPCLDCAVVRNFRKANCATSADAICGDCPLG 120
Db 61 ECGFGYGEDAQCVTRLHREKEDWGFKCKPCLDCAVVRNFRKANCATSADAICGDCPLG 120
Qy 121 FYRKTCLVGFQDMCEVPCGDPPEPPHPCASKVNLVKIASTASSPRDTALAAVICSALAT 180
Db 121 FYRKTCLVGFQDMCEVPCGDPPEPPHPCASKVNLVKIASTASSPRDTALAAVICSALAT 180
Qy 181 VLLALLILCIYKROFMKPKSWLSRSDIQYNGSELSCFDRPQLHEYAHRAACCCRRD 240
Db 181 VLLALLILCIYKROFMKPKSWLSRSDIQYNGSELSCFDRPQLHEYAHRAACCCRRD 240
Qy 241 SVOTCGPVRLLPSCMCCBEACSPNATLGGCVHSAASLQARNAGPAGEMVPTFFGSLTQSI 300
Db 241 SVOTCGPVRLLPSCMCCBEACSPNATLGGCVHSAASLQARNAGPAGEMVPTFFGSLTQSI 300
Qy 301 CGEFSDAWPLMQNPMGMDNISFCDSYPELTGEDIHSLNPELESSTLSDNSSQDLVGGAV 360
Db 301 CGEFSDAWPLMQNPMGMDNISFCDSYPELTGEDIHSLNPELESSTLSDNSSQDLVGGAV 360
Qy 361 PVQSHSENFTAATDLSRYNN--TLVESASTQDALTMRSOLDQESGAIHPATQTSIQ 417
Db 359 -ALESSGNVSESTSPRHGDTGTWQETLAQDAQRTPSQGGWEDRENLNLAAPTAFQDA 416

RESULT 4
Q9JLL3
ID Q9JLL3 PRELIMINARY; PRT; 416 AA.
AC Q9JLL3;
DT 01-OCT-2000 (TEMBLrel. 15, Created)
DT 01-OCT-2000 (TEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TEMBLrel. 15, Last annotation update)
DE TAJ-ALPHA LONG.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Eby M.T., Jasmin A., Kumar A., Sharma K., Chaudhary P.M.;
RT "TAJ, a Novel Member of the Tumor Necrosis Factor Receptor Family,
```

RT Activates the c-Jun N-terminal Kinase Pathway and Mediates Caspase-independent Cell Death.";
RL J. Biol. Chem. 275:15336-15342(2000).
DR EMBL: AF167552; AAF1825.1; -
SQ SEQUENCE 416 AA; 45294 MW; 19CA2B75DD7B9D49 CRC64;

Query Match 69.3%; Score 1563.5; DB 11; Length 416;
Best Local Similarity 70.4%; Pred. No. 7.5e-137;
Matches 295; Conservative 34; Mismatches 85; Indels 5; Gaps 3;

```
QY 1 MALKVLEOEKTFLLVLLGYLSKVCETGDCRQOEFRDRSGNCVPCNOCGPGMELSK 60
DB 1 MALKVLPPLHRTVLFALFLHLACKVSCETGDCRQOEFKDRSGNCVLCKQCGPGMELSK 60
QY 61 ECGFGYGEDAQCVCRLHREFKEDWGFCCKPCLDCAVNVRFKANCATSDAICGDCPLG 120
DB 61 ECGFGYGEDAQCVCPRPHREFKEDWGFCCKPCADCALVNRFORANCSTSDAVCGDCPLG 120
QY 121 FYRKTGLVGFQDMCVPCGDDPPPPYEPHCASKVNLVKIATASSPRDTALAAVICSALAT 180
DB 121 FYRKTGLVGFQDMCVPCGDDPPPPYEPHCCTSKVNLVKISSTVSSPRDTALAAVICSALAT 180
QY 181 VLLALLILCVYCKQFMEKPSWSLSRSDIOYNGSELSCLDPRPOLHEYAHRACCCRRD 240
DB 181 VLLALLILCVYCKQFMEKPSWSLSRSDIOYNGSELSCFDPQRLRHCARACCCYHRD 240
QY 241 SVOTCGPVRLLPSMCEACSPNATLGGVHSAASLQARNAGPAGVMVPTFFGSILTOSI 300
DB 241 SAPMGPVHLIPSLCCSEARSARAVLGGGLSRPTTLQERNPASVGNWTPAFFGVSRSI 300
QY 301 CGEFSADWPLMONGMGNISFCDSPYELTGEDIHSLNPEL 341
DB 301 CAEFSADWPLMONGPLGGDS-SLDCSYPELTGDTNLSNPEM 340
QY 361 PVQSHSENFATDLSRYNN--TLVESASTQDALWRSQDOESGAIHPATQTSLOEA 417
DB 359 -ALESSGNVSESTDSPRHGDGTGVMEQTALQADQRTPSQGWEDRENLMPTAFQDA 416
RESULT 5
QYQXW7 PRELIMINARY: PRT: 348 AA.
AC Q9QXW7
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE TNFRSF19.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Hu S., Tamada K., Ni J., Vincenz C., Chen L.;
RT "Characterization of TNFRSF19, a novel member of tumor necrosis factor
RT receptor superfamily.";
RL Genomics 62:103-107(1999).
DR EMBL: AF173166; AAF19795.1; -
DR INTERPRO: IPR001368; -
DR PFM: PF00020; TNFR_C6; 2.
DR PROSITE: PS00552; TNFR_NGFR_1; UNKNOWN_2.
DR PROSITE: PS00550; TNFR_NGFR_2; 1.
SQ SEQUENCE 348 AA; 38450 MW; 013C799638F8E333 CRC64;
```

Query Match 65.3%; Score 1472.5; DB 11; Length 348;
Best Local Similarity 77.7%; Pred. No. 1.7e-128;
Matches 265; Conservative 24; Mismatches 51; Indels 1; Gaps 1;

```
QY 1 MALKVLEOEKTFLLVLLGYLSKVCETGDCRQOEFRDRSGNCVPCNOCGPGMELSK 60
DB 1 MALKVLPPLHRTVLFALFLHLACKVSCAGDCRQOEFKDRSGNCVLCKQCGPGMELSK 60
```

```
QY 61 ECGFGYGEDAQCVCRLHREFKEDWGFCCKPCLDCAVNVRFKANCATSDAICGDCPLG 120
DB 61 ECGFGYGEDAQCVCPRPHREFKEDWGFCCKPCADCALVNRFORANCSTSDAVCGDCPLG 120
QY 121 FYRKTGLVGFQDMCVPCGDDPPPPYEPHCASKVNLVKIATASSPRDTALAAVICSALAT 180
DB 121 FYRKTGLVGFQDMCVPCGDDPPPPYEPHCCTSKVNLVKISSTVSSPRDTALAAVICSALAT 180
QY 181 VLLALLILCVYCKQFMEKPSWSLSRSDIOYNGSELSCLDPRPOLHEYAHRACCCRRD 240
DB 181 VLLALLILCVYCKQFMEKPSWSLSRSDIOYNGSELSCFDPQRLRHCARACCCYHRD 240
QY 241 SVOTCGPVRLLPSMCEACSPNATLGGVHSAASLQARNAGPAGVMVPTFFGSILTOSI 300
DB 241 SAPMGPVHLIPSLCCSEARSARAVLGGGLSRPTTLQERNPASVGNWTPAFFGVSRSI 300
QY 301 CGEFSADWPLMONGMGNISFCDSPYELTGEDIHSLNPEL 341
DB 301 CAEFSADWPLMONGPLGGDS-SLDCSYPELTGDTNLSNPEM 340
RESULT 6
QYQJHF1 PRELIMINARY: PRT: 214 AA.
AC Q9JHF1
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DE DTROY (TAJ-ALPHA SHORT).
GN DTROY.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Kojima T., Morikawa Y., Copeland N.G., Gilbert D.J., Jenkins N.A.,
RA Senba E., Kitamura T.;
RT "TROY, a newly identified member of the tumor necrosis factor receptor
RT superfamily, exhibits a homology with Eder and is expressed in
RT embryonic skin and hair follicles.";
RL J. Biol. Chem. 275:20742-20747(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Eby M.T., Jasmin A., Kumar A., Sharma K., Chaudhary P.M.;
RT "TAJ, a Novel Member of the Tumor Necrosis Factor Receptor Family,
RT Activates the c-Jun N-terminal Kinase Pathway and Mediates Caspase-
RT Independent Cell Death.";
RL J. Biol. Chem. 275:15336-15342(2000).
DR EMBL: AB040433; BAB03268.1; -
DR EMBL: AF167553; AAF1826.1; -
SQ SEQUENCE 214 AA; 23564 MW; ECC63981C37482B8 CRC64;
```

Query Match 43.3%; Score 977; DB 11; Length 214;
Best Local Similarity 84.6%; Pred. No. 8e-83;
Matches 176; Conservative 10; Mismatches 22; Indels 0; Gaps 0;

```
QY 1 MALKVLEOEKTFLLVLLGYLSKVCETGDCRQOEFRDRSGNCVPCNOCGPGMELSK 60
DB 1 MALKVLPPLHRTVLFALFLHLACKVSCETGDCRQOEFKDRSGNCVLCKQCGPGMELSK 60
QY 61 ECGFGYGEDAQCVCRLHREFKEDWGFCCKPCLDCAVNVRFKANCATSDAICGDCPLG 120
DB 61 ECGFGYGEDAQCVCPRPHREFKEDWGFCCKPCADCALVNRFORANCSTSDAVCGDCPLG 120
QY 121 FYRKTGLVGFQDMCVPCGDDPPPPYEPHCASKVNLVKIATASSPRDTALAAVICSALAT 180
DB 121 FYRKTGLVGFQDMCVPCGDDPPPPYEPHCCTSKVNLVKISSTVSSPRDTALAAVICSALAT 180
QY 181 VLLALLILCVYCKQFMEKPSWSLSR 208
|||||
```

Db 181 VLLALLILCVYCKRQFMKKPSKLP 208

RESULT 7

ID Q9JLL2 PRELIMINARY; PRT; 150 AA.

AC Q9JLL2;

DT 01-OCT-2000 (TReMBLrel. 15, Created)

DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)

DT 01-OCT-2000 (TReMBLrel. 15, Last annotation update)

DE TAJ-BETAL.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RA Eby M.T., Jasmin A., Kumar A., Sharma K., Chaudhary P.M.;

RT "TAJ, a Novel Member of the Tumor Necrosis Factor Receptor Family,

RT Activates the c-Jun N-terminal Kinase Pathway and Mediates Caspase-

RL Independent Cell Death.";

RL J. Biol. Chem. 275:15336-15342(2000).

DR EMBL; AF167554; AAF71827.1; -.

SQ SEQUENCE 150 AA; 16728 MW; 4A1B2E93ABEF7FF43 CRC64;

Query Match 32.2%; Score 725; DB 11; Length 150;

Best Local Similarity 82.6%; Pred. No. 1.2e-59;

Matches 123; Conservative 9; Mismatches 17; Indels 0; Gaps 0;

QY 1 MALKVLLEQEKTEFTLLVLGLYLSKVTCTGDCRQEQFRDRSGNCVPCNQCQPGMELSK 60

DB 1 MALKVLPLHRTVLFATLLHLLACKVSCETGDCRQEQFKDRSGNCVLCQCGPGMELSK 60

QY 61 ECGFGYGEDAQCVTCRLHRFKEDWGQCKPCLDCAVNRFOKANSATSDAICGDCPLG 120

DB 61 ECGFGYGEDAQCVPCPHRFKEDWGQCKPCADALVNRFORANGSHTSDAYCGDCPLG 120

QY 121 FYRKTLLGVQDMQPCGPPPPYEPHC 149

DB 121 FYRKTLLGVQDMQPCGPPPPYEPHC 149

RESULT 8

ID Q9R187 PRELIMINARY; PRT; 448 AA.

AC Q9R187;

DT 01-MAY-2000 (TReMBLrel. 13, Created)

DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)

DT 01-OCT-2000 (TReMBLrel. 15, Last annotation update)

DE ECTODERMAL DYSPLASIA RECEPTOR.

GN EDAR OR DL.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=99364417; PubMed=10431242;

RA Headon D.J., Overbeek P.A.;

RT "Involvement of a novel Tnf receptor homologue in hair follicle

RT Induction.";

RL Nat. Genet. 22:370-374(1999).

DR EMBL; AF160502; AAD50425.1; -.

DR MGD; MGI:1343498; Edar.

KW Receptor.

SQ SEQUENCE 448 AA; 48434 MW; FCCAF38F3D6BB971 CRC64;

Query Match 8.7%; Score 197; DB 11; Length 448;

Best Local Similarity 28.2%; Pred. No. 3.6e-10;

Matches 61; Conservative 32; Mismatches 83; Indels 40; Gaps 11;

QY 16 LVLVLLGLSKVTCETGDCRQEQFRDR-SGNCVPCNQCQPGMELSKGCGFG-YGEDAQCV 73

DB 13 LPVLVVLMSAKAEDSNGENEYHNQTTGLCQCCPPCRGPEPYMSCGVTGKDDYGCY 72

QY 74 TCRHFRKEDWGQCKPCLDCAVNRFOKANC-----SATSDAICGDCPLPGFY----RKT 125

DB 73 PCPAERFSKG-GYQICRRHKDC---EGFFRATVLTTPGDMENDAECCGCLPGYTMLENRPR 128

QY 126 KLGVFQDMQPCGDPDPPEPHCAKSNVLVKI-----ASTASSPRDTA-----L 170

DB 129 NIYG---WVCYSC-LLAPPNTKECVGATSGASANFFCTSGSSTLSLSPFQHAHKELSGQHL 184

QY 171 AAVICSALATVL---LALLILCVYCKRQFMKKPS 203

DB 185 ATALLIATSTIFIMATIAIVLIIMFY---ILKTKPS 216

RESULT 10

Q9UND9

ID Q9UND9 PRELIMINARY; PRT; 448 AA.

AC Q9UND9;

DT 01-MAY-2000 (TReMBLrel. 13, Created)

DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)

DT 01-MAY-2000 (TReMBLrel. 13, Last annotation update)

DE ECTODYSPLASIN-A RECEPTOR PROTEIN.

GN EDAR.

OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99364416; PubMed=10431241;
 RA Monreal A.W., Ferguson B.M., Headon D.J., Street S.L., Overbeek P.A.,
 RA Zonana J.;
 RT "Mutations in the human homologue of mouse dl cause autosomal
 RT recessive and dominant hypohidrotic ectodermal dysplasia.";
 RL Nat. Genet. 22:366-369(1999).
 DR EMBL; AF130996; AAD50077.1; .
 DR EMBL; AF130990; AAD50077.1; JOINED.
 DR EMBL; AF130991; AAD50077.1; JOINED.
 DR EMBL; AF130992; AAD50077.1; JOINED.
 DR EMBL; AF130993; AAD50077.1; JOINED.
 DR EMBL; AF130994; AAD50077.1; JOINED.
 DR EMBL; AF130995; AAD50077.1; JOINED.
 KW Receptor.
 SQ SEQUENCE 448 AA; 48572 MW; AC8F80F79CB255EA CRC64;

Query Match 8.5%; Score 191; DB 4; Length 448;
 Best Local Similarity 28.7%; Pred. No. 1.3e-09;
 Matches 62; Conservative 30; Mismatches 84; Indels 40; Gaps 12;

QY 16 LVLVLLGYLSKVTCTGDCRQOEFRRD-SGNCVPCNQCQPGMELSKGFG-YGDAOCV 73
 DB 13 LPLVVLVSLMCSARAESYNGENEYNOTGLQCPCPGGEEPYLSGCGYTKDEDYGCV 72

QY 74 TCRHREKEDWGFKCKPCCLDCAVNRFQKANC-----SATSDAICGDLPGFY-----RT 125
 DB 73 PCPAEKFSKG-GYQICRRHKDC---EGFRATVLPFGDMENDAECPCLPGYMYLENRPR 128

QY 126 KLIVGFQDMECVCPGDPDPPEPHCASKNLVKI-----ASTASSPRDTA-----L 170
 DB 129 NIYG---MVCYSC-LAPNTKECVGATSGASANFPGTSGSSTLSPFQHAHKLMSGQHL 184

QY 171 AAVICSALATVL---LALLILCVYCKRQFMKKPS 203
 DB 185 ATALLIAMSTIFMAIAVLIIMFY-----ILTKPS 216

RESULT 11
 Q9PVD4 PRELIMINARY; PRT; 387 AA.
 AC Q9PVD4
 DT 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
 DT 01-OCT-2000 (Tremblrel. 15, Last annotation update)
 DE P75-LIKE TRANSMEMBRANE PROTEIN FULLBACK.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipiloidea; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Hick E., Sun B.I., Collins-Racie L., LaVallie E., Sive H.L.;
 RT "Identification and Characterization of fullback, a Novel Posteriorly-
 RT Expressed Xenopus Gene.";
 RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF131890; AAD54072.1; .
 DR HSP; P07174; INGR.
 DR INTERPRO; IPR000488; .
 DR INTERPRO; IPR001368; .
 DR PFAM; PF00020; TNFR_c6; 4.
 DR PFAM; PF00531; death; 1.
 DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_3.
 DR PROSITE; PS50017; DEATH_DOMAIN; 1.
 DR PROSITE; PS50050; TNFR_NGFR_2; 4.
 KW Transmembrane.

SQ SEQUENCE 387 AA; 42066 MW; 1A386A239C7C8A82 CRC64;
 Query Match 7.6%; Score 170.5; DB 13; Length 387;
 Best Local Similarity 23.6%; Pred. No. 8.7e-08;
 Matches 69; Conservative 35; Mismatches 93; Indels 95; Gaps 15;

QY 16 LVLVLLGYLSKVTCTGDCRQOEFRRD-SGNCVPCNQCQPGMELSKGFGYGEDAQCVTC 75
 DB 12 LLLLSKISAEDVCESG-----LYTNSGKC--CSLCPAGFGVVVPCG---DSDTKCEPC 60

QY 76 RLHRPKEDWGFG-----KCKPCCLDCAVNRFQKANCATSDAIC-----GDC 117
 DB 61 -----IENSTFSDVRSAAKAKQPCFTQCSPSLTLESNCTREODTVCRCPEROYLDNSGIC 115

QY 118 LP-----GFKRTKLVGFQDMECVPC-----G 139
 DB 116 LPCQLCSKGGHGVVSOCITNKNTVQLCSGGFYSEVK---SSPCLPCRTECKETEVOIG 172

QY 140 DPPPPEPHCASK-VNLVK-----IASTASS-----PRDTA--LAAVICSALATVLLALL 186
 DB 173 DCVPQHDILCDKQVPILKRTGEGENGTSAGSPHPIDQNSKNIIPVYCSILAAVVVGLI 232

QY 187 ILCVYCKRQFMKKPSWSLSRQDI--QYNGSELS-----CLDRPOLHEYAH 231
 DB 233 AYVAFKCYTCTCKQKKQAKARAGELATSTEGEKLHNDSGVFLDTHSLOEPNH 284

RESULT 12
 Q9N092 PRELIMINARY; PRT; 430 AA.
 AC Q9N092
 DT 01-OCT-2000 (Tremblrel. 15, Created)
 DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
 DT 01-OCT-2000 (Tremblrel. 15, Last annotation update)
 DE UNNAMED PORTEIN PRODUCT.
 OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
 OC Cercopitheciinae; Macaca.
 OX NCBI_TaxID=9541;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K.,
 RA Suzuki Y., Sugano S., Hashimoto K.;
 RT "Isolation of full-length cDNA clones from macaque brain CDNA
 RT libraries.";
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB046039; BAB01621.1; .
 SQ SEQUENCE 430 AA; 45850 MW; BABDE92593E1E859 CRC64;

Query Match 6.4%; Score 144.5; DB 6; Length 430;
 Best Local Similarity 21.3%; Pred. No. 2.5e-05;
 Matches 57; Conservative 29; Mismatches 83; Indels 99; Gaps 8;

QY 51 QCGPGMELSKGFGYGEDAQCVTCRLHRFKEDWGFKQCKPCCLDCAVNRFQKANCATS 110
 DB 31 QCGPG-----EEDPLNPGQGTLCRPPPGTFSAAWSSPCQPHARSLQRLAQQVGTATQ 86

QY 111 DAICGDLPGFYKRTKLVGFQDMECVCPGDPDPPEPHCASKNL-----VK 157
 DB 87 DTLCGDCWPGWFG-----PWGVRVPCQPCSWAPLGIHGCDGEMRRARRGVE 133

QY 158 IASTASS-----PRDTALA-AVICASALATVLLALLILCVYCKRQFMKK 201
 DB 134 VAAAGASSGGETRQPGNGTRAGGPEETAQYAVI--AIVPVFCLMGLLGLVLC----- 183

QY 202 PWSLSRQDIQYNGSELSCLDRPOLHEVAHRACCCRRDSVQTCGVRLLPSMCCEEACS 261
 DB 184 -----NLLKRGYHCTAHK-----EVG 200

QY 262 PNPATIGCGVHSAASLIQARNAGPAGEMV 289

Db 201 PGPGGGSGINPAYRTEDVNEGTIGLV 228

RESULT 13

Q9Z0W1
ID Q9Z0W1 PRELIMINARY; PRT; 417 AA.
AC Q9Z0W1;
DT 01-MAY-1999 (Tremblrel. 10, Created)
DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)
DT 01-MAY-2000 (Tremblrel. 13, Last annotation update)
DE NERVE GROWTH FACTOR RECEPTOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A;
RX MEDLINE=99077793; PubMed=9857182;
RA Tuffreau C., Benjean J., Blondel D., Kieffer B., Flament A.;
RT "Low-affinity nerve-growth factor receptor (p75NTR) can serve as a
RT receptor for rabies virus";
RL EMBO J. 17:7250-7259(1998).
DR EMBL; AF105292; AAD17943.1;
DR HSSP; P07174; INGR.
DR INTERPRO: IPR000488;
DR INTERPRO: IPR000561;
DR INTERPRO: IPR000734;
DR INTERPRO: IPR001368;
DR PFAM; PF00020; TNFR_C6; 4.
DR PROSITE; PS00420; TNFR_NGFR_1; 3.
DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
DR PROSITE; PS50017; DEATH_DOMAIN; 1.
DR PROSITE; PS50050; TNFR_NGFR_2; 4.
KW Receptor.
SQ SEQUENCE 417 AA; 44686 MW; 5D7A4510DB8AF9B2 CRC64;

Query Match 6.3%; Score 142; DB 11; Length 417;

Best Local Similarity 22.4%; Pred. No. 4.2e-05;

Matches 93; Conservative 50; Mismatches 178; Indels 94; Gaps 23;

QY 7 LEQETFTLLVLLG--YLCKVTCETGDCRQOEFDRSGNCVPCNQCGMELSKCGF 64
Db 1 MRLRLLLLLLLLVSGGAKETCTG-----MYTHSGEC--CKACNLGEGVAQPCG- 51
QY 65 GYGEDAQCVCRLHREKED--WGFOCKPCLDCAVNVRFQKNCATSDAICGDCLPGFY 122
Db 52 --ANQTVCEPCLDSTVFSVDVSTATEPCKPCTECLGL-QSMAPCVADDAVC-RCSYGY 107
QY 123 RYTKLVGFQDME-----CVPCGDPPPPYEPHCASKNVLV-----KIATASSPRDTAL 170
Db 108 -----QDEETGRCEACSVCG-VGSLGVFSQDKQNTVCECPGTYSDANHVDPCL 158
QY 171 AAVICSAATVLLALLILCVYKRFMEKKPSWSLSRSODIQNGSELSCLDRLPQLHEYA 230
Db 159 PCTVCEDTERQLRE----CTPWADAEEETIPGRWITRTPPE--GSDVT---TPSTQE-- 207
QY 231 HRACCCCRDRSVOTCGPVR-LLPMSMCEEACSPNATLPGCVHSAASLQARNAGPAGEMV 289
Db 208 -----PEAPERDLIASTVAD-----TVITVMGSSQPVVTR--GTADNLI 245
QY 290 PTFPGSLTSQICEFS-----DAMPLQNMPPMGDNISFCDSYPELTGEDIHSLNPELESST 345
Db 246 PIVYCSILAAVVGVLVYIAFKRNWSCONKQGANSPVNTQTPPEGEKLSH-----DSGI 300
QY 346 SLDSNSSQDLVGGAVPQSHSENFATDLSRYNNLTVESASTQDALTWRSOLDQ 400
Db 301 SVDSQSQSHD-----QOHTQ--TASQAALKGDNLYSSL-----PLTKREEVEK 342

RESULT 14

O14865
ID O14865 PRELIMINARY; PRT; 426 AA.
AC O14865;
DT 01-JAN-1998 (Tremblrel. 05, Created)
DT 01-JAN-1998 (Tremblrel. 05, Last sequence update)
DT 01-OCT-2000 (Tremblrel. 15, Last annotation update)
DE DEATH RECEPTOR 3 BETA.
GN DR3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98113360; PubMed=9446802;
RA Warzocha K., Ribeiro P., Charlot C., Renard N., Coiffier B.,
RA Salles G.;
RT "A new death receptor 3 isoform: expression in human lymphoid cell
RT lines and non-Hodgkin's lymphomas";
RL Biochem. Biophys. Res. Commun. 242:376-379(1998).
DR EMBL; AF026070; AAC39556.1;
DR HSSP; P19438; INCF.
DR INTERPRO: IPR000488;
DR INTERPRO: IPR000561;
DR INTERPRO: IPR001368;
DR PFAM; PF00020; TNFR_C6; 2.
DR PFAM; PF00531; death; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
DR PROSITE; PS50017; DEATH_DOMAIN; 1.
DR PROSITE; PS50050; TNFR_NGFR_2; 1.
SQ SEQUENCE 426 AA; 45950 MW; 371AA7F16AD29C16 CRC64;

Query Match 6.3%; Score 142; DB 4; Length 426;

Best Local Similarity 25.2%; Pred. No. 4.3e-05;

Matches 66; Conservative 26; Mismatches 70; Indels 100; Gaps 14;

QY 34 CROQEFDRSGNC--VPCNQCG--POMELSKCGFGYGEDAQCVTCRLHREKEDWGFGKC 89
Db 95 CDEQASQVALENCASVADTRCGCKPGFV--EC-----QVSCQVSSSPF-----YC 138
QY 90 KPCLDCAVNVRFQKNCATSDAICGDCLPGFYKTKLVGFQDMECVPCGDPPPPYEPHC 149
Db 139 QPCLDQCALHRTLLCS--RRDFDCGTCLPGFYE-----HGDGCVSCTPTPP----- 184
QY 150 ASKVNVLKIASTASSPRDTALAAVICSAL-----ATVLLALLILCVYCKRQPMKK 201
Db 185 -----SLAGAPWGVAVQSAVPLSVAGRGVGVFWQVLLAGLVPLLL----- 225
QY 202 PSWSLSRSODIQNGSELSCLDRLPQLHEYAHRAACCCQCRDRSVQTCGVRLLPSMCCE----- 257
Db 226 -----GATLT-----YTYRH-----CWPBK--PLVTADAEAGM 250
QY 258 EACSPNPATLPGCVHSAASLQA 279
Db 251 EALTTPPPATHLSPDLSAHTLLA 272

RESULT 15

O72735
ID O72735 PRELIMINARY; PRT; 186 AA.
AC O72735;
DT 01-AUG-1998 (Tremblrel. 07, Created)
DT 01-AUG-1998 (Tremblrel. 07, Last sequence update)
DT 01-OCT-2000 (Tremblrel. 15, Last annotation update)
DE A53R PROTEIN.
GN A53R.
OS Cowpox virus (CPV).
OC Viruses; GSDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.

```
OX NCBI_TaxID-10243;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN-GRI-90;
RX MEDLINE-98229462; PubMed-9568042;
RA Shchelkunov S.N., Saifonov P.F., Totmenin A.V., Petrov N.A.,
RA Ryazankina O.I., Gutorov V.V., Kotwal G.J.;
RT "The genomic sequence analysis of the left and right species-specific
RT terminal region of a cowpox virus strain reveals unique sequences and
RT a cluster of intact ORFs for immunomodulatory and host range
RT proteins";
RL Virology 243:432-460(1998).
DR EMBL; Y15035; CAA75273.1; -.
DR HSSP; P25942; ICDF.
DR INTERPRO; IPR001368; -.
DR PFAM; PF00020; TNFR_C6; 2.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_2.
DR PROSITE; PS00050; TNFR_NGFR_2; 2.
DR PRODOM; PD000771; -. 1.
SQ SEQUENCE 186 AA; 20482 MW; D2342F1040A00AE3 CRC64;

Query Match          6.1%; Score 137.5; DB 12; Length 186;
Best Local Similarity 28.0%; Pred. No. 4.4e-05;
Matches 46; Conservative 18; Mismatches 69; Indels 31; Gaps 11;

QY 11 KTFFTLLVLLGYLSCKVTCE-----TGDCRQOEFRDRSGN-CVPCNQCGPGMEL 58
   | : : : | : : | : | : | : | : | : | : | : | : | : | : |
Db 4 KSLAVACFIL-YITTLVTADITPLPPHAPVNGSCDEGEYLDKRHNQC--CNQCPGGEFA 60

QY 59 SKECGFGYGED-AQCVCRLHREKEDMGFK-CKPCLDCAVVNRFOKANCATSDAICGD 116
   | | | | : | : | : | : | : | : | : | : | : | : | : | : |
Db 61 KVRCS---GSDNTKGERCPHTYTAIPNYSNGCHQCKCP-TGSFQKVKCTGTQNSKC-S 115

QY 117 CLPGFYRKTGLVGFD-MECVPCGDPPEPY-----EPHCAS 151
   | | | | : | : | : | : | : | : | : | : | : | : | : | : |
Db 116 CLPGWICATDSSQTECDRCDCVPSKRCPCGFGGIDEQGNPICKS 159
```

Search completed: February 16, 2001, 21:09:00
Job time: 235 sec

THIS PAGE BLANK (USPTO)

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 2, 2001, 01:56:55 ; Search time 4027.99 Seconds
(without alignments)
2207.677 Million cell updates/sec

Title: us-09-380-276A-1
Perfect score: 1269
Sequence: 1 atggcttaaaagtgtact.....ggcagcagactgggtccctg 1269

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 7991742 seqs, 3503743858 residues
Total number of hits satisfying chosen parameters: 15983484

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST.*
1: gb_est1.*
2: gb_est2.*
3: gb_est3.*
4: gb_est4.*
5: gb_est5.*
6: gb_est6.*
7: gb_est7.*
8: gb_est8.*
9: gb_est9.*
10: gb_est10.*
11: gb_est11.*
12: gb_est12.*
13: gb_est13.*
14: gb_est14.*
15: gb_est15.*
16: gb_est16.*
17: gb_est17.*
18: gb_est18.*
19: gb_est19.*
20: gb_est20.*
21: gb_est21.*
22: gb_est22.*
23: gb_est23.*
24: gb_est24.*
25: gb_est25.*
26: gb_est26.*
27: gb_est27.*
28: gb_est28.*
29: gb_est29.*
30: gb_est30.*
31: gb_est31.*
32: gb_est32.*
33: gb_est33.*
34: gb_est34.*
35: gb_est35.*
36: gb_est36.*
37: gb_est37.*
38: gb_est38.*
39: gb_est39.*
40: gb_est40.*
41: em_estba.*
42: em_estfun.*
43: em_esthum1.*

44: em_esthum2.*
45: em_esthum3.*
46: em_esthum4.*
47: em_esthum5.*
48: em_esthum6.*
49: em_esthum7.*
50: em_esthum8.*
51: em_esthum9.*
52: em_esthum10.*
53: em_esthum11.*
54: em_esthum12.*
55: em_esthum13.*
56: em_esthum14.*
57: em_esthum15.*
58: em_esthum16.*
59: em_esthum17.*
60: em_esthum18.*
61: em_esthum19.*
62: em_esthum20.*
63: em_estin1.*
64: em_estin2.*
65: em_estin3.*
66: em_estin4.*
67: em_estov1.*
68: em_estov2.*
69: em_estpl1.*
70: em_estpl2.*
71: em_estpl3.*
72: em_estpl4.*
73: em_estpl5.*
74: em_estrol1.*
75: em_estrol2.*
76: em_estrol3.*
77: em_estrol4.*
78: em_estrol5.*
79: em_estrol6.*
80: em_estrol7.*
81: em_estrol8.*
82: em_estrol9.*
83: em_estrol10.*
84: em_estrol11.*
85: em_estrol12.*
86: em_estrol13.*
87: gb_est41.*
88: gb_est42.*
89: gb_est43.*
90: gb_est44.*
91: gb_est45.*
92: gb_est46.*
93: gb_est47.*
94: gb_est48.*
95: gb_est49.*
96: gb_est50.*
97: gb_est51.*
98: gb_est52.*
99: gb_est53.*
100: gb_est54.*
101: gb_est55.*
102: gb_est56.*
103: gb_est57.*
104: gb_est67.*
105: gb_est68.*
106: gb_est69.*
107: gb_est70.*
108: gb_est71.*
109: gb_est72.*
110: gb_est73.*
111: gb_est74.*
112: em_esthum21.*
113: em_esthum22.*
114: em_esthum23.*
115: em_estom1.*
116: em_estom2.*

117: em_estpl6:*
 118: em_estpl7:*
 119: em_estpl8:*
 120: em_estpl9:*
 121: em_estpl10:*
 122: em_estpl11:*
 123: em_estpl12:*
 124: em_estpl13:*
 125: em_estpl14:*
 126: em_estpl15:*
 127: em_estpl16:*
 128: em_estpl17:*
 129: em_estpl18:*
 130: em_estpl19:*
 131: em_estpl20:*
 132: em_estpl21:*
 133: em_estpl22:*
 134: em_estpl23:*
 135: em_estpl24:*
 136: em_estpl25:*
 137: em_estpl26:*
 138: em_estpl27:*
 139: em_estpl28:*
 140: em_estpl29:*
 141: em_estpl30:*
 142: em_estpl31:*
 143: em_estpl32:*
 144: em_estpl33:*
 145: em_estpl34:*
 146: em_estpl35:*
 147: em_estpl36:*
 148: em_estpl37:*
 149: em_estpl38:*
 150: em_estpl39:*
 151: em_estpl40:*
 152: em_estpl41:*
 153: em_estpl42:*
 154: em_estpl43:*
 155: em_estpl44:*
 156: em_estpl45:*
 157: em_estpl46:*
 158: em_estpl47:*
 159: em_estpl48:*
 160: em_estpl49:*
 161: em_estpl50:*
 162: em_estpl51:*
 163: em_estpl52:*
 164: em_estpl53:*
 165: em_estpl54:*
 166: em_estpl55:*
 167: em_estpl56:*
 168: em_estpl57:*
 169: em_estpl58:*
 170: em_estpl59:*
 171: em_estpl60:*
 172: em_estpl61:*
 173: em_estpl62:*
 174: em_estpl63:*
 175: em_estpl64:*
 176: em_estpl65:*
 177: em_estpl66:*
 178: em_estpl67:*
 179: em_estpl68:*
 180: em_estpl69:*
 181: em_estpl70:*
 182: em_estpl71:*
 183: em_estpl72:*
 184: em_estpl73:*
 185: em_estpl74:*
 186: em_estpl75:*
 187: em_estpl76:*
 188: em_estpl77:*
 189: em_estpl78:*

190: gb_gss25:*
 191: gb_gss26:*
 192: gb_gss27:*
 193: gb_gss28:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	302.2	23.8	395	106	BE306459	BE306459 601103459
2	296.4	23.4	454	147	W56829	W56829 xdl6e11.r1
3	274.8	21.7	282	28	AL036000	AL036000 DKFZp564K
4	241.2	19.0	534	135	BE757704	BE757704 212225 MA
5	203	16.0	401	1	AA003356	AA003356 mg49d01.r
6	192.8	15.2	369	91	AA478317	AA478317 19558 MAR
7	174.8	13.8	358	1	AA036247	AA036247 ml74d03.r
8	157.6	12.4	258	133	BB542020	BB542020 BB542020
9	155	12.2	643	159	AQ563354	AQ563354 HS_5335_B
10	125.8	9.9	646	159	AQ544065	AQ544065 RPCI-11-3
11	124.4	9.8	275	31	AV111112	AV111112 AV111112
12	120.8	9.5	404	8	AA495217	AA495217 fa04d10.r
13	113.8	9.0	450	158	AQ514075	AQ514075 HS_5184_A
14	95	7.5	1110	193	CNS050TC	AL347097 Tetraodon
15	91.2	7.2	414	91	AW527025	AW527025 UI-R-B01-
16	80.2	6.3	381	21	AI551729	AI551729 vf11e02.y
17	67.4	5.3	442	109	BE554624	BE554624 ur48c11.y
18	59	4.6	405	150	AQ173919	AQ173919 HS_3204_A
19	42.6	3.4	443	11	AA759377	AA759377 ah54a10.s
20	41.4	3.3	551	12	AA814296	AA814296 nz07d08.s
21	39.4	3.1	397	13	AA860208	AA860208 ak48c10.s
22	39.2	3.1	266	128	BB350382	BB350382 BB350382
23	39.2	3.1	407	146	W32428	W32428 zc05c12.s1
24	39	3.1	559	3	AA161105	AA161105 z058c05.s
25	38.8	3.1	706	109	BE535395	BE535395 601058548
26	38.8	3.1	925	190	CNS0091P	AL053013 Drosophila
27	38.8	3.0	391	21	AI522266	AI522266 t184f06.x
28	38	3.0	597	97	AW968349	AW968349 EST380424
29	37.8	3.0	458	88	AW303441	AW303441 xv19b01.x
30	37.8	3.0	482	139	BF018062	BF018062 uc95a06.x
31	37.6	3.0	510	29	AU060928	AU060928 AU060928
32	37.6	2.9	319	103	BB219800	BB219800 BB219800
33	37.4	2.9	343	96	AW877284	AW877284 MR4-PT005
34	37.4	2.9	472	7	AA417295	AA417295 zu18c03.s
35	37.4	2.9	968	193	CNS056T4	AL323761 Tetraodon
36	37.4	2.9	1002	191	CNS0206F	AL208896 Tetraodon
37	37.2	2.9	344	37	AV630854	AV630854 AV630854
38	37.2	2.9	372	89	AW312781	AW312781 5078 MARC
39	37.2	2.9	910	190	CNS0060N	AL065629 Drosophila
40	37	2.9	366	8	AA542636	AA542636 fa08d10.r
41	36.8	2.9	447	17	AI217695	AI217695 qh26d07.x
42	36.8	2.9	465	38	AW015051	AW015051 UI-H-B10-
43	36.8	2.9	465	87	AW181919	AW181919 xj68d07.x
44	36.8	2.9	689	109	BE532858	BE532858 601234740

ALIGNMENTS

RESULT 1

BE306459

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

BE306459 395 bp mRNA
 601103459F1 NCI_CGAP_Lu29 Mus musculus cdna clone IMAGE:3495566 5',
 mRNA sequence.
 BE306459
 BE306459.1 GI:9159707
 EST.
 house mouse.

13-JUL-2000

ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 395)
NIH-MGC <http://www.ncbi.nlm.nih.gov/MGC/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: L14W8546 row: f column: 15
High quality sequence stop: 395.
Location/Qualifiers
1..395

source
/organism="Mus musculus"
/strain="C57BL/6J (f1)"
/db_xref="taxon:10090"
/clone="IMAGE:349556"
/clone_lib="NCI-CCAP-Lu29"
/tissue_type="spontaneous tumor, metastatic to mammary."
Stem cell origin.
/lab_host="DH10B"
/note="Organ: lung; Vector: pCMV-SPORT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
BASE COUNT 88 a 101 c 120 g 86 t
ORIGIN

Query Match 23.8%; Score 302.2; DB 106; Length 395;
Best Local Similarity 85.3%; Pred. No. 2.8e-78;
Matches 337; Conservative 0; Mismatches 58; Indels 0; Gaps 0;
QY 56 tactaggctattgtcatgtaagtgaactgtgtaacaggagactgtgacagcaagaat 115
DB 1 TCCTACTCCACTTGGCATGTAAGTGAGTTGCGAACCCGGAGATTGCGAGCAGGAAT 60
QY 116 tcaggagatcggtctggaactgtttccctgcaacagatgtggccagcagctggtgt 175
DB 61 TCAGGATCGATCTGGAACACTGTGCTCTGCAACAGTGGCGGACCTGGCATGGAGTTGT 120
QY 176 ctaaggaatgtgcttcggtatgggagatgcacagtggtgacgtgcccgtgcaca 235
DB 121 CCAAGGAATGTGGCTTCGGCTATGGGAGGATGCACAGTGTGTCCTGCGAGCCGACCC 180
QY 236 ggttcaggagagactggggctcccaagaatgcaacccctgtctgagctgcagtggtga 295
DB 181 GGTTCAGGAAGACTGGGGTTTCCAGAGTGTAAAGCGGTGCGGACTGTGCGCTGGTGA 240
QY 296 accgtttcagaagcacaattttcagcaccagcagtgatccatctcggggactcttgc 355
DB 241 ACCGCTTTTCAGAGGCCAACTGCTCACACACAGGATGTGCTCTGCGGGGACTGCGCTGC 300
QY 356 caggattttatagaagcagaactgttcggtttcagaacatgagtggtgtgcttgg 415
DB 301 CAGGATTTACCGAAGACCAACTGGTGGTTTTCAGACATGGAGTGTGTGCGCTGCG 360
QY 416 gagaccctctctcttacgcaacgcagctgtgcc 450
DB 361 GAGACCCACTCTCTCTACGAACACACACTGTACC 395

RESULT 2
W56629 454 bp mRNA EST
LOCUS

DEFINITION zdi6ell.r1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone
IMAGE:340844 5', mRNA sequence.
ACCESSION W56629
VERSION W56629.1 GI:1358487
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 454)
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman,
M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J.,
Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston,
R., Williamson, A., Wohlmann, P. and Wilson, R.
The WashU-Merck EST Project
Unpublished (1995)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1373 Std Error: 0.00
Seq primer: mob.REGA+ET.

FEATURES
Location/Qualifiers
1..454
/organism="Homo sapiens"
/db_xref="GDB:1266219"
/db_xref="taxon:9606"
/clone="IMAGE:340844"
/clone_lib="Soares_fetal_heart_NbHH19W"
/sex="unknown"
/dev_stages="19 weeks"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ: heart; Vector: pT7T3D (Pharmacia) with a
modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTTACCAATCTGAAGTGGGAGCGCGCATCTTTTCTTTTCTTTTCTTTT 3'], RI
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT7T3 vector
(Pharmacia). Library went through one round of
normalization to a Cot = 5. Library constructed by
M.Fatima Bonaldo. This library was constructed from the
same fetus as the fetal lung library, Soares fetal lung
NbHH19W."

BASE COUNT 132 a 96 c 88 g 138 t
ORIGIN

Query Match 23.4%; Score 296.4; DB 147; Length 454;
Best Local Similarity 99.7%; Pred. No. 1.5e-76;
Matches 297; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 972 ctcttactgaactcactggaagacattctctctcaatccagacttgaagctc 1031
DB 1 CTCCTATCTGAACCTCACTGGAGAGACATTCATCTCTCAATCCAGAACTTGAAGCTC 60
QY 1032 aacgtcttggattcaaatagcagtcagatttgggtggggctgtctccagtcagtc 1091
DB 61 AACGCTTTGGATTCAATAGCAGTCAGATTTGGTTGGTGGGGCTGTTCAGTCCAGTC 120
QY 1092 tcaattctgaaacttacagcagctactgatttattctagataataacacacactggtaga 1151
DB 121 TCATTCTGAAAACCTTACAGCAGCTACTGATTATCTAGATATAACACACACTGGTAGA 180
QY 1152 atcagcatcaactcagatgcactaactatgagaagccagctagatcaggaagtgggc 1211
DB 181 ATCAGCATCAACTCAGTAGTCCTAACTATGAGAGCCAGCTAGATCAGGAGGTGGCGC 240
QY 1212 tatcatccaccagcactcagacgtccctccaggtaaggcagcagctgggttcctcg 1269

```

Db 241 TGTCATCCAGCCAGCTCAGAGTCCCTCCAGGTAAAGCAGGAGTGGTCCCTG 298
|||||
RESULT 3
AL036000 282 bp mRNA EST 29-FEB-2000
LOCUS DKF2p564K1022_r1 564 (synonym: hfbr2) Homo sapiens cDNA clone
DEFINITION DKF2p564K1022 5', mRNA sequence.
ACCESSION AL036000
VERSION AL036000.1 GI:5405629
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 282)
AUTHORS Wambutt R., Heubner D., Mewes H.W., Gassenhuber J. and Wiemann S.
TITLE EST (Wambutt, et al.)
JOURNAL Unpublished (1999)
COMMENT Contact: Wambutt R
MIPS
Am Klopferpitz 18a D-82152 Martinsried, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by AGOWA (Berlin/Germany) within the cDNA sequencing
consortium of the German Genome Project.
SI sequence also available.
This clone (DKF2p564K1022) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
FEATURES
source
1..282
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="DKF2p564K1022"
/clone_lib="564 (synonym: hfbr2)"
/tissue_type="brain"
/dev_stage="fetal"
/lab_host="Xl-2blue"
/note="Vector: pAMPl; site_1: NotI; site_2: SalI"
BASE COUNT 57 a 85 c 75 g 63 t
ORIGIN

```

```

Query Match 21.7%; Score 274.8; DB 28; Length 282;
Best Local Similarity 98.6%; Pred. No. 3.1e-70;
Matches 276; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 365 ataggagaggaactgtcggtttcaagacatggagtgtgcctgtggagaccctc 424
|||||
Db 3 ATAGGAAGAGCAACTTGTGGCTTTCAGACATGGAGTGTGCTTGTGGAGACCCCTC 62
|||||
Qy 425 ctctctctacgaaccgcactgtgccagcaaggtccaacctcgtgaagatcgcgctccacgg 484
|||||
Db 63 CTCCTCTTACGAACCCGACTGTGCCAGCAAGGTCAACCTCGTAGATCGCTCCACGG 122
|||||
Qy 485 cctccagccacgggacacacggcgtgctcgtctatctcagcgcctcgtggcacccctc 544
|||||
Db 123 CCTCAGCCACGGGACAGCGCGCTGGCTTATCTGCANCGCTCTGGCCACCCGTC 182
|||||
Qy 545 tgcctgcccctgctcatcctctgctcatctattgtaagagacagtttatgagaagaac 604
|||||
Db 183 TGCTGGCCCCGCTCATCTCTGTGTCTATCTATTGTAGAGACAGCTTATGTAGAGANAC 242
|||||
Qy 605 ccagctggtctctgctggttcacagacattccagtacaacgg 644
|||||
Db 243 CCAGCTGGTCTCTCGGTTCGANGACATTCAGTACTACGG 282
|||||

```

```

RESULT 4
BE757704

```

```

LOCUS BE757704 534 bp mRNA EST 15-SEP-2000
DEFINITION 212225 MARC 2BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION BE757704
VERSION BE757704.1 GI:10171696
KEYWORDS EST.
SOURCE cow.
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
REFERENCE 1 (bases 1 to 534)
AUTHORS Smith, T.P.L., Casas, E., Stone, R.T., Heaton, M.P., Grosse, W.M.,
Bennett, G.A., Fahrnkug, S.C., Freking, B.A., Rohrer, G.A., Laegreid
W.W. and Keele, J.W.
TITLE Design and use of four pooled tissue normalized cDNA libraries for
EST discovery in cattle
JOURNAL Unpublished (2000)
COMMENT Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
PCR Primers
FORWARD: AGAAACACGCTATGACCAT
BACKWARD: GTTTCCCGAGTCAGCAGC
Plate: 65 row: C column: 2
Seq primer: ATTAGTGACACTATAG.
FEATURES
source
1..534
Location/Qualifiers
/organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="MARC 2BOV"
/tissue_type="pooled"
/lab_host="DH10B"
/note="Vector: pCMV SPOR6; site_1: XbaI; site_2: XhoI;
Library made from pooled tissue from testis, thymus,
semitendinosus muscle, longissimus muscle, pancreas,
adrenal, and endometrium."
BASE COUNT 122 a 117 c 171 g 124 t
ORIGIN

```

```

Query Match 19.0%; Score 241.2; DB 135; Length 534;
Best Local Similarity 83.6%; Pred. No. 3.4e-60;
Matches 286; Conservative 0; Mismatches 53; Indels 3; Gaps 1;

Qy 1 atgctttaaagtgtctactagaacaagagaaacgtttttcactcttttagtattacta 60
|||||
Db 196 ATGCTTCAACAGTGTCTACTCAGGCAACAGAAA--FCTTTCAGGGTTGTAGTTTACTA 252
|||||
Qy 61 ggctattgtctgaagtgtactgtgaaacagggagactgtgacagcaagaattcagg 120
|||||
Db 253 GCCTGTTTGGCATGTGGAGTGATTGTGAAACAGGAGACTGTGACAGCAGGAATTACAG 312
|||||
Qy 121 gatcgtctggaactgtgttccctcgaaccagtgtggtggtggtggtggtggtggtggt 180
|||||
Db 313 GACCAGTTCAGAACTGTGTCTGTGCAAGCAGTGTGGCCAGGCGATGGAGTTGTCCAG 372
|||||
Qy 181 gaatggtcttggcgtatgggagagatgcacagtgtgacgtgcgcgtgcacaggttc 240
|||||
Db 373 GAATGTGCTTTGGCTACGGGGAGGAGCGCCAGTGTGTGAAGTGGCCGCGCAGGTTTC 432
|||||
Qy 241 aaggagactggggctctccagaaatgcagccctgtctgactgcgcagtggtgaaaccgc 300
|||||
Db 433 AAGGAGACTGGGCTCTCAGAAAGTGCACGCGTGCCTGGACTGCGCCCTGCTGAGCCGC 492
|||||
Qy 301 ttccagaaggcaaatgttccagccaccagtgtgcaatctgc 342
|||||
Db 493 TTCAGAAGCCCAACTGCTCGGCCACTTGGCGAGCGCGCTCTGC 534
|||||

```

```
RESULT 5
AA003356 401 bp mRNA EST 19-JUL-1996
LOCUS mg49g01.r1 Soares mouse embryo NBME13.5 14.5 Mus musculus cDNA
DEFINITION clone IMAGE:427152 5', mRNA sequence.
ACCESSION AA003356
VERSION AA003356.1 GI:1446796
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 401)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
Waterston, R.
The WashU-HMI Mouse EST Project
Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:261704
Seq primer: ETPRimer
High quality sequence stop: 345.
FEATURES
Location/Qualifiers
1..401
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:427152"
/clone_lib="Soares mouse embryo NBME13.5 14.5"
/sex="unknown"
/tissue_type="embryo"
/dev_stage="13.5-14.5dpc total fetus"
/lab_host="DH10B"
/note="vector: p7T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer [5'
TGTTACCAATCTGAAGTGGGAGCGCGCGGAAATTTTTTTTTTTTTTTTTT
T 3'] , on equal amounts of mRNA from 2 13.5dpc and 2
14.5dpc embryos [total RNA provided by Minoru Ko, Wayne
State Univ., from 2 ]; double-stranded cDNA was ligated to
Eco RI adaptors (Pharmacia), digested with Not I and
cloned into the Not I and Eco RI sites of the modified
p7T3 vector. Library went through one round of
normalization, and was constructed by Bento Soares and
M.Fatima Bonaldo."
BASE COUNT 92 a 96 c 128 g 85 t
ORIGIN

Query Match 16.0%; Score 203; DB 1; Length 401;
Best Local Similarity 78.8%; Pred. No. 6e-49;
Matches 242; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

QY 1 atggcttttaaaagtctactagacaagaagaaagctttttcactcttttagtatacta 60
||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 95 ATGGCACTCAAGGCTCTACTCTACACAGAGCGGTCTCTCGCTGCCATTCCTCTCTA 154

QY 61 gactatttgcataaagtactgtgaacacagagagactgtagacagcaagaattcagg 120
||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 155 CTCACCTGGCAGTAAAGTAGTGTCCGAACCGGAGATTGAGGAGCAGGAGAAATTCAG 214
```

```
QY 121 gatcggctctgaaactgtgttccctgcacaccagtgtggccaggcatggagtgtgtctaag 180
||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 215 GATCGATCTGGAAACTGTGTCTCTGCAACAGTGGACCTGGCATGGAGTTGTTCCAAG 274

QY 181 gaatgtgcttcggctatgggagagatgcacagtggtgtgacgtgcggctgcacagggttc 240
||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 275 GAATGTGGCTTCGGCTATGGGAGGATGCACAGTGTGTGCCCTGCGAGCCGCGCGGTTC 334

QY 241 aaggaggactgggcttccagaaatgcagccctctctggactgcagtggtgaaccgc 300
||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 335 AAGGAAGACTGGGGTTTCCAGAAGTGTAAAGCATGTGCGGACTGTGCGCTGGTGAACCGC 394

QY 301 tttcaga 307
|||||
DB 395 TGTCTAGA 401

RESULT 6
AA478317 369 bp mRNA EST 07-JUL-2000
LOCUS AW478317
DEFINITION 19558 MARC 2B0V Bos taurus cDNA 5', mRNA sequence.
ACCESSION AW478317
VERSION AW478317.1 GI:7048423
KEYWORDS EST.
SOURCE cow.
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
1 (bases 1 to 369)
Smith, T.P.L., Casas, E., Stone, R.T., Heaton, M.P., Grosse, W.M.,
Bennett, G.A., Fahrenkrug, S.C., Freking, B.A., Rohrer, G.A., Laegreid
,W.W. and Keeler, J.W.
Design and use of four pooled tissue normalized cDNA libraries for
EST discovery in cattle
Unpublished (2000)
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@mail.marc.usda.gov
Single pass sequencing. Bases called and trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 20
and -minmatch 12 options.
PCR Primers
FORWARD: AGGAACAGCTATGACCAT
BACKWARD: GTTTCCTCCAGTCACGAGC
Plate: 10 row: M column: 8
Seq primer: ATTGAGTGACACTATAG.
FEATURES
Location/Qualifiers
1..369
/organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="MARC 2B0V"
/tissue_type="pooled"
/lab_host="DH10B"
/note="vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI;
Library made from pooled tissue from testis, thymus,
semitendinosus muscle, longissimus muscle, pancreas,
adrenal, and endometrium."
BASE COUNT 60 a 115 c 115 g 79 t
ORIGIN

Query Match 15.2%; Score 192.8; DB 91; Length 369;
Best Local Similarity 72.9%; Pred. No. 6.1e-46;
Matches 248; Conservative 0; Mismatches 92; Indels 0; Gaps 0;

QY 736 gggccgggtgcgttctccatccatgctgtgaggagcctgcagcccaaccgcgcg 795
||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 26 GGGCCAGTCACCTTGTCCCTCCCGGTGCTGTGTGGGGCTGCGGCATTGCGCCGGGAC 85
```

Qy	796	actcttggttggtgggtgcattctctgcagcagtcattcttcagggcaagaacacgagccagcc	855		
Db	86	ACTCTCTGGTTGTCAGGGGGCCTGCAAGGGCCACACTTCAGGACAGAAACACAGGTCACGCG	145		
Qy	856	ggggagatggtgcgcgactttcttcggatccctccacgcagctccatctgtggcgagttttca	915		
Db	146	GGGAGGCGGATTCCCACTTCTTTGGGTGCCCTGTCAAGGTCCTCTGTGGCGAGTCTTCA	205		
Qy	916	gatgcctggcctctgatgcagaaatcccatgggtggtgacacatctctttttgtgactct	975		
Db	206	GAGCGCTGGCCTCTGATGACGAATCCCGGTGGTGGTGACGATGTCTCTCTCTCGCACTCC	265		
Qy	976	tactctgaactcactgaggaagacattctctctcaatccagaaacttgaagatccaacy	1035		
Db	266	TGCCCTGAGCTCCCTGGAGAAGACGCTCACTCTCTCGACCCAGAGACACAAGCTTGGCT	325		
Qy	1036	tcttggattcaaatagcagctcaagattggttggtgggg	1075		
Db	326	TCCCTGGACTCAGACAGCAGCTGGGGGTCTGGTGGTGGGG	365		
RESULT 7					
AA036247	358 bp	mrna	EST		
LOCUS	m174803.r1	Soares mouse p3NMF19.5	Mus musculus cDNA clone		
DEFINITION	IMAGE:472300 5', mRNA sequence.				
ACCESSION	AA036247				
VERSION	AA036247.1	GI:1509376			
KEYWORDS	EST.				
SOURCE	house mouse.				
ORGANISM	Mus musculus				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
AUTHORS	1 (bases 1 to 358) Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Scheilenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.				
TITLE	The WashU-HIMI Mouse EST Project				
JOURNAL	Unpublished (1996)				
COMMENT	Contact: Marra M/Mouse EST Project WashU-HIMI Mouse EST Project Washington University School of Medicinep 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: mouseest@watson.wustl.edu This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information. MGI:283044				
Seq primer:	-28M13 rev2 from Amersham				
High quality sequence stop:	747.				
Location/Qualifiers	1. .358 /organism="Mus musculus" /db_xref="taxon:10090" /clone="IMAGE:472300" /clone_lib="Soares mouse p3NMF19.5" /dev_stage="19.5 dpc total fetus" /lab_host="DH10B (ampicillin resistant)" /note="Vector: pT7T3D (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCATCTGAAGTGGAGCGGCGGCATTTTTTTTTTTTTTTT 3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo. RNA was kindly provided by Dr. Minoru KO (Wayne State University)."				
BASE COUNT	81 a	98 c	110 g 69 t		

ORIGIN

Query Match 13.8%; Score 174.8; DB 1; Length 358;
 Best Local Similarity 78.6%; Pred. No. 1.3e-40;
 Matches 209; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

QY 1 atgagctttaaagtctactagacaagaagaaaacgtttttcactctcttttagtattacta 60
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 92 ATGGCACTCAAGTCTCTACCTCTACACAGGACGGTGCTCTTCGCTGCGCATTCCTTCCTA 151
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 61 ggcatttgcataagtgactgtgaaacaggagactgtgagacgaagaattcagg 120
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 152 CTCACCTGGCATGTAAGTGCAGTTCGGAACCGGAGATTCCAGGCAGCAGGAATTCAG 211
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 121 gatcgcttgaaacgtgttccctgcacacagatgtggccaggcatggagtgtctaaag 180
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 212 GATCGATCTCGAAGCTGTGCTCTCGCAACAGTCCGGACCTGGCATGGAGTTGTCTCCAAG 271
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 181 gaatgtgcttcggctatggggaggaTgcacagtgtgtgacgtgcggctgcacagattc 240
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 272 GAATGTGGCTTCGGCTATGGGAGGATGCACAGTGTGTGCCCTGCAGCGCCAGCGGTTC 331
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 241 aaggaggactggggcttccagaaatg 266
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 332 AAGGAAGACTGGGGTTTCCAGAAGTG 357
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 8

BB542020
 LOCUS
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

BB542020 258 bp mRNA EST 31-JUL-2000
 BB542020 RIKEN full-length enriched, 0 day neonate eyeball Mus
 musculus cDNA clone EL30118C08 3', mRNA sequence.
 BB542020.1 GI:9613243
 EST.
 house mouse.
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
 AUTHORS
 Kono, H., Aizawa, K., Akahira, S., Akiyama, J., Arakawa, T., Carninci
 P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N.,
 Hirozane, T., Hori, F., Ishii, Y., Ishikawa, J., Ishikawa, T., Itoh, M.,
 Izawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N.,
 Kiyosawa, H., Kojima, Y., Kondo, S., Koya, S., Kurinara, C., Kusakabe, M.,
 Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Ode, H., Okazaki, Y.,
 Ono, T., Owa, C., Saito, H., Sakai, C., Sato, K., Shibata, K., Shibata
 Y., Shigemoto, Y., Shingagawa, A., Shiraki, T., Sogabe, Y., Sugahara, Y.,
 Suzuki, H., Suzuki, H., Tagawa, A., Takahashi, F., Tominaga, N., Toya
 T., Tsunoda, Y., Watahiki, A., Watanabe, S., Yamamura, T., Yamanaka, I.,
 Yano, R., Yasunishi, A., Yokota, T., Yoshida, K., Yoshiki, A., Yoshino
 M., Muramatsu, M. and Hayashizaki, Y.

RIKEN Mouse ESTs (Konno, H., et al.)
 Unpublished (2000)

TITLE
 JOURNAL
 COMMENT

Contact: Yoshihide Hayashizaki
 Genome Exploration Research Group, Life Science Tsukuba Center,
 Genome Science Laboratory
 The Institute of Physical and Chemical Research (RIKEN), Genomic
 Sciences Center
 3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
 Tel: +81-298-36-9013
 Fax: +81-298-36-9098
 Email: genome-res@rct.riken.go.jp/
 URL: http://genome.rtc.riken.go.jp/
 Carninci, P., Nishiyama, Y., Westover, A., Itoh, M., Nagaoka, S., Sasaki
 N., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
 Thermostabilization and thermoactivation of the model enzymes by
 trehalose and its application for the synthesis of full length
 cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
 Itoh, M., Kitsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J.,
 Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki
 Y. and Hayashizaki, Y.

BASE COUNT

Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)
Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)

Please visit our web site (<http://genome.rtc.riken.go.jp>) for further details.

FEATURES

source

Location/Qualifiers

```
1. .258
  /organism="Mus musculus"
  /db_xref="taxon:10090"
  /clone="E130118G08"
  /clone_lib="RIKEN full-length enriched, 0 day neonate
  eyeball"
  /tissue_type="eyeball"
  /dev_stage="0 day neonate"
  /lab_host="DH10B"
  /note="Site_1: SalI; Site_2: BamHI; cDNA library was
  prepared and sequenced in Mouse Genome Encyclopedia
  Project of Genome Exploration Research Group in Riken
  Genomic Sciences Center and Genome Science Laboratory in
  RIKEN. Division of Experimental Animal Research in Riken
  contributed to prepare mouse tissues. 1st strand cDNA was
  primed with a primer [5'
  GAGAGAGAGCGGCCCAACTCGAGTTTTTTTTTTTTTNN 3'], cDNA was
  prepared by using trehalose thermo-activated reverse
  transcriptase and subsequently enriched for full-length by
  cap-trapper. Second strand cDNA was prepared with the
  primer adapter of sequence [5'
  GAGAGAGATTTCGAGTAAATTAATCCCGCCCCCCC 3']. cDNA
  was cleaved with BamHI and XhoI. Vector: a modified
  pBluescript KS(+) after bulk excision from Lambda FLC I."
  55 a 77 c 66 g 60 t
```

BASE COUNT

ORIGIN

```
Query Match      12.4%; Score 157.6; DB 133; Length 258;
Best Local Similarity 80.7%; Pred. No. 1.4e-35;
Matches 184; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

Qy 221 cgtccgctcacaggttcaggagactgggcttcagaaatgaagccctgtctgg 280
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1  CTTGAGCCCCCACCCTGTTCAAGAACTGGGCTTCCAGAAAGTGAAGCCATGTGGCG 60
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 281 actgcagtggtgaaccgcttcagaaggcaaatgttcagccaccagtgatgcacat 340
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61  ACTTTGCGCTGTGTAACCGCTTTCAGAGGCCCACTGCTCACACCACTGATGCTTTT 120
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 341 gcggggactgcttcaggatttataggaagacgaaactgtcggtttcaagacatgg 400
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 121 GCGGGAGTGCCTGCCAGGATTTTACCGGAAGACCAACTGGTTGTTTCAAGACATGG 180
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 401 agtgtgctctgtgagaccctcctcctctctacgaaccgactgtg 448
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 181 AGTGTGCTCCCTGGAGACCACCTCTCCTCTAGAACACACACTGTG 228
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
```

RESULT 9

```
AQ563354      643 bp      DNA      GSS      29-MAY-1999
LOCUS      HS_5335_B2_B03_07A RPCI-11 Human Male BAC Library Homo sapiens
DEFINITION      genomic clone Plate=911 Col=6 Row=D, DNA sequence.
```

ACCESSION AQ563354

VERSION AQ563354.1

KEYWORDS GSS.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS

Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D., and
Hood, L.

TITLE

JOURNAL

MEDLINE

COMMENT

Sequence-tagged connectors: A sequence approach to mapping and
scanning the human genome
Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
99380589

Contact: Mahairas GG, Wallace JC, Hood L

High Throughput Sequencing Center

University of Washington

401 Queen Anne Avenue North, Seattle, WA 98109, USA

Tel: (206) 616-3618

Fax: (206) 616-3887

Email: jwallaceu.washington.edu

Clones are derived from the human BAC library RPCI-11. For BAC

library availability, please contact Pieter de Jong

(pieter@dejong.med.buffalo.edu). Clones may be purchased from

BACPAC Resources (<http://bacpac.med.buffalo.edu/ordering.bac.htm>)

or from Resear h Genetics (info@resgen.com). BAC end Web Server:

<http://www.husc.washington.edu>

Plate: 911 row: D column: 6

Seq primer: T7

Class: BAC ends

High quality sequence stop: 643.

Location/Qualifiers

1. .643

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="Plate=911 Col=6 Row=D"

/clone_lib="RPCI-11 Human Male BAC Library"

/sex="male"

/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;

Male blood DNA was isolated from one randomly chosen donor

and partially digested with a combination of EcoRI and

EcoRI Methylase. Size selected DNA was cloned into the

pBACe3.6 vector at EcoRI sites"

BASE COUNT 151 a 154 c 158 g 167 t 13 others

ORIGIN

Query Match

Best Local Similarity 12.2%; Score 155; DB 159; Length 643;

Matches 170; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

Qy 445 tgtgccagcaaggtcaacctcgtggaagatcggtccagcgcctccagccacggacacg 504

Db 315 TGTGCCAGCAAGGTCAACCTCGTGAAGATCGGTTNCACGGCTCCAGCCACGGACAGC 374

Qy 505 gcgctggctgcggttatctgcagcgtctggccaccgctcctgctggcctgctatcttc 564

Db 375 GCGCTGTGCTGCCGCTATCTGCAGCGCTCTGGCCACCGCTCTGCTCATCTC 434

Qy 565 tgtgtcatctattgaagacagatttatggagaagaacccagctggtctctcggtca 624

Db 435 TGTGTCACTATTGTAAGAGACAGTNTATGGAGAGAAACCCAGCTGTAAAGTTGAGCT 494

Qy 625 caggacattcagtaacaac 642

Db 495 CATTACATNTCTTATCAC 512

RESULT 10

AQ544065

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

J.C.

J.C.

J.C.

J.C.

J.C.

J.C.

J.C.

J.C.

J.C.

J.C.

J.C.

TITLE Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready Map Building

JOURNAL Unpublished (1997)

COMMENT Other_GSSs: RPCI-11-315F10.TJ
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0208
Email: hbest@igf.org

Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieter@edj.med.buffalo.edu). Clones may be purchased from BACPAC Resources (<http://bacpac.med.buffalo.edu/ordering>) or from Research Genet cs (inforesgen.com). BAC end search page: http://www.tigr.org/tldb/hungen/bac_end_search/bac_end_search.html.
Seq primer: T7
Class: BAC ends.

FEATURES
Source

Location/Qualifiers
1. 646
/organism="Homo sapiens"
/db_xref="GDB:7620705"
/db_xref="taxon:9606"
/clone="RPCI-11-315F10"
/clone_lib="RPCI-11"
/sex="Male"
/cell_type="Lymphocytes"
/note="Vector: pBAC3.6; Site_1: EcoRI; Site_2: EcoRI; RPCI11 Human Male BAC Library"

BASE COUNT 175 a 135 c 145 g 191 t

Query Match 9.9%; Score 125.8; DB 159; Length 646;
Best Local Similarity 94.9%; Pred. No. 4.8e-26;
Matches 130; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 611 ggtctcgagtcacaggacattcagtaacagcgtctgaagctgtctgtcttgacagac 670
|||||
Db 263 GGTCTCGCGGTCCAGGACATTCAGTACACGGCTCTGAGCTGTCTGTGTGACAGAC 322
|||||
QY 671 ctgagctccacgaataatgcccacagagcctgctgccagtgccgcctgactcagtgacga 730
|||||
Db 323 CTCAGTCCACGAATATGCCACAGAGCCTGCTGCCAGTGCCGCCGTGACTCAGTCAGAC 382
|||||
QY 731 cctgcgggcccgggtgcgc 747
|||||
Db 383 CCGCGGTAAGTTTCAGC 399

RESULT 11
LOCUS AV111112 275 bp mRNA EST 29-JUN-1999
DEFINITION AV111112 Mus musculus C57BL/6J 10-day embryo Mus musculus cdna clone 2600016N17, mRNA sequence.

ACCESSION AV111112
VERSION AV111112.1 GI:5265192
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 275)
Carninci, P., Shibata, K., Ozawa, Y., Konno, H., Itoh, M., Aizawa, K., Akahira, S., Akiyama, J., Fukuda, S., Fukunishi, Y., Funayama, T., Hara, A., Hayatsu, N., Hori, F., Ishikawa, T., Itoh, M., Izawa, M., Kawai, J., Kikuchi, N., Kojima, Y., Matsuyama, T., Naitsuma, H., Oda, H., Owa, C., Sato, K., Shibata, Y., Shigemoto, Y., Shiraki, T., Sogabe, Y., Sugahara, Y., Suzuki, H., Suzuki, H., Tateno, M., Tomaru, Y., Tomimaga, N., Watanabe, S., Yagane, M., Yamamura, T., Yokota, T., Yoshino, M., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y.

REFERENCE
AUTHORS RIKEN Mouse ESTs

TITLE

JOURNAL
COMMENT

Unpublished (1999)
Contact: Chie Owa
Genome Science Laboratory
RIKEN
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-9145
Fax: 81-298-36-9098
Email: genome-res@rtc.riken.go.jp

Thermostabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA (Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))
Transcriptional sequencing: A method for DNA sequencing using RNA polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
Please visit our web site (<http://genome.rtc.riken.go.jp>) for further details.

FEATURES
Source

Location/Qualifiers
1. 275
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="2600016N17"
/clone_lib="Mus musculus C57BL/6J 10-day embryo"
/sex="mixed"
/dev_stage="10-day embryo"

BASE COUNT 77 a 86 c 55 g 57 t

ORIGIN

Query Match 9.8%; Score 124.4; DB 31; Length 275;
Best Local Similarity 71.3%; Pred. No. 9.1e-26;
Matches 164; Conservative 0; Mismatches 66; Indels 0; Gaps 0;

QY 245 aggaactgggctccagaataatgcaagcctgtctgactgcagtggtgaaccgcttc 304
|||||
Db 43 AGAAAGTGGTTTCCAGAGTAAGAACCCATTGCCCAACCTGCCCTGTAGAACCCCTATC 102
|||||
QY 305 agaagcgaaattgttcagccaccagtgatgcatctgcgggactctgtccaggatttt 364
|||||
Db 103 TGAGGACCCATTGCTCACACACACACTGATGCTCTGCGGGGACTGCCTGCCAAGATTTT 162
|||||
QY 365 ataggaagcagaaactgtcgctcttcagagcaatggagtggtgctcttgagagacctc 424
|||||
Db 163 ACCAGAAAGACCAACACTGGTTGGTTTTCAGACATGAGTGCTGTCCTCGGAGACCCAC 222
|||||
QY 425 ctctccttaccgaaccgcacactgtgccagcaaggtcaacctcgtaagatc 474
|||||
Db 223 CTCTCCCTACGAAACACACAGTGTGCTGATGTGCCAAGTGGCAGACGACC 272

RESULT 12

LOCUS AA495217 404 bp mRNA EST 27-JUN-1997
DEFINITION fa04d10.r1 zebrafish ICRFzfls Danio rerio cdna clone 10E17 5', mRNA sequence.

ACCESSION AA495217
VERSION AA495217.1 GI:2225645
KEYWORDS EST.
SOURCE zebrafish.
ORGANISM Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi; Cypriniformes; Cyprinidae; Rasbora; Danio.

REFERENCE
AUTHORS 1 (bases 1 to 404)
Clark, M., Lehrach, H., Appel, B., Eisen, J., Johnson, S., Marra, M., Jost, S., Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Dodt, S., Kucaba, T., Lacy, M., Le, N., Lennon, G., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie, T., Waterston, R. and Willson, R.

TITLE WashU Zebrafish EST Project
JOURNAL Unpublished (1997)
COMMENT Contact: Steve Johnson
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Actinopterygii, Neopterygii; Teleostei; Euteleostei; Neoteleostei; Eurypterygii; Ctenosquamata; Acanthomorpha; Eucanthomorpha; Holacanthopterygii; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontidae; Tetraodontidae; Tetraodon. 1 (bases 1 to 1110)

Roest-Crolius, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher, C., Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and Weissenbach, J.

Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis

Unpublished

2 (bases 1 to 1110)

Roest-Crolius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C., Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F., Saurin, W. and Weissenbach, J.

Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence

Unpublished

3 (bases 1 to 1110)

Genoscope.

Direct Submission

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at <http://www.genoscope.cns.fr/Tetraodon>.

FEATURES

source

1. .1110

Location/Qualifiers

/organism="Tetraodon nigroviridis"

/db_xref="taxon:99883"

/clone="042M15"

/clone_lib="c"

/notes="Genoscope sequence ID : COBC042AG08tl-end : T3"

222 a 293 c 292 g 281 t 22 others

BASE COUNT

ORIGIN

Query Match 7.5%; Score 95; DB 193; Length 1110;

Best Local Similarity 70.6%; Pred. No. 7.4e-17;

Matches 139; Conservative 0; Mismatches 57; Indels 1; Gaps 1;

QY 179 aggaatggtcctcggtatggggagatgcacagtgtagcgtgcgggtgcacaggt 238

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 706 AGGAATGTGCTTTGGCTACGAGAGATGCCGGTGTGTCCCTGTCTGGAGCGCGCT 765

||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 239 tcaagagagactgggcttcagaaatcgaagcctgtctgactgccaagtgtggaacc 298

||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 766 TCAAGAGAGAGCGCGNCTCGAAGAGTGCAGAGCGCTGCCTGGACTGCGGGCTCATCAACC 825

||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 299 gcttcagaagcgaatgttcagccaccagtgatgcacatc-gcggggactgctgcca 357

||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 826 GCTTCCAGAGGCGCACTGTCTCCACCAGCAACGCAAGTGTGTGGAGACTGCTGCCC 885

||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 358 ggattttataggaagac 374

||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 886 GGGTCACTCAGCAGGCC 902

||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 15

AW527025/c

LOCUS

AW527025 414 bp mRNA EST 06-MAR-2000

DEFINITION

UI-R-B01-ajg-f-10-0-UI.s1 UI-R-B01 Rattus norvegicus cDNA clone

UI-R-B01-ajg-f-10-0-UI 3', mRNA sequence.

ACCESSION

AW527025

VERSION

AW527025.1 GI:7169439

KEYWORDS

EST.

SOURCE

Norway rat.

ORGANISM

Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;

Rattus.

REFERENCE

AUTHORS

Bonaldo, M.F., Lennon, G. and Soares, M.B.

Search completed: March 2, 2001, 09:58:55
Job time: 28920 sec

THIS PAGE BLANK (USPTO)

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 2, 2001, 09:58:55 ; Search time 4027.99 Seconds
(without alignments)
2964.446 Million cell updates/sec

Title: US-09-380-276A-2
Perfect score: 1704
Sequence: 1 gggaacgtagaactctccaa.....gaccacagatatacttttc 1704

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 7991742 seqs, 3503743858 residues 15983484
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*

1:	gb_est1.*
2:	gb_est2.*
3:	gb_est3.*
4:	gb_est4.*
5:	gb_est5.*
6:	gb_est6.*
7:	gb_est7.*
8:	gb_est8.*
9:	gb_est9.*
10:	gb_est10.*
11:	gb_est11.*
12:	gb_est12.*
13:	gb_est13.*
14:	gb_est14.*
15:	gb_est15.*
16:	gb_est16.*
17:	gb_est17.*
18:	gb_est18.*
19:	gb_est19.*
20:	gb_est20.*
21:	gb_est21.*
22:	gb_est22.*
23:	gb_est23.*
24:	gb_est24.*
25:	gb_est25.*
26:	gb_est26.*
27:	gb_est27.*
28:	gb_est28.*
29:	gb_est29.*
30:	gb_est30.*
31:	gb_est31.*
32:	gb_est32.*
33:	gb_est33.*
34:	gb_est34.*
35:	gb_est35.*
36:	gb_est36.*
37:	gb_est37.*
38:	gb_est38.*
39:	gb_est39.*
40:	gb_est40.*
41:	em_estba.*
42:	em_estfun.*
43:	em_esthum1.*
44:	em_esthum2.*
45:	em_esthum3.*
46:	em_esthum4.*
47:	em_esthum5.*
48:	em_esthum6.*
49:	em_esthum7.*
50:	em_esthum8.*
51:	em_esthum9.*
52:	em_esthum10.*
53:	em_esthum11.*
54:	em_esthum12.*
55:	em_esthum13.*
56:	em_esthum14.*
57:	em_esthum15.*
58:	em_esthum16.*
59:	em_esthum17.*
60:	em_esthum18.*
61:	em_esthum19.*
62:	em_esthum20.*
63:	em_estin1.*
64:	em_estin2.*
65:	em_estin3.*
66:	em_estin4.*
67:	em_estov1.*
68:	em_estov2.*
69:	em_estpl1.*
70:	em_estpl2.*
71:	em_estpl3.*
72:	em_estpl4.*
73:	em_estpl5.*
74:	em_estro1.*
75:	em_estro2.*
76:	em_estro3.*
77:	em_estro4.*
78:	em_estro5.*
79:	em_estro6.*
80:	em_estro7.*
81:	em_estro8.*
82:	em_estro9.*
83:	em_estro10.*
84:	em_estro11.*
85:	em_estro12.*
86:	em_estro13.*
87:	gb_est41.*
88:	gb_est42.*
89:	gb_est43.*
90:	gb_est44.*
91:	gb_est45.*
92:	gb_est46.*
93:	gb_est47.*
94:	gb_est48.*
95:	gb_est49.*
96:	gb_est50.*
97:	gb_est51.*
98:	gb_est52.*
99:	gb_est53.*
100:	gb_est54.*
101:	gb_est55.*
102:	gb_est56.*
103:	gb_est57.*
104:	gb_est67.*
105:	gb_est68.*
106:	gb_est69.*
107:	gb_est70.*
108:	gb_est71.*
109:	gb_est72.*
110:	gb_est73.*
111:	gb_est74.*
112:	em_esthum21.*
113:	em_esthum22.*
114:	em_esthum23.*
115:	em_estom1.*
116:	em_estom2.*

117: em_estpl6:*
118: em_estpl7:*
119: em_estpl8:*
120: em_estpl9:*
121: em_estpl10:*
122: em_estpl11:*
123: em_estpl12:*
124: em_estpl13:*
125: em_estpl14:*
126: em_estpl15:*
127: em_estpl16:*
128: em_estpl17:*
129: em_estpl18:*
130: em_estpl19:*
131: em_estpl20:*
132: em_estpl21:*
133: em_estpl22:*
134: em_estpl23:*
135: em_estpl24:*
136: em_estpl25:*
137: em_estpl26:*
138: em_estpl27:*
139: em_estpl28:*
140: em_estpl29:*
141: em_estpl30:*
142: em_estpl31:*
143: em_estpl32:*
144: em_estpl33:*
145: em_estpl34:*
146: em_estpl35:*
147: em_estpl36:*
148: em_estpl37:*
149: em_estpl38:*
150: em_estpl39:*
151: em_estpl40:*
152: em_estpl41:*
153: em_estpl42:*
154: em_estpl43:*
155: em_estpl44:*
156: em_estpl45:*
157: em_estpl46:*
158: em_estpl47:*
159: em_estpl48:*
160: em_estpl49:*
161: em_estpl50:*
162: em_estpl51:*
163: em_estpl52:*
164: em_estpl53:*
165: em_estpl54:*
166: em_estpl55:*
167: em_estpl56:*
168: em_estpl57:*
169: em_estpl58:*
170: em_estpl59:*
171: em_estpl60:*
172: em_estpl61:*
173: em_estpl62:*
174: em_estpl63:*
175: em_estpl64:*
176: em_estpl65:*
177: em_estpl66:*
178: em_estpl67:*
179: em_estpl68:*
180: em_estpl69:*
181: em_estpl70:*
182: em_estpl71:*
183: em_estpl72:*
184: em_estpl73:*
185: em_estpl74:*
186: em_estpl75:*
187: em_estpl76:*
188: em_estpl77:*
189: em_estpl78:*

190: gb_gss25:*
191: gb_gss26:*
192: gb_gss27:*
193: gb_gss28:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match %	Score	Length	DB	ID	Description
1	302.2	17.7	395	106	BE306459	BE306459 601103459
2	274.8	16.1	282	28	AL036000	AL036000 DKFp584K
3	273.8	16.1	454	147	W56629	W56629 xdl6e11.r1
4	264.8	15.5	534	135	BE757704	BE757704 212225 MA
5	215.6	12.7	401	1	AA003356	AA003356 mg4901.r
6	192.8	11.3	369	91	AA478317	AA478317 19558 MAR
7	186.6	11.0	358	1	AA036247	AA036247 ml74803.r
8	165	9.7	325	140	D82546	D82546 HUMHBC4158
9	163	9.7	461	140	D82492	D82492 HUMHBC4526
10	165	9.7	489	140	D82272	D82272 HUMHBC4271
11	165	9.7	515	140	D82308	D82308 HUMHBC4605
12	164	9.6	417	140	D82482	D82482 HUMHBC4476
13	160	9.4	392	140	D82504	D82504 HUMHBC4605 H
14	157.6	9.2	258	133	BB542020	BB542020 BB542020
15	155	9.1	643	159	AQ563354	AQ563354 HS_5335_B
16	152.4	8.9	157	140	D82323	D82323 HUMHBC4706
17	125.8	7.4	646	159	AQ544065	AQ544065 RPCI-11-3
18	124.4	7.3	275	31	AV111112	AV111112 AV111112
19	120.8	7.1	404	8	AA495217	AA495217 fa04d10.r
20	113.8	6.7	450	158	AQ514075	AQ514075 HS_5184_A
21	112.4	6.6	414	91	AW527025	AW527025 UI-R-B01-
22	95	5.6	1110	193	CNS050TC	AL347097 Tetraodon
23	86.8	5.1	381	21	AI551729	AI551729 vfl1e02.y
24	80	4.7	425	31	AV167843	AV167843 AV167843
25	67.4	4.0	442	109	BE554624	BE554624 ur48c11.y
26	59	3.5	405	150	AQ173919	AQ173919 HS_3204_A
27	58	3.4	485	28	AL120773	AL120773 DKFp762C
28	42.6	2.5	443	11	AA759377	AA759377 ah54a10.s
29	41.4	2.4	551	12	AA814296	AA814296 nz07d08.s
30	40.2	2.4	255	7	AA445805	AA445805 vfl1e02.r
31	39.4	2.3	397	13	AA860208	AA860208 ak48c10.s
32	39.4	2.3	465	147	W47341	W47341 zc34h02.s1
33	39.2	2.3	266	128	BB350382	BB350382 BB350382
34	39	2.3	407	146	W32428	W32428 zc05c12.s1
35	39	2.3	559	3	AA161105	AA161105 zc05c05.s
36	38.8	2.3	706	109	BE535395	BE535395 601058548
37	38.8	2.3	925	190	CNS0091P	AL053013 Drosophila
38	38.6	2.3	502	13	AA925878	AA925878 UI-R-A1-e
39	38.6	2.3	552	134	BE104177	BE104177 UI-R-BX0-
40	38.6	2.3	554	17	AI171746	AI171746 EST217728
41	38.6	2.3	555	17	AI179276	AI179276 EST222969
42	38.2	2.2	1082	193	CNS05NLR	AL345528 Tetraodon
43	38	2.2	391	21	AI522266	AI522266 t184f06.x
44	38	2.2	597	97	AA968349	AA968349 EST380424
45	37.8	2.2	458	88	AW303441	AW303441 xvl19b01.x

ALIGNMENTS

RESULT 1

BE306459

LOCUS

DEFINITION

BE306459

ACCESSION

VERSION

KEYWORDS

SOURCE

BE306459

601103459f1 NCI_CGAP_Lu29

mus musculus

CDNA clone IMAGE:3495566 5'

EST

13-JUL-2000

395 bp

mRNA

sequence.

BE306459

BE306459.1

GI:9159707

EST.

house mouse.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 454)
AUTHORS Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P., and Wilson, R.
TITLE The WashU-Merck EST Project
JOURNAL Unpublished (1995)
COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LML; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1373 Std Error: 0.00
Seq primer: mob.REGA+ET.
FEATURES
1..454
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="GB:1266219"
/db_xref="taxon:9606"
/clone="IMAGE:34084"
/clone_lib="Soares_fetal_heart_NbHH19W"
/sex="unknown"
/dev_stage="19 weeks"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ: heart; Vector: pT73D (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCATCTCAAGTGGAGCGCGCGCATCTTTTCTTTTCTTTT 3'] double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT73 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by M.Fatima Bonaldo. This library was constructed from the same fetus as the fetal lung library, Soares fetal lung NBHH19W."

BASE COUNT 132 a 96 c 88 g 138 t
ORIGIN
Query Match 16.1%; Score 273.8; DB 147; Length 454;
Best Local Similarity 99.3%; Pred. No. 1.6e-70;
Matches 275; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1016 ctcttaccctgaactcactggaagacattctctctcaatccagaaacttgaaagctc 1075
Db 1 CTCTTATCTGAACTCACTCGAAGACATTCATCTCTCAATCCAGAACTTGAAAGCTC 60
QY 1076 aacgtcttggattcaaatagcagctcaagatttgggtgggtgggtggttcacgtccagtc 1135
Db 61 AAGCTCTTTGGATTCAAAATAGCAGTCAAGATTGGTTGGTGGGGCTGTTCCAGTCCAGTC 120
QY 1136 tcattctgaaactttacagcagctactgatttatctatagatataaacaacactggtaga 1195
Db 121 TCATTTCTGAAACTTTTACAGCAGCTACTGATTTATCTAGATATAAACAACACACTGGTAGA 180
QY 1196 atcagatcaactcaggatgcactaactatgagaagccagctagatcagagagtggtgcgc 1255
Db 181 ATCAGCATCAACTCAGGATGCATTAAGTATGAGAACCCAGCTAGATCAGGAGAGTGCGCG 240
QY 1256 tataatcccccagcactcagacgtccctccaggaa 1292
Db 241 TGTTCATCCAGCCGCACTCAGACGTCCTCCAGGTA 277

RESULT 4
BE757704

LOCUS BE757704 534 bp mRNA EST 15-SEP-2000
DEFINITION 212225 MARC 2BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION BE757704
VERSION BE757704.1 GI:10171696
KEYWORDS EST.
SOURCE Bos taurus
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
REFERENCE 1 (bases 1 to 534)
AUTHORS Smith, T.P.L., Casas, E., Stone, R.T., Heaton, M.P., Grosse, W.M., Bennett, G.A., Fahrenkrug, S.C., Freking, B.A., Rohrer, G.A., Lagreid, W.W., and Keele, J.W.
TITLE Design and use of four pooled tissue normalized cDNA libraries for EST discovery in cattle
JOURNAL Unpublished (2000)
COMMENT Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 18 and -minmatch 12 options.
PCR PRIMERS
FORWARD: AGGAACACGCTATGACCAT
BACKWARD: GTTTCCTCCAGTCACGACG
Plate: 65 row: C column: 2
Seq primer: ATTTAGGTGACATATAG.
FEATURES
Location/Qualifiers
1..534
/organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="MARC 2BOV"
/tissue_type="pooled"
/lab_host="DH10B"
/note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI;
Library made from pooled tissue from testis, thymus, semilendonsus muscle, longissimus muscle, pancreas, adrenal, and endometrium."

BASE COUNT 122 a 117 c 171 g 124 t
ORIGIN
Query Match 15.5%; Score 264.8; DB 135; Length 534;
Best Local Similarity 82.9%; Pred. No. 8.5e-68;
Matches 315; Conservative 0; Mismatches 62; Indels 3; Gaps 1;
QY 7 gtagaactctcccaataataacatttgataagaagaatggcttcaaaagtgtactag 66
Db 158 GAAGACGCTCTTCAACCCAGAAATACATTTAATAGACGAATGGCTTCAACAGCTGCTACTCA 217
QY 67 aacagagagaaacgcttttcaactcttttagtattactagctattgttcattgtaaaagtga 126
Db 218 GGCAACAGAAA---TCTTCCAGCTGTGTAGTTTACTAGCTCTTTGGCATGTGGAGTGA 274
QY 127 ctgtgaaacagagagactgtagacacagaatctcgggagatcggtctggaactgtgttc 186
Db 275 TTTGTGAACAGAGAGACTGTGGACAGCAGGAATTCAGGGACCACTGAGGAAGCTGTGTTC 334
QY 187 cctgcaacagctgtggccagcagctgaggtgtctgaaggaatgtggtctcggtatgggg 246
Db 335 TGTGCAAGCAGTGTGGCCAGGCAATGTGTGTCACAGGAATGTGGCTTTGGCTAGCGGG 394
QY 247 aggatgcacagtggtgacggtgccggtgcacaggttcaaggaggactggggtcttcaga 306
Db 395 AGGACGCCCACTGTGTGAAGTGGCCGCGCACAGGTTCAAGGAGGACTGGGGCTCTCAGA 454
QY 307 aatgcaagccctgtctggagactgcagagtggtgaaaccgcttccagagggcaaatgttcag 366
Db 455 AGTGAAGCCGTCCTGGAGCTGCTGAGCCCTGCTGAGCCCTTCCAGAGGCCCACTGCTCGG 514


```
Db 1 CCTACATGAGAGCTTCTCTGCCACAAAAGTGACTTCAAAGACGGATGGTTGAGCTGCG 60
QY 1600 agcctatgagattgtggacataatacaagaacagaataatgcctcatctatttttcag 1659
|||||
Db 61 AGCCTATGAGATGTGGACATATACAGAAACAGAAATGCCCTCATGCTTATTTTCATG 120
QY 1660 gtgattgtggttttcaagactgaagaccagagatatacttttc 1704
|||||
Db 121 GTGATTGTGGTTTACAAAGACTGAAGACCCAGAGTATACTTTTC 165

RESULT 9
LOCUS D82492
DEFINITION HUMHC4526 Human pancreatic islet Homo sapiens cDNA, mRNA sequence.
ACCESSION D82492
VERSION D82492.1 GI:1183664
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 461)
Takeda,J.
Human pancreatic islet ESTs
Unpublished (1995)
Contact: Jun Takeda
Institute for Molecular and Cellular Regulation, Gunma University
3-39-15 Showa-machi, Maebashi Gunma 371, Japan
Tel: 272-20-8856
Fax: 272-20-8896
Email: jtakeda@sb.gunma-u.ac.jp.
Location/Qualifiers
1. 461
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="Human pancreatic islet"
/note="Vector: Lambda ZAPII; Site.1: Eco RI; Site.2: Xho
I; mRNA was prepared from normal adult human islets. cDNA
was directionally synthesized from the Xho I in the vector
to the EcoRI site. cDNA was size fractionated to remove
sequences <1000 bp in size."
BASE COUNT 137 a 91 c 96 g 134 t 3 others
ORIGIN

Query Match 9.7%; Score 165; DB 140; Length 461;
Best Local Similarity 100.0%; Pred. No. 5.3e-38;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1540 cctacatgagaagcttctgtccacaaagtgaactcaagaacgagatgggtgagctggc 1599
|||||
Db 1 CCTACATGAGAGCTTCTCTGCCACAAAAGTGACTTCAAAGACGGATGGTTGAGCTGCG 60
QY 1600 agcctatgagattgtggacataatacaagaacagaataatgcctcatctatttttcag 1659
|||||
Db 61 AGCCTATGAGATGTGGACATATACAGAAACAGAAATGCCCTCATGCTTATTTTCATG 120
QY 1660 gtgattgtggttttcaagactgaagaccagagatatacttttc 1704
|||||
Db 121 GTGATTGTGGTTTACAAAGACTGAAGACCCAGAGTATACTTTTC 165

RESULT 10
LOCUS D82272
DEFINITION HUMHC4271 Human pancreatic islet Homo sapiens cDNA, mRNA sequence.
ACCESSION D82272
VERSION D82272.1 GI:1183487
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```

```
REFERENCE
AUTHORS Takeda,J.
TITLE Human pancreatic islet ESTs
JOURNAL Unpublished (1995)
COMMENT Contact: Jun Takeda
Institute for Molecular and Cellular Regulation, Gunma University
3-39-15 Showa-machi, Maebashi Gunma 371, Japan
Tel: 272-20-8856
Fax: 272-20-8896
Email: jtakeda@sb.gunma-u.ac.jp.
Location/Qualifiers
1. 489
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="Human pancreatic islet"
/note="Vector: Lambda ZAPII; Site.1: Eco RI; Site.2: Xho
I; mRNA was prepared from normal adult human islets. cDNA
was directionally synthesized from the Xho I in the vector
to the EcoRI site. cDNA was size fractionated to remove
sequences <1000 bp in size."
BASE COUNT 144 a 94 c 110 g 138 t 3 others
ORIGIN

Query Match 9.7%; Score 165; DB 140; Length 489;
Best Local Similarity 100.0%; Pred. No. 5.4e-38;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1540 cctacatgagaagcttctgtccacaaagtgaactcaagaacgagatgggtgagctggc 1599
|||||
Db 1 CCTACATGAGAGCTTCTCTGCCACAAAAGTGACTTCAAAGACGGATGGTTGAGCTGCG 60
QY 1600 agcctatgagattgtggacataatacaagaacagaataatgcctcatctatttttcag 1659
|||||
Db 61 AGCCTATGAGATGTGGACATATACAGAAACAGAAATGCCCTCATGCTTATTTTCATG 120
QY 1660 gtgattgtggttttcaagactgaagaccagagatatacttttc 1704
|||||
Db 121 GTGATTGTGGTTTACAAAGACTGAAGACCCAGAGTATACTTTTC 165

RESULT 11
LOCUS D82308
DEFINITION HUMHC4605 Human pancreatic islet Homo sapiens cDNA, mRNA sequence.
ACCESSION D82308
VERSION D82308.1 GI:1183724
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 515)
Takeda,J.
Human pancreatic islet ESTs
Unpublished (1995)
Contact: Jun Takeda
Institute for Molecular and Cellular Regulation, Gunma University
3-39-15 Showa-machi, Maebashi Gunma 371, Japan
Tel: 272-20-8856
Fax: 272-20-8896
Email: jtakeda@sb.gunma-u.ac.jp.
Location/Qualifiers
1. 515
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="Human pancreatic islet"
/note="Vector: Lambda ZAPII; Site.1: Eco RI; Site.2: Xho
I; mRNA was prepared from normal adult human islets. cDNA
was directionally synthesized from the Xho I in the vector
to the EcoRI site. cDNA was size fractionated to remove
sequences <1000 bp in size."
FEATURES
source
```

```
BASE COUNT      153 a   102 c   113 g   141 t   6 others
ORIGIN

Query Match      9.7%; Score 165; DB 140; Length 515;
Best Local Similarity 100.0%; Pred. No. 5.5e-38;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1540 cctacatgagaagctctctgcacaaaagtgcattcaagaacgagatgggtgagctgac 1599
Db 1 CCTACATGAGAAGCTTCTCTGCCACAAAAGTGACTTCAAAGACGAGGATGGGTGAGCTGGC 60

QY 1600 agcctatgagattgtgacataaacaagaacagaaatgccctcatgcttatttttc 1659
Db 61 AGCCTATGAGATTGTGCACATATAACAAGAACAGAAATGCCCTCATGCTTATTTCATG 120

QY 1660 gtgattgtggtttacaagactgaagaccagaggtatactttttc 1704
Db 121 GTGATTGTGGTTTACAAGACTGAAGACCCAGAGTATACTTTTTC 165

RESULT 12
D82482
LOCUS      D82482      417 bp      mRNA      EST      09-FEB-1996
DEFINITION HUMHBC4476 Human pancreatic islet Homo sapiens cDNA, mRNA sequence.
ACCESSION  D82482
VERSION     D82482.1 GI:1183621
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 417)
AUTHORS     Takeda, J.
TITLE       Human pancreatic islet ESTs
JOURNAL     Unpublished (1995)
COMMENT     Contact: Jun Takeda
            Institute for Molecular and Cellular Regulation, Gunma University
            3-39-15 Showa-machi, Maebashi Gunma 371, Japan
            Tel: 272-20-8856
            Fax: 272-20-8896
            Email: jtakeda@sb.gunma-u.ac.jp.
FEATURES    Location/Qualifiers
             1..392
             /organism="Homo sapiens"
             /db_xref="taxon:9606"
             /clone_lib="Human pancreatic islet"
             /note="Vector: Lambda ZAPII; Site_1: Eco RI; Site_2: Xho
             I; mRNA was prepared from normal adult human islets. cDNA
             was directionally synthesized from the Xho I in the vector
             to the EcoRI site. cDNA was size fractionated to remove
             sequences <1000 bp in size."
BASE COUNT   126 a   77 c   86 g   122 t   6 others
ORIGIN

Query Match      9.6%; Score 164; DB 140; Length 417;
Best Local Similarity 99.4%; Pred. No. 1e-37;
Matches 164; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1540 cctacatgagaagctctctgcacaaaagtgcattcaagaacgagatgggtgagctgac 1599
Db 1 CCTACATGAGAAGCTTCTCTGCCACAAAAGTGACTTCAAAGACGAGGATGGGTGAGCTGGC 60

QY 1600 agcctatgagattgtgacataaacaagaacagaaatgccctcatgcttatttttc 1659
Db 61 AGCCTATGAGATTGTGCACATATAACAAGAACAGAAATGCCCTCATGCTTATTTCATG 120

QY 1660 gtgattgtggtttacaagactgaagaccagaggtatacttttc 1704
Db 121 GTGATTGTGGTTTACAAGACTGAAGACCCAGAGTATACTTTTTC 165

RESULT 13
D82504
LOCUS      D82504      392 bp      mRNA      EST      09-FEB-1996
DEFINITION HUMHBC4605 Human pancreatic islet Homo sapiens cDNA, mRNA sequence.
ACCESSION  D82504
VERSION     D82504.1 GI:1183160
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 392)
AUTHORS     Takeda, J.
TITLE       Human pancreatic islet ESTs
JOURNAL     Unpublished (1995)
COMMENT     Contact: Jun Takeda
            Institute for Molecular and Cellular Regulation, Gunma University
            3-39-15 Showa-machi, Maebashi Gunma 371, Japan
            Tel: 272-20-8856
            Fax: 272-20-8896
            Email: jtakeda@sb.gunma-u.ac.jp.
FEATURES    Location/Qualifiers
             1..392
             /organism="Homo sapiens"
             /db_xref="taxon:9606"
             /clone_lib="Human pancreatic islet"
             /note="Vector: Lambda ZAPII; Site_1: Eco RI; Site_2: Xho
             I; mRNA was prepared from normal adult human islets. cDNA
             was directionally synthesized from the Xho I in the vector
             to the EcoRI site. cDNA was size fractionated to remove
             sequences <1000 bp in size."
BASE COUNT   115 a   70 c   84 g   112 t   11 others
ORIGIN

Query Match      9.4%; Score 160; DB 140; Length 392;
Best Local Similarity 97.0%; Pred. No. 1.5e-36;
Matches 160; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1540 cctacatgagaagctctctgcacaaaagtgcattcaagaacgagatgggtgagctgac 1599
Db 1 CCTACATGAGAAGCTTCTCTGCCACAAAAGTGACTTCAAAGACGAGGATGGGTGAGCTGGC 60

QY 1600 agcctatgagattgtgacataaacaagaacagaaatgccctcatgcttatttttc 1659
Db 61 AGCCTATGAGATTGTGCACATATAACAAGAACAGAAATGCCCTCATGCTTATTTCATG 120

QY 1660 gtgattgtggtttacaagactgaagaccagaggtatacttttc 1704
Db 121 GTGATTGTGGTTTACAAGACTGAAGACCCAGAGTATACTTTTTC 165

RESULT 14
BB542020
LOCUS      BB542020      258 bp      mRNA      EST      31-JUL-2000
DEFINITION RIKEN full-length enriched, 0 day neonate eyeball Mus
            musculus cDNA clone E130118G08 3', mRNA sequence.
ACCESSION  BB542020
VERSION     BB542020.1 GI:9613243
KEYWORDS    EST.
SOURCE      house mouse.
ORGANISM    Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 258)
AUTHORS     Konno, H., Aizawa, K., Akahira, S., Akiyama, J., Arakawa, T., Carninci
            P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N.,
            Hirozane, T., Hori, F., Ishii, Y., Ishikawa, J., Ishikawa, T., Itoh, M.,
            Izawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N.,
            Kiyosawa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C., Kusakabe, M.,
            Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y.,
            Ono, T., Owa, C., Saito, H., Sakai, C., Sato, K., Shibata, K., Shibata
            Y., Shigemoto, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Suganara, Y.,
```


Qy 609 tgtgtcatctattgttaagagacagtttatggagaagaacccagctggtctctgcggtca 668
|||||
Db 435 TGTGTCATCTATTGTAAGAGACAGTNTATGGAGAAGAAACCCAGCTCTAAGTGTGAGCT 494
|||||
Qy 669 caggacattcagtacaac 686
|||
Db 495 CATTACATNTCTTATCAC 512
|||

Search completed: March 2, 2001, 09:59:02
Job time: 28927 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 2, 2001, 12:59:17 ; Search time 8955.7 Seconds
(without alignments)
1942.344 Million cell updates/sec

Title: US-09-380-276A-5
Perfect score: 1269
Sequence: 1 atggcttaaaagtgtact.....ggcagcgactgggttccttg 1269

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
Searched: 1118133 seqs, 6853842396 residues
Total number of hits satisfying chosen parameters: 2236266

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*
1: gb_bal.*
2: gb_ba2.*
3: gb_om.*
4: gb_ov.*
5: gb_ph.*
6: gb_pl1.*
7: gb_pl2.*
8: gb_pr1.*
9: gb_pr2.*
10: gb_pr3.*
11: gb_ro.*
12: gb_sy.*
13: gb_un.*
14: em_fun.*
15: em_hum1.*
16: em_hum2.*
17: em_in.*
18: em_om.*
19: em_or.*
20: em_ov.*
21: em_pat.*
22: em_ph.*
23: em_pl.*
24: em_ro.*
25: em_sts.*
26: em_sy.*
27: em_un.*
28: em_vl.*
29: gb_htg1.*
30: gb_htg2.*
31: gb_in1.*
32: gb_in2.*
33: em_ba1.*
34: em_ba2.*
35: em_hum3.*
36: em_hum4.*
37: gb_pr4.*
38: gb_htg3.*
39: gb_htg4.*
40: gb_htg5.*
41: gb_htg6.*
42: gb_htg7.*
43: em_htg1.*

44: em_htg2.*
45: em_htg3.*
46: em_hum5.*
47: gb_pl3.*
48: gb_pr5.*
49: gb_htg8.*
50: gb_htg9.*
51: gb_htg10.*
52: gb_htg11.*
53: gb_htg12.*
54: gb_htg13.*
55: gb_htg14.*
56: gb_in3.*
57: gb_htg15.*
58: gb_htg16.*
59: gb_htg17.*
60: em_htg4.*
61: em_htg5.*
62: em_htg6.*
63: em_htg7.*
64: em_hum6.*
65: gb_htg18.*
66: gb_htg19.*
67: gb_htg20.*
68: gb_htg21.*
69: gb_htg22.*
70: gb_htg23.*
71: gb_vil.*
72: gb_vil2.*
73: gb_ba3.*
74: em_htg8.*
75: em_htg9.*
76: em_htg10.*
77: gb_pr6.*
78: gb_pr7.*
79: gb_sts1.*
80: gb_sts2.*
81: gb_pat1.*
82: gb_pat2.*
83: em_htg0.*
84: gb_htg24.*
85: gb_pr8.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	1264.2	99.6	1364	8	AB040434	AB040434 Homo sapi
2	1256.2	99.0	1489	37	AF167555	AF167555 Homo sapi
3	732.4	57.7	3964	11	AB040432	AB040432 Mus muscu
4	729.2	57.5	1678	11	AF167552	AF167552 Mus muscu
5	680.8	53.6	1075	11	AF173166	AF173166 Mus muscu
6	449	35.4	744	11	AB040433	AB040433 Mus muscu
7	449	35.4	886	11	AF167553	AF167553 Mus muscu
8	428.8	33.8	143608	67	AL161422	AL161422 Homo sapi
9	428.8	33.8	178256	66	AL139080	AL139080 Homo sapi
10	314	24.7	591	11	AF167554	AF167554 Mus muscu
11	73	5.8	188351	67	AL353136	AL353136 Homo sapi
12	73	5.8	205736	51	AC023560	AC023560 Homo sapi
13	65.4	5.2	205736	51	AC023560	AC023560 Homo sapi
14	43.6	3.4	160214	54	AC034198	AC034198 Homo sapi
15	43.6	3.4	180511	42	AC018836	AC018836 Homo sapi
16	43.6	3.4	209876	10	AC011599	AC011599 Homo sapi
17	42	3.3	207166	42	AC018843	AC018843 Homo sapi
18	38.8	3.1	200948	38	AC010331	AC010331 Homo sapi
19	38.8	3.1	204573	41	AC016589	AC016589 Homo sapi
20	38.4	3.0	145934	67	AL353611	AL353611 Homo sapi
21	38.4	3.0	148018	67	AL159992	AL159992 Homo sapi

c 22 38.4 3.0 171491 50 AC022606 AC022606 Homo sapi
 23 37.8 3.0 108774 70 AP001862 AP001862 Homo sapi
 24 37.8 3.0 177014 8 AC004063 AC004063 Homo sapi
 25 37.8 3.0 189239 53 AC026557 AC026557 Homo sapi
 26 37.6 3.0 38532 73 SCE94 AL04928 Streptomy
 c 27 37.6 3.0 186797 49 AC021965 AC021965 Homo sapi
 28 37.6 3.0 188351 67 AL353136 AL353136 Homo sapi
 c 29 37.4 2.9 32354 73 SCD84 AL353816 Streptomy
 c 30 37.4 2.9 73868 55 AC055762 AC055762 Homo sapi
 31 37 2.9 154378 7 AP001383 AP001383 Oryza sat
 32 37 2.9 159099 69 AL359749 AL359749 Homo sapi
 33 37 2.9 171031 51 AC024503 AC024503 Homo sapi
 c 34 36.8 2.9 680 4 CHRC1A201 J00821 Chicken alp
 35 36.8 2.9 162025 9 AC005730 AC005730 Homo sapi
 c 36 36.6 2.9 15355 1 AE005026 AE005026 Halobacte
 c 37 36.6 2.9 166712 39 AC012213 AC012213 Homo sapi
 c 38 36.4 2.9 2890 10 AF030177 AF030177 Homo sapi
 c 39 36.4 2.9 2921 8 AB003723 AB003723 Homo sapi
 40 36.4 2.9 32723 32 CSM88 234802 Caenorhabdi
 41 36.4 2.9 41906 73 SC5C7 AL031515 Streptomy
 42 36.2 2.9 3154 56 LMCCR2 X69521 L.migratori
 43 36.2 2.9 31261 32 CELF33G12 U41278 Caenorhabdi
 c 44 36.2 2.9 71412 54 AC040891 AC040891 Homo sapi
 c 45 36.2 2.9 159397 53 AC027040 AC027040 Homo sapi

ALIGNMENTS

RESULT 1
 LOCUS AB040434 1364 bp mRNA PRI 22-JUL-2000
 DEFINITION Homo sapiens mRNA for hTROY, complete cds.
 ACCESSION AB040434
 VERSION AB040434.1 GI:9392329
 KEYWORDS hTROY.
 SOURCE Homo sapiens cDNA to mRNA.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (sites)
 AUTHORS Kojima,T., Morikawa,Y., Copeland,N.G., Gilbert,D.J., Jenkins,N.A.,
 Senba,E. and Kitamura,T.
 TITLE hTROY, a newly identified member of the tumor necrosis factor
 receptor superfamily, exhibits a homology with Edar and is
 expressed in embryonic skin and hair follicles
 J. Biol. Chem. 275 (27), 20742-20747 (2000)
 20347167
 JOURNAL 2 (bases 1 to 1364)
 MEDLINE Kojima,T. and Kitamura,T.
 REFERENCE Direct Submission
 AUTHORS Submitted (23-MAR-2000) to the DDBJ/EMBL/GenBank databases, Tetsuo
 TITLE Kojima, Chugai Research Institute for Molecular Medicine, Inc.,
 CytoKine Research Program; 153-2 Nagai, Niihari, Ibaraki 300-4101,
 Japan (E-mail:kojima@cimed.com, Tel:81-298-306211,
 Fax:81-298-306270)
 COMMENT Sequence updated (06-Apr-2000).
 FEATURES
 source
 1..1364
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 37..1308
 /gene="hTroy"
 37..1308
 /gene="hTroy"
 /codon_start=1
 /product="hTROY"
 /protein_id="BAB03269.1"
 /db_xref="GI:9392330"
 /translation="WALKVLEQETFFLLVLGVLSCKVTCESGDCRQORFRDRSG
 NCVPNOCSPGHLSKEGFGYGEAQCVCRLHRPKEDWGWKCKPCLDCAVNRQ
 KANCATSDAICGDCUPGYRNTKLGVFQDMCEVCPGDPPTPIEPHCAKSNVLKIAS
 TASSPRDTALAAVIGSALATVLLALLILCVIYKQFMKPKPSWSLSODIYNGSEL

SCFDRPQLHEYAHRRACCCQRRDSVQTCVPVRLPLSMCCCEASPNPALTGCGVHSAAS
 LQARNAAGEMVFFPFGSLTOSIGCEFSWAMPNMGDNISFCDSYSPELTGEDI
 HSLNLESSTSLDSNSQDLVGVAPVQSHSENFTAATDLRYNNTLVSQASTQDAL
 TWRSQDDQESGAVIHPATQTSLOVQRQLSL*
 BASE COUNT 325 a 351 c 358 g 330 t
 ORIGIN
 Query Match 99.6%; Score 1264.2; DB 8; Length 1364;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 1266; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 atgctctttaaagtctactagacaagaagaaacgtttttcactcttttagtattacta 60
 |||||
 Db 37 ATGGCTTTAAAGTGTACTAGAACAGAGAAACGTTTTTCACTCTTTTAGTATTACTA 96
 |||||
 QY 61 ggctatttgcatagtataaagtacttgaacacaggagactgttagacagcaagaattcaag 120
 |||||
 Db 97 GGCTATTGTCTATGTAAGTGTACTTGTGAATCAGGAGACTGTAGACAGCAAGAAATTCAGG 156
 |||||
 QY 121 gacgctctggaactgtgttccctgcaaccagtggtggccagcagcatgagttgtctaaag 180
 |||||
 Db 157 GATCGGTGTGAAACGTGTGTCTCCCTGCACACAGTGTGGCCAGCATGGAGTGTCTTAAG 216
 |||||
 QY 181 gaatgtggtctcggtctatggggagagatgcacagtggtgacgtgcccgggtgcacaggttc 240
 |||||
 Db 217 GAATGTGGCTTCGGCTATGGGAGGATGCACACTGTGTGACGTGCCGGCTGCACAGGTTTC 276
 |||||
 QY 241 aaggagactggggcttccagaataatgcaagccctgtctggactgcagtcggtgaaccgc 300
 |||||
 Db 277 AAGGAGGACTGGGGCTTCCAGAAATGCAAGCCCTGTCTGGACTGCCGAGTGGTGAACCGC 336
 |||||
 QY 301 ttccagaagcaaatgttcagccaccagtgatgccatctgcgggactgcttgccagga 360
 |||||
 Db 337 TTTCAAGGCAAAATTTGTCAGCCACCAAGTGTGCCATCTGCCGGGACTCTCTGCCAGGA 396
 |||||
 QY 361 ttttaaggagaagcaaaactgtcgcttttcaagacatggagtggtgctcttgagagac 420
 |||||
 Db 397 TTTTATAGGAAGACGAAACTTGTGCGCTTTTCAAGACATGAGTGTGTGCTTCTGGAGAC 456
 |||||
 QY 421 cttctctctcttaagaacccgactgtgccagcaaggtcaaacctcgtgaagatcgagtc 480
 |||||
 Db 457 CTTCTCTCTCTTACGAACCCGACTGTGCCAGCAAGGTCAACCTCGTGAAGATCGCGTCC 516
 |||||
 QY 481 acggtccacagccacgggacacggcgctggtgcgcttatctgcagcgcctctggccacc 540
 |||||
 Db 517 ACGGCTTCCAGCCACCGGACACGGGCGTGGCTGCTGCTTATCTGCAGCGCTCTGGCCACC 576
 |||||
 QY 541 gtcctgtggccctgtctcatctctgtgtcatctattgttaagagacagtttatggagaag 600
 |||||
 Db 577 GTCCTGTGCGCCCTGTCTCATCTCTGTGTCTATTATTGAAGAGACAGATTTATGGAGAG 636
 |||||
 QY 601 aaaccagctggtctctggtgtcacaggacattcagtaaacagggctctgagctgctggt 660
 |||||
 Db 637 AAACCCAGCTGGTCTCTGCGGTCACAGGACATTCAGTACAAACGGCTCTGAGCTGTCTGT 696
 |||||
 QY 661 cttagacagacctcagctccacgaatgcccacagacgctgctgctgctgctgctgctgac 720
 |||||
 Db 697 TTTGACAGACCTCAGCTCCACGAATATGCCACAGAGACCTTCTGCCAGTCCGCCCGTGC 756
 |||||
 QY 721 tcagtgacagacctgcggggcggtgctctgtctccatccatctgtgtgtgagggagctgct 780
 |||||
 Db 757 TCAGTGCAGACCTCGCGGCGGTCGCTTGTCTCCATCCATGCTGCTGTGAGGAGGCGCTGC 816
 |||||
 QY 781 agcccaaccccgcgactctgtgtgtgggtgcttcttctgacccagctcttcaaggaga 840
 |||||
 Db 817 AGCCCCAAACCCGCGACTCTTGTGTTGTGGGTGCATTTCTGCAGCCAGTCTTTCAGGCAAGA 876
 |||||
 QY 841 aacgagggccacggggagagtggtgcgacttctctcgatccctcacgagctccatc 900
 |||||
 Db 877 AAGCGAGGCCACCGCGGGAGATGTTGCCACACTTTCTTCTCGGATCCCTCACGAGTCCATC 936
 |||||
 QY 901 tgtggcgagtcttcagatgcctggtcctctgtagagaatcccatgggtgtgtagacaatc 960

Db 937 TGTGGCGAGTTTTCAGATGCCCTGGCCTCTGATGCAGAAATCCATCGGTGGTGACAACATC 996
Qy 961 tcttttttgactcttactgaactactgagagagacattctctcaatccagaa 1020
Db 997 TCTTTTGTGACTCTTATCCTGAATCTACTGGAGAAGACATTCATCTCTCAATCCAGAA 1056
Qy 1021 cttgaagctcaacgtcttttgattcaaatagcagtcgaagatttggttgggtgggctgtt 1080
Db 1057 CTTGAAGCTCAACGCTCTTGATTCAAATAGCAGTCAAGATTTGGTGGGGCTGTT 1116
Qy 1081 ccagtcagctctcttctgaataactttacagcagctactgatttcttagatatataaac 1140
Db 1117 CCAGTCCAGCTCTCATCTCTGAATCTTACAGCAGCTACTGATTTATCTAGATATAACAAC 1176
Qy 1141 acactggttagaagcagcactcaactcagatgcactaactatgagagccagctagatcag 1200
Db 1177 ACACGTGGTAGAATGAGTCAACTCAGGATGCACCTAACTATGAGAAGCCAGCTAGATCAG 1236
Qy 1201 gagagtggtcgctatcatccaccagccactcagacgctcctccaggttaagcagcagctg 1260
Db 1237 GAGAGTGGGCTGTCTATCCACCAGCCACTCAGACGTCCTCCAGGTAAAGCAGGACTG 1296
Qy 1261 ggttccctg 1269
Db 1297 GGTTCCTCG 1305

RESULT 2
AF167555 1489 bp mRNA PRI 25-MAY-2000
LOCUS Homo sapiens TAJ-alpha mRNA, complete cds.
DEFINITION AF167555
ACCESSION AF167555
VERSION AF167555.1 GI:8071643
KEYWORDS human.
SOURCE
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1489)
AUTHORS Eby,M.F., Jasmin,A., Kumar,A., Sharma,K. and Chaudhary,P.M.
TITLE TAJ, a Novel Member of the Tumor Necrosis Factor Receptor Family,
Activates the c-Jun N-terminal Kinase Pathway and Mediates
Caspase-Independent Cell Death
J. Biol. Chem. 275 (20), 15336-15342 (2000)
10809768
JOURNAL 2 (bases 1 to 1489)
PUBMED Chaudhary,P.M.
REFERENCE Direct Submission
AUTHORS Submitted (12-JUL-1999) Internal Medicine, UT Southwestern Medical
TITLE Center, 5323 Harry Hines Blvd., Dallas, TX 75235-8593, USA
JOURNAL
FEATURES
source 1..1489
/organism="Homo sapiens"
/db_xref="taxon:9606"
65..1336
/codon_start=1
/product="TAJ-alpha"
/protein_id="AAF71828.1"
/db_xref="GI:8071643"
CDS
translation="MALKVLLLEQKFTFTLLVLLGYSCKVTCEGDCRQGFRRDRSG
NCVPCQCGPMELSKCEGFGYGEDACVACRLHRFKEDWGFQKPCCLDCAVVNRFO
KANCSDATDGLPCGFYRKTKLVGFQDMCEVPCGDPDPPEPHCAASKVNLVKIAS
TASSPRDTALAAVICSALATVLLALLILCVLYCKQFMEKKPSLSRSDIQYNETEL
SCFDRPQIUEHAHRACQCRDSVQTCGFRVLLPSMCCCEACSPNPATLGGCVHSAAS
LOARNPAGMEVPTFFGLSTQISGEEFSDAWPLMNPMPGMDNIFSDQSYBELTGEDI
HSLNPLESSTSLDSNSQDLVGGAVPVQSHSENFTAAITDLRSYNNLTIVESASTODAL
TMRSDQESGAVIHPTQTSLOVQRQLGSL"
BASE COUNT 361 a 366 c 380 g 382 t
ORIGIN

Query Match 99.0%; Score 1256.2; DB 37; Length 1489;

Best Local Similarity 99.4%; Pred. No. 0;
Matches 1261; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
Qy 1 atgggttttaagaagtctactagaacaagagaaaaacgttttttcaactctttttagtatacta 60
Db 65 ATGGCTTTAAAGTCTACTAGAACAAAGAAAAAGCTTTTTCACCTCTTTTATGATTACTA 124
Qy 61 ggcattttgcatgtataaagtactgtgaaacagagagactgtagacagcaagaattcagg 120
Db 125 GGCATTTTTGTCTATGTAAAGTGACTTTGTGAATCAGGAGACTGTAGACAGCAAGAATTCAG 184
Qy 121 gatcggtctgaaacactgtgttccctgcaacacagtgctgggcccaggcatggagtgttctaag 180
Db 185 GATCGCTCTGGAACACTGTGTTCCTTCACCAACAGTGTGGGCCAGGCATGGAGTGTCTAAG 244
Qy 181 gaattggtctcggtatggggagagatgcacagatgtgtgacgtgcggtgcacaggttc 240
Db 245 GAATGTGGCTTCGGGTATGGGGAGGATGCACAGTGTGTGGCGTGCACAGGTTTC 304
Qy 241 aaggaggtactggggtcttcagaaaaatgcagccctctctggactgcgagtggtgaaccgc 300
Db 305 AAGGAGGACTGGGGCTTCAGAAATGCAAGCCCTGTCTGGACTGGCAGTGTGAACCCG 364
Qy 301 ttccagaaggcaaatgtttcagccaccagtgatgccatctcgcgggactgcttgcaga 360
Db 365 TTTTCAGAAAGGCAAAATGTTTCAGCCACCAGTGATGCCATCTCGGGGACTGCTTGCAGGA 424
Qy 361 ttttatagaagaacgaaactgtcggctttcaagacatggagtggtgcttctgtgagac 420
Db 425 TTTTATAGAAAGACGAAACTTTCGGCTTTTCAAGACATAGAGTGTGTGCTTTGTGGAGAC 484
Qy 421 cctctctctcttagaaccgcactgtgcagcaaggtcacaacctcgtgaagatcgcgtcc 480
Db 485 CTTCTCTCTCTTACGAACCCGACCTGTGCCACAGGTCACCTCTGTGAAGATTCGGTCC 544
Qy 481 acggctctcagccccagggacacgctggtgctgctgttatctgcagcgtctctgcccacc 540
Db 545 ACGGCTCTCAGCCACGCGGACACGCGCTGCTGCGTATCTGCAGCGCTCTGCGCCACC 604
Qy 541 gtctctgtggccctctcactctctgtctcatctatttgaagagacagtttatggagaag 600
Db 605 GTCTCTGTGGCCCTCTCTATCTCTGTGTCTATTTGTAAGAGACAGTFTTTATGAAAAAG 664
Qy 601 aaacccagctgtctctgcggtcagagacatttcagtaacaacgctctcgtgctctgt 660
Db 665 AAACCCAGCTGTCTCTGCGGTTCACAGGACATTCAGTACAAACAGACTGAGCTGTCTGT 724
Qy 661 cttgacagacctcagctccacgaatatgccacagagcctgctgcccagtgccgcgctgac 720
Db 725 TTTGACAGACCTCAGCTCCACGAATATGCCACAGAGCCTGCTGCCAGTGCCTGCGCGTGAC 784
Qy 721 tcagtgacagacctgcggccggtgcgctgtgctcccatccatgctgtgtgagagagcctgc 780
Db 785 TCAGTGCAGACCTGCGGGCCGGTGGCTGCTCCCATCCATCTGTGTGTGAGAGGCGCTGC 844
Qy 781 agcccccaacccgcgactcttgggtgtggtgctctcttcggatccccctcagcagtcac 840
Db 845 AGCCCCAACCCGCGGACTCTTGGTGTGGGGTGCACTTCTGCAGCCAGCTCTTCAGGCAAGA 904
Qy 841 aacgcagggccccgcgggagatggtgcccgaactttcttcggatccccctcagcagtcac 900
Db 905 AACGCAGGCCACGCGGGGAGATGGTCCGACTTTCTTCGGATCCCTCACGAGTCCATC 964
Qy 901 tgtggcgagttttcagatgcctcggcctctgtagcagaatccccatgggtgtgtgacaaatc 960
Db 965 TGTGGCAGCTTTTTCAGATGCCCTGGCCTCTGTATGCAGAAATCCCATGGGTGGTGACAAATC 1024
Qy 961 tcttttttgactcttctcctgaactcactgcagagacatctcctcctcattccattccagaa 1020
Db 1025 TCTTTTGTGACTCTTATCTCTGAATCTCAGTGGAGAAGACATTCATCTCTCAATCCAGAA 1084
Qy 1021 cttgaaagctcaacgtcttttgattcaaatagcagtcgaagatttggtggtgggctgtt 1080

Db 1085 CTTGAAAGCTCAACGCTCTTTGGATTCAAAATAGCAGTCAAGATTGGTTGGTGGGCTGTT 1144
 QY 1081 ccagtcagctctattctgaaactttacagcagctactgatttatctagataaacaac 1140
 Db 1145 CCAGTCCAGTCTCATCTGAAACTTTACAGCAGCTACTGATTATCTAGATATACAAAC 1204
 QY 1141 acactggtagaatcagcatcaactcaggatgcactaactatgagaagccagctagatcag 1200
 Db 1205 ACATGCTAGTAATCAGCATCACTCAGGATGCACCTAACTAATATGAGAAGCCAGCTAGATCAG 1264
 QY 1201 gagatggcgctatccaccagccactcagacgtccctccagtaaggcgagctg 1260
 Db 1265 GAGATGGCGCTGTCTACCCAGCCACTCAGACGCTCCCTCCAGGTAAAGCAGCTG 1324
 QY 1261 ggtccctg 1269
 Db 1325 GGTTCCTG 1333

RESULT 3
 AB040432 3964 bp mRNA ROD 22-JUL-2000
 LOCUS Mus musculus mRNA for TROY, complete cds.
 DEFINITION
 AB040432
 ACCESSION
 VERSION
 AB040432.1 GI:9392325
 KEYWORDS
 TROY.
 SOURCE
 Mus musculus cDNA to mRNA.
 ORGANISM
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 Senba, E. and Kitamura, T.
 Kojima, T., Morikawa, Y., Copeland, N.G., Gilbert, D.J., Jenkins, N.A.,
 1 (sites)
 TROY, a newly identified member of the tumor necrosis factor
 receptor superfamily, exhibits a homology with Edar and is
 expressed in embryonic skin and hair follicles
 J. Biol. Chem. 275 (27), 20742-20747 (2000)
 20347167
 2 (bases 1 to 3964)
 Kojima, T.
 Direct Submission
 Submitted (23-MAR-2000) to the DDBJ/EMBL/GenBank databases. Tetsuo
 Kojima, Chugai Research Institute for Molecular Medicine, Inc.,
 Cytokine Research Program; 153-2 Nagai, Niihari, Ibaraki 300-4101,
 Japan (E-mail: Kojima@climmed.com, Tel:81-298-306211,
 Fax:81-298-306270)

FEATURES
 Location/Qualifiers
 1..3964
 /organism="Mus musculus"
 /db_xref="taxon:10090"
 127..1377
 /gene="Troy"
 127..1377
 /gene="Troy"
 /note="a member of TNFR superfamily exhibits a homology
 with Edar"
 /codon_start=1
 /product="TROY"
 /protein_id="BAB03267.1"
 /db_xref="GI:9392325"
 /translation="WALKVPLHRTVLFPAAILLHLACKVSCETGDCRQBFKDRSG
 NCVLKCQPGMELSKCEGFGYGEDAQCVCPHRFKEDWGFQKPCADCALVNRFO
 RANCSHTSDAVGDCCLPGFYRTKLGVFODMECVCPGPPPEPHCTSKVNLVITSS
 TVSSPDRLAAVICALATVLLALILCVYCKRQFMKKPSWSILRSODIYNGSEL
 SFDPQLRHCRACCCQYHRDSAPWYGVPHLIPSLCCCEARSAVILGGLRSPFT
 LNPNPASVGDWTPAFVGSVRSICAEFSDWLMQNPGLGDSLSLSDSYPELTGDTN
 SLNPENASALDSSGGDLAGTAALSSGNSVSESTDSPRHGDITGTWQDTLAQDAQR
 TPSQGWEDRENILNAMPATFQDA"
 BASE COUNT 984 a 958 c 980 g 1041 t 1 others
 ORIGIN
 Query Match 57.7%; Score 732.4; DB 11; Length 3964;

Best Local Similarity 74.8%; Pred. No. 3.5e-187;
 Matches 932; Conservative 0; Mismatches 311; Indels 3; Gaps 1;
 QY 1 atggtcttaaaagtgtactacagaagaagaaacgttttttcaactcttttagtattacta 60
 Db 127 ATGGCACTCAAGTCTCACTTACACAGCAGCGTCTCTTCGCTGCCATCTCTCTTA 186
 QY 61 ggtatttgcataagtgacttgtgaacagagagactgttagacagcaagaattcagg 120
 Db 187 CTCACCTGGCATGTAAAGTGAGTTGCGAAACCGGAGATTGACAGGACGAGGANTTCAAG 246
 QY 121 gatcggtctggaaactgtttccctgtcaaccagtgtgggcccagggcatggagttgtctaa 180
 Db 247 GATCGATCTGGAACCTGTGTCTCTGCAAAACAGTGGCGACCTGGCATGGAGTTGTCCAAG 306
 QY 181 gaatgtggtctcggtatggggaggatgcacagtgtgtgacgtgcccgggtgcacaggttc 240
 Db 307 GAATGTGGCTTCGGCTATGGGAGGATGCACAGTGTGTGCTGTGCGGACGTGGCTGTGAACCGC 366
 QY 241 aaggagactgggctctccagaaatgcaagccctgtctggaactgcgcagtgtgtgaaccgc 300
 Db 367 AAGGAAGCTGGGGTTTCCAGAAAGTGTAAAGTGTGCGGACGTGGCTGTGAACCGC 426
 QY 301 ttccagaaggaatgttctcagccaccagtgtgcccactctgcgggactgtctgtgccagga 360
 Db 427 TTTTCAGAGGGCCAACTGCTCACACACAGTGTGCTGTGCGGGGACTGCCTGCCAGGA 486
 QY 361 tttataggaagcgaactgtcggtcttccagacatgtgagtggtgtgctgtgagagac 420
 Db 487 TTTTACCGGAAGACCAAACTGGTTGGTTTTCAGAGATGGAGTGTGTGCGCTCGGAGAC 546
 QY 421 cctcctcctcttaccgaacccagctgtgccagcaagctcaacctgtgaagatcgcgtcc 480
 Db 547 CGACCTCTCCCTACGACACCACTGTACCGAAGGTAACCTTTGTGAAGATCTCTCC 606
 QY 481 acggctccagcccaaggagacagcgctgtggtgcgttatctgcagcgcctctggccacc 540
 Db 607 ACCGTCTCCAGCCCTCGGGACACGGCGCTGGCTGCGCTCATCTGCAGTGTCTTGGCCACG 666
 QY 541 gtctctggtggtcctctcctctgtgtatctattgttaagagacagtttattggaag 600
 Db 667 GTGCTGCTCGCCCTGTCTATCTCTGTGTCTATCTACTGCAAGAGGAGGATTCATGGAGAAG 726
 QY 601 aaaccagctgtgtctgcggtcacaggacattcagacaaacggtctgtgagctgtcgtgt 660
 Db 727 AAACCCAGCTGGTCTCTGCGGTACAGGACATTCAGTACAAATGGCTGTGAGCTGTCTATGC 786
 QY 661 cttyacagacctcagctccacgaatatgccacagagcgtgtgctgcagtgcccggtgac 720
 Db 787 TTTTGACACAGCTCGGCTCCGCCACTGTGCCCATAGAGCATGCTGTGAGTATCACCGGGAC 846
 QY 721 tcaagtgcagacctgcgggcggctgtgctgtctcccatcctgtgtgctgtgagggagcctgc 780
 Db 847 TCAGCCCCAATGTATGGGCGCTGTACCTGATTCGCGTCTGTGTGTGTGAAGAGGCCCCG 906
 QY 781 agcccaaacccgcgactctgtgtgggtgtcattctcagcagcagctctcaggaaga 840
 Db 907 AGTCTCTGCCGAGCTGTGCTGTGGCTGTGGCTGTGCTGTCTCCCACTACCTCCAGGAGAGA 966
 QY 841 aacgagggccagccggggagagtgtgtgcgaactttcttoggatccctcagcagctccatc 900
 Db 967 AACCCGGCTCTGTGGGGACAGATGCCACCTTCTTCGGGTCTGTGTTCCTCCGTTCATC 1026
 QY 901 tgtggcaggttttcagatgctggtcctctgtatgcagaaatccctatgggtgtgagcaacatc 960
 Db 1027 TGGCGTGAATTTTCTGATGCTGGCTCTGCTGCAAAATCCTCTGGGTGTGTGTTCCTCCG 1083
 QY 961 tcttttgtgactcttctcctgaactcactgcagagacattcattctcctcaatccagaa 1020
 Db 1084 TCTCTGTGTGACTTATCTCTGAACCTCAGTGGAGAGATACCAATTCCTTCATCCCGAA 1143
 QY 1021 cttgaaagctcaacgtcttttggattcaaaatagcagtcagagattgtgtgtggtggtcgtt 1080

Db	1144	ACGAAGCCGAGCATCTCTGGATTCCAGTGGCGGCCGAGATCTGGCTGGGACAGCTGCT	1203
Qy	1081	ccagtcagctctcattctgaaactttacagcagctactgatttatctagataatacaac	1140
Db	1204	CTAGAGTCTTCTGGGAATGTTTTCAGAACTTACTGACTCACTAGACATGCTGACACTGGT	1263
Qy	1141	acactggtaaatcagcatcaactcagcagatgcactaactatgagaagcagctagatcag	1200
Db	1264	ACAGTCTGGAGAGCAGCGCTAGCTCAGGATGCTCAAGAGACTCCAAAGCAGGAGGCTGG	1323
Qy	1201	gagagtggcctcatccaccagcagcactcagacgtccctccag	1246
Db	1324	GAAGACAGGAARACCTGAATCTAGCCATGCCACACCCCTTCCAGG	1369
RESULT	4		
AF167552			
LOCUS	AF167552	1678 bp	25-MAY-2000
DEFINITION	Mus musculus TAJ-alpha long mRNA, complete cds.	rod	
ACCESSION	AF167552		
VERSION	AF167552.1	GI:8071637	
KEYWORDS	house mouse.		
SOURCE	Mus musculus		
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
REFERENCE	1 (bases 1 to 1678)		
AUTHORS	Eby, M.T., Jasmán, A., Kumar, A., Sharma, K. and Chaudhary, P.M.		
TITLE	TAJ, a Novel Member of the Tumor Necrosis Factor Receptor Family, Activates the c-Jun N-terminal Kinase Pathway and Mediates Caspase-Independent Cell Death		
JOURNAL	J. Biol. Chem. 275 (20), 15336-15342 (2000)		
PUBMED	10809768		
REFERENCE	2 (bases 1 to 1678)		
AUTHORS	Chaudhary, P.M.		
TITLE	Direct Submission		
JOURNAL	Submitted (12-JUL-1999) Internal Medicine, UT Southwestern Medical Center, 5323 Harry Hines Blvd., Dallas, TX 75235-8593, USA		
FEATURES	Location/Qualifiers		
source	1..1678		
	/organism="Mus musculus"		
	/db_xref="taxon:10090"		
CDS	72..1322		
	/codon_start=1		
	/product="TAJ-alpha long"		
	/protein_id="AAF1825.1"		
	/db_xref="GI:8071638"		
	/translation="MALKVLPHRTVFLRAILLHLACKVSCETGDCRQEQEKPKDRSG NCVLCKGQGMELSKCEGFGYGEQACVPCPHRFKEDMGQKPKPCADCALVNRFG RANCSHTDAVCGDCLPGFYRRTKLGFQDMCEVCGDPDPPEPHCTSKVNLVKRIS TVSSPRTALAAVICSALATVLLALLILCVYCKRQFMKKPSURSQDIOYNGSEL SCDPRLRHCAHRCACVYHRDSAPWGPVHLIPSLCEARSARAVLGCGLRSPPT LOERNPAGVHTWPAFGSVRSICAEFSDAWPLMONPLGGSSSLCDSYPELTGDTN SLNPENSTASLDSSGGQDLAGTAAVLALESSGNVSESTDSPRHGDTGTWVEOTLQAQDAQR TPSQGWEDRENILNLAFTAFODA"		
BASE COUNT	371 a 467 c 466 g 374 t		
ORIGIN			
Query Match	57.5%;	Score 729.2;	DB 11; Length 1678;
Best Local Similarity	74.6%;	Pred. No. 2.5e-186;	
Matches 930;	Conservative	0; Mismatches 313;	Indels 3; Gaps 1;
Qy	1	atgctttaaagtgcctactagaacagagaaaaacgttttccactcttttagtattacta	60
Db	72	ATGGCATCAAGGTCCTACCTCTACACAGCAGCGGTGCTCTTCGCTGCCATCTCTTCTCTA	131
Qy	61	ggctattgtcatgaaagtactgtgaaacagagagactgtagacagcaagaattcagg	120
Db	132	CTCCACCTGGCATGTAAGTGAGTTGGCAACCGGACATTCCAGGACAGCAAGGAATTCAG	191
Qy	121	gacgtgtctgaaactgtgtccctgcacacagtgctggcgccagcatggagtgcttaag	180

Db	192	GATCGATCTGGAAACTGTGTCTCTCTGCAAAACAGTGCAGACTGGCATGTGGAGTTGTCTCCAG	251
Qy	181	gaatgtggcttcggtctatgggagatgcacagttgtgtgacgtgccggctgcacaggttc	240
Db	252	GAATGTGGCTTCGGCTATGGGGAGGATGCACAGTGTGTGCCCTTCAGGCCGCGACGGTTC	311
Qy	241	aaggaggactgggggttcacagaaatgcaagccctgtctggtactgcgcagtggtgaaaccgc	300
Db	312	AAGGAAGACTGGGGTTTCCAGAAAGTGTAAAGCATGTGCGGACTGTGGGCTGTGTAACCGC	371
Qy	301	tttcagaagcgaattgttcagccaccagtatgccattctgcgtgggactcttgcaccaga	360
Db	372	TTTCAGAGGGCCAACTGTCACACACCACTGATGTGTCTCGGGGACTGCCTGCCAGGA	431
Qy	361	ttttaaggaaacgaactctgcgtcttcaagacatggagttgtgtccttggagagac	420
Db	432	TTTTTACCGGAACCAACTGGTTGGTTTCAAGACATGGAGTGTGTCCCTGCGGAGAC	491
Qy	421	cctctcctctcttacgaaccgcgtgtgccagcaaggtccaacctctgtgaagatcggtcc	480
Db	492	CCACCTCTCTCCCTAGCAACCACTGTACCAGCAAGGTGAACCTTGTGAAGATCTCCTCC	551
Qy	481	acggctccagcccaagggaacagcgctggctccgttatctcagcgcctctggaccac	540
Db	552	ACCGTCTCCAGCCCTCGGACACGGCGTGGCTGCCGTCACTGCAGTGTCTGGCCACG	611
Qy	541	gtcctgtggcctgcctcactctgtgtcatctatttgaagagacagtttatatggagaag	600
Db	612	GTGCTGCTCGCCCTGCTCATCTCTGTGTCTACTCTACATGCAAGAGGCAGTTCATCGAGAAG	671
Qy	601	aaaccagctgtctctgcgtgtcacaggacattcagtaacaacgctctgagctgtctgt	660
Db	672	AAACCCAGCTGGTCTCTGGCGTACAGGACATTCAATGCAATGCTGTAGCTGTCTCATGC	731
Qy	661	cttgacagacctcagtcacagaaatatgccacagagcgtctgccagtcgccgcgctgac	720
Db	732	TTTTGACCAACGCTCGGCTCGCCACACTGTGCCCATAGAGCATGCTGTCACTATFACACGGGAC	791
Qy	721	tcagtgcagacctggggcggtgtgcctgtgtcccatccatgtctgtgagggagcgctgc	780
Db	792	TCAGCCCCAATGTATGGGCGCTGTTCACTGTATTCGTCCTTGTGCTGTGAAGAGGCCCGC	851
Qy	781	agcccaacccggcgactcttggtgtgggtgtgcattctgcagccagtccttcaggccaaga	840
Db	852	AGCTGCTCCGAGCTGTGCTTGGCTGTGGCTGTGCCTTCTCCACTACCTCCAGGAGAGA	911
Qy	841	aacgcaggccagccgggagatggtgcgactttcttcggatccctcagcagtcctc	900
Db	912	AAACCGGCTCTGTGGGGAAACAGATGCCAGCGCTTCTTTGGGCTGTGTTCCCGTTCCTATC	971
Qy	901	tgtggcgagtttccagatccttgccctctgatgcagaatcccatgggtgggtgacaacatc	960
Db	972	TGCGCGGAGTTTTCGATGCCCTGGGCTCTGATGTCAGAAATCCTCTGCGGCGGTG---ACAGC	1028
Qy	961	tcttttgtgactcttactcctgaactcactgcaggaagacattcatctctcaatcccgaa	1020
Db	1029	TCCTCTGTGACTCTTATCCTGAACTCACTGGAGAAGATACCAATTCCTTCAATCCCGAA	1088
Qy	1021	cttgaagctcaacgctcttcttgattcaaatagcagtcgaagatttgggttgggtggggcgtct	1080
Db	1089	AACGAAGACACAGCATCTCTGGAATTTCCAGTGGCGGCCAGGATCTGGCTGGGACAGCTGCT	1148
Qy	1081	ccagtcagctctcattctgaaaactttacagcagctactgtatttatctagataataaac	1140
Db	1149	CTAGACTTCTGGGAATGTTTCAGAAATCTACTGACTCACCTAGACATGGTGTGACACTGGT	1208
Qy	1141	acactggtagaatcacgcatcaactcaggtatgcactaaactatgaaagccagctagatcag	1200
Db	1209	ACAGTCTGGGAGCAGCGTAGCTCAGGATGTCTAAAGGACTCCAAGCCAAAGGAGGCTGG	1268
Qy	1201	gagatggcgctatatccaccaccagccactcagactccctccagg	1246
Db	1269	GAAGACAGGGAACCTGAATCTAGCCATGCCACAGCGCTTCCAGG	1314

	Query Match	57.5%	Score 729.2	DB 11	Length 1678
	Best Local Similarity	74.6%	Pred. No. 2.5e-186		
	Matches 930	Conservative 0	Mismatches 313	Indels 3	Gaps 1
Qy	1	atgctttaaagtgctactagaacaagagaaaaacgtttttcacctcttttagtattacta	60		
Db	72	ATGCGACTCAAGGTCTTACCTCTACACGAGACGGTGCTCTTCGGTCGCATCTCTTCTCTA	131		
Qy	61	ggctattgttcattgaaagtgaacttgtgaacaggagactgtgacagcaagaattcagg	120		
Db	132	CTCCACCTGGCATGTAAAGTGAGTTGCGAAACCGAGATTGCGAGGCAGCAGGAATTC AAG	191		
Qy	121	gateggtctggaaactgtgttccctgcacaacagtgctgggccaggcatggagttgtctaa	180		

RESULT	5
AFI73166	
LOCUS	AF173166 1075 bp mRNA ROD 26-DEC-1999
DEFINITION	Mus musculus TNFRSF19 mRNA, complete cds.
ACCESSION	AF173166
VERSION	AF173166.1 GI:6635354
KEYWORDS	house mouse.
SOURCE	Mus musculus
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. Hu,S., Tamada,K., Ni,J., Vincenz,C. and Chen,L. Characterization of TNFRSF19, a novel member of the tumor necrosis factor receptor superfamily
JOURNAL	Genomics 62 (1), 103-107 (1999)
MEDLINE	20054362
REFERENCE	2. (bases 1 to 1075) Hu,S.
AUTHORS	Direct Submission
TITLE	Submitted (29-JUL-1999) Department of Immunology, Mayo Clinic and Foundation, 200 First Street SW, Rochester, MN 55903, USA
JOURNAL	Location/Qualifiers
FEATURES	source 1..1075 <code>/organism="Mus musculus"</code> <code>/db_xref="taxon:10090"</code> 28..1074 <code>/codon_start=1</code> <code>/product="TNFRSF19"</code> <code>/protein_id="AAF19795.1"</code> <code>/db_xref="GI:6635355"</code> <code>/translation="MALKVLPLHRTLVLAIFLLHLACKVSCAGDCRQOEKDRSG NCVLKQCGRMBELSECEGYGEDAQCPREHRKEGDFOKFCAPCADCALVNRFQ RWCSHTSDAVAGDCLPGFVKTKLVGFQDMECVPQDPPIPEPHCTSKVNLVKISS TNSSPRDTLAAVICSLATYLLALLILCVYKRQFMFKPKSWLSRPQDIQYNGLSS CDFQNPRLRHRCARCCQYHRDSAPMYGPVHLIPSLCCEARSARAVLGCGLRSPT LOENPASVGNTWPAFPFGSVSRISCAEFSDAWPMLQNPLGSSLDSDYPDLTGDTN SLNPELCPRFDL"</code>
BASE COUNT	211 a 308 c 296 g 259 t 1 others
ORIGIN	
Query Match	53.6%; Score 680.8; DB 11; Length 1075;
Best Local Similarity	78.9%; Pred. No. 3.1e-173;
Matches 824; Conservative	0; Mismatches 217; Indels 3; Gaps 1;
Qy	1 atggcgttaaagtgctactagaacaagagaaaaacgtttccactcttttagtattacta 60
Db	28 ATGGCACTCAAGGTCTTACCTTACACAGGACGGTGCTCTTCGCTGCCATTCTCTCTTA 87
Qy	61 ggctatttgtcatgaagtgtacctgtgaaacaggagactgtatagacgaagaattcagg 120
Db	88 CTCACCCTGGCATGAAGTGAAGTGGCGAAGCCGGAGATTGCAGGCAGCAGGAATTCAA 147
Qy	121 gatcggtctgaaaactgtgtccctgcacaacagtgtggccagcatggaattctctaag 180
Db	148 GATCGATCTGGAAACTGTGTCTCTGCAACAGTGGCGACCTGGCATGGAGTTGTCCAAG 207
Qy	181 gaatgtggcttcggctatgggagagatgcacagtgtgtgacgtgccggctgcacaggttc 240
Db	208 GAATGTGGCTTCGGCTATGGGAGAGATGCACAGTGTGTCCTTCAGGCCGCACCGGTT 267
Qy	241 aagagagactgggcttcgaagaaatgcaagccctgtctgtgactgcgagtggtgaaccgc 300
Db	268 AAGGAAGACTGGGTGTTCCAGAAGTGTGAAGCCATGTGCGGACTGTGGGCTGGTGAACCG 327
Qy	301 tticagaagccaattgttcagcccaccagtgatccatctcgcgggagactcttcagcaga 360
Db	328 TTTTCAGAGGCCCACTGCTCACACACAGTAGTGTGTGTGCGGGGACTTGCTGCCAGGA 387
Qy	361 ttttataggagaacgaacactgtcggttttcaagacatgagtggtgtgcttggagac 420

Db	388	TTTTACGGGAAGACCAAACTGGTTGGTTTTTTCAGACATGGAGTGTGTGCCCTGCGGAGAC	447
Qy	421	ctctctctccttacaaacgcgaactgtccgaacaaggtcaacctcgtgaagatcgcgtcc	480
Db	448	CCACCTCCTCCCTACGAACACCACTGTACCAGAGGTGAACCTTGTGAAGATCTCCCTCC	507
Qy	481	acggctccacgcacgcggacacggcgctggctgcgttatctatgcagcgctctgagccacc	540
Db	508	ACCGTCTCCAGCCCTCGGGACACGGCGCTGGCTGCGGTCACTGTCAGTGCCTGCGCCACG	567
Qy	541	gtcctgtggccctgtctatcctctctgttcaatcttatgttaagagacagtttatggaggaag	600
Db	568	GTGCTGCTCGCCCTGCTCATCCCTGTGTGTCTCATCTACTGCAAGAGGCAGTTCTATGGAGAAG	627
Qy	601	aaacacagctggctctctgtcggttcacagagacattcagtaacaacgcgtctgagctgtcgtgt	660
Db	628	AAACCCAGCTGGTCTCTGGCGGCCACAGGACATTCAGTACAATGGCTCTGTAGCTGTTCATGC	687
Qy	661	cttgacagacctcagctccacgaatatgccacagagcctgtcgcagtgccgcgcgtgac	720
Db	688	TTTGACCAAGCCTCGGCTCCGCCACTGTGCCCATAGACATGCTGTCTAGTATCACCGGGAC	747
Qy	721	tcagtgacagctgcggcgcggtgcgcctctgtcctccatccatgtctgtgagagagcctgc	780
Db	748	TCAGCCCCAATGTATGGCGCTGTTCACCTGATTCGGTCCCTTGTGTGTGAAGAGCGCCGC	807
Qy	781	agcccaaacccggcgactcttggttgggggtgcattcttcagccagctcttcaggacaaga	840
Db	808	AGCTTCGCCGAGCTGTGCTTGGCTGTGGGCTGCGTTCCTCCACATACCCCTCCAGGAGAGA	867
Qy	841	aaqcgagcccgccgggagatggtgcgcgaactcttcttcggatccctcacgcagtcacac	900
Db	868	AACCCGGCTTCTGTGGGAACAGATGCCAGCGCTCTTTGGTCTCTTTCCCGTTCATC	927
Qy	901	tgtgpgagtttccagatgcctggcctctgatgcagaatccccatgggtgggtgacaacac	960
Db	928	TGCGCGAGTTTTCTGATGCTGGCTCTGATGCAGAAATCCCTGTGGCGGTG---ACAGC	984
Qy	961	tcttttggactcttatactcgaactcaactcaggaagacattcattctctcaatccagaa	1020
Db	985	TCTCTGTGACTTATATCTGAATCTCACTGGGAAGATACCAATTCCTCAATCCAGAG	1044
Qy	1021	cttgaaagctcaacgctctttggat	1044
Db	1045	ATGCTGTGCTTTGTTTCGGGAT	1068
RESULT	6		
LOCUS	AB040433		
DEFINITION	AB040433	744 bp mRNA	22-JUL-2000
ACCESSION	AB040433	Mus musculus mRNA for dTROY, complete cds.	
VERSION	AB040433.1	GI:9392327	
KEYWORDS		dTROY.	
SOURCE		Mus musculus cDNA to mRNA.	
ORGANISM		Mus musculus	
REFERENCE		Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi	
AUTHORS		Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; N	
TITLE		Kojima,T., Morikawa,Y., Copeland,N.G., Gilbert,D.J., Jenkins,N.	
JOURNAL		Senba,E. and Kitamura,T.	
MEDLINE		dTROY, a newly identified member of the tumor necrosis factor	
REFERENCE		receptor superfamily, exhibits a homology with Edar and is	
AUTHORS		expressed in embryonic skin and hair follicles	
JOURNAL		J. Biol. Chem. 275 (27), 20742-20747 (2000)	
TITLE		20347167	
REFERENCE		2 (bases 1 to 744)	
AUTHORS		Kojima,T. and Kitamura,T.	
JOURNAL		Direct Submission	
MEDLINE		Submitted (23-MAR-2000) to the DDBJ/EMBL/GenBank databases. Tel	
REFERENCE		Kojima, Chugai Research Institute for Molecular Medicine, Inc.,	
AUTHORS		Cytokine Research Program; 153-2 Nagai, Niihari, Ibaraki 300-41	
JOURNAL			

Japan (E-mail: kojimat@immed.com, Tel: 81-298-306211,
Fax: 81-298-306270)

```
FEATURES
Source
  1. .744
  Location/Qualifiers
    /organism="Mus musculus"
    /db_xref="taxon:10090"
    /chromosome="14"
    67. .711
    /gene="dTroy"
    67. .711
    /gene="dTroy"
    /note="a member of TNFR superfamily exhibits a homology
    with Edar."
    /product_start=1
    /product="dTroy"
    /protein_id="BAB03268.1"
    /db_xref="GI:9392328"
    /translation="MALKVLPLHRTVLFALILFLHLACKVSCETGDCRQOEFKDRSG
    NCVLCKQCGPMELSKEGFGYEDAQVCPKPHRFKEDWGFQCKPCADCALVNRFO
    RANGSHTSDAVCGDCLPGFYRKTLVGFQDMCEVPCGDPFPPEPHCTSKYNLVRISS
    TVSSPRDTALAAVTCSALATVLLALLILCVYCKRQPMKKPSKLPCLSLCTVK"
BASE COUNT 162 a 208 c 211 g 163 t
ORIGIN
Query Match 35.4%; Score 449; DB 11; Length 744;
Best Local Similarity 82.4%; Pred. No. 1.5e-110;
Matches 515; Conservative 0; Mismatches 110; Indels 0; Gaps 0;
QY 1 atggttttaaaagtctactagaagaagaaacgtttttcactcttttagtattacta 60
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 67 ATGGCACTCAAGGTCCTACTCTACACAGGACGGTGCTCTCGCTGCCATTCTTCTCTA 126
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 61 ggcattttgctaaagtctgtgaacagagactgtagacagacaagaattcag 120
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 127 CTCACCTGGCATGTAAGTGTGCGAACCAGGAGATTGACGACGACGAATTCAG 186
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 121 gatcggtctggaactgtgttccctgcaaccagtggtggccaggcatgagttgtctaa 180
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 187 GATCGATCTGGAACATGTCTCTCTCAACACAGTGGGACCTGGCATGGAGTTGTCCAAG 246
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 181 gaatgtggttcggctatgggagagatgcacagtgtgtgacgtgcccggctgcacaggttc 240
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 247 GAATGTGGCTTCGGCTATCGGGAGGATGCACAGTGTGTGTCCTGCGGCGACCCGGTTC 306
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 241 aaggagactggggtcttcagaaatgcagaccctgtctggaactgcgcagtggtgaaccgc 300
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 307 AAGGAAGACTGGGGTTCACAGAAGTGTAAAGCATGTGCGGACTGTGCGTGGTGAACCCG 366
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 301 ttccagaagcgaattgttcagccaccagtgatgccatctgcggggactgcttgccagga 360
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 367 TTTCAGAGGCCCAACTGCTACACACACACAGTGTGTGTCGGGGACTGCTGCCAGGA 426
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 361 tttttagagaagacgaactctgcgcttcttaagacatggagtgtgtgcttgtggagac 420
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 427 TTTTACCGGAAGACCAAACTGTGTGTTTCAAGACATGAGTGTGTGTCCTCGCGAGAC 486
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 421 cctcctcctccttacgaacgcacagtgtccagcaaggtcaaacctcgtgaagatcgctcc 480
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 487 CCACCTCTCTCCCTACGAACACACACTGTACACAGGCTGAACCTGTGGAAGATCTCTCC 546
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 481 acggcctccagccacgggacacg9cgctggctggttcattctgcagcgccttggccacc 540
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 547 ACCGTCTCCAGCCCTCGGACACACGGCGCTGGCTGCGGTATCTGCAGTGTCTGGCCAG 606
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 541 gtctctgctggcctgctcactctctgtgtcactctatgttaagagacagtttatggagaag 600
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 607 GTGCTCTCGCCCTGCTCATCTGTGTGTCTACTCTACTGCAAGGCGAGTTCATGGAGAAG 666
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 601 aaacccagctgtgctctcggttcac 625
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 667 AAACCCAGCTGTAAAGTCCCATCC 691
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
```

```
RESULT 7
LOCUS AF167553 886 bp mRNA ROD 25-MAY-2000
DEFINITION Mus musculus TAJ-alpha short mRNA, complete cds.
ACCESSION AF167553
VERSION AF167553.1 GI:8071639
KEYWORDS
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 886)
Eby, M.T., Jasmin, A., Kumar, A., Sharma, K. and Chaudhary, P.M.
TAJ, a Novel Member of the Tumor Necrosis Factor Receptor Family,
Activates the c-Jun N-terminal Kinase Pathway and Mediates
Caspase-independent Cell Death
J. Biol. Chem. 275 (20), 15336-15342 (2000)
10809768
REFERENCE 2 (bases 1 to 886)
AUTHORS Chaudhary, P.M.
TITLE Direct Submission
JOURNAL Submitted (12-JUL-1999) Internal Medicine, UT Southwestern Medical
Center, 5323 Harry Hines Blvd., Dallas, TX 75235-8593, USA
FEATURES
source
  1. .886
  /organism="Mus musculus"
  /db_xref="taxon:10090"
  /clone_lib="Soares p3NMF19.5"
  72. .716
  /note="decoy receptor"
  /codon_start=1
  /product="TAJ-alpha short"
  /protein_id="AAF71826.1"
  /db_xref="GI:8071640"
  /translation="MALKVLPLHRTVLFALILFLHLACKVSCETGDCRQOEFKDRSG
  NCVLCKQCGPMELSKEGFGYEDAQVCPKPHRFKEDWGFQCKPCADCALVNRFO
  RANGSHTSDAVCGDCLPGFYRKTLVGFQDMCEVPCGDPFPPEPHCTSKYNLVRISS
  TVSSPRDTALAAVTCSALATVLLALLILCVYCKRQPMKKPSKLPCLSLCTVK"
BASE COUNT 204 a 245 c 247 g 190 t
ORIGIN
Query Match 35.4%; Score 449; DB 11; Length 886;
Best Local Similarity 82.4%; Pred. No. 1.5e-110;
Matches 515; Conservative 0; Mismatches 110; Indels 0; Gaps 0;
QY 1 atggttttaaaagtctactagaagaagaaacgtttttcactcttttagtattacta 60
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 72 ATGGCACTCAAGGTCCTACTCTACACAGGACGGTGCTCTCGCTGCCATTCTTCTCTA 131
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 61 ggcattttgctaaagtctgtgaacagagactgtagacagacaagaattcag 120
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 132 CTCACCTGGCATGTAAGTGTGCGAACCAGGAGATTGACGACGACGAATTCAG 191
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 121 gatcggtctggaactgtgttccctgcaaccagtggtggccaggcatgagttgtctaa 180
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 192 GATCGATCTGGAACATGTCTCTCTCAACACAGTGGGACCTGGCATGGTGTGCCAG 251
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 181 gaatgtggttcggctatgggagagatgcacagtgtgtgacgtgcccggctgcacaggttc 240
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 252 GAATGTGGCTTCGGCTATGGGAGGATGCACAGTGTGTGTCCTGCGGCGACCCGGTTC 311
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 241 aaggagactggggtctccagaagaatgcagccctgctggaactgcgaatggtgaaccgc 300
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 312 AAGGAAGACTGGGGTTCAGAAAGTGTAAAGCCATGTCGGGACTGTGCGTGGTGAACCCG 371
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 301 ttccagaagcgaattgttcagccaccagtgatgccatctgcggggactgcttgccagga 360
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 372 TTTACAGAGGCCCAACTGCTCACACACACACTGTATGCTGCGGGACTGCTGCCAGGA 431
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 361 tttttagagaagacgaactgtcggcttctcaagacatggagtgtgtgcttgtggagac 420
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
```

Db 432 TTTTACGGGAAGCAAACTGGTTGTTTTTCAAGACATGAGTGTGTGCCCTCGGAGAC 491
 QY 421 cctcctcctcttacgaacccagctgtgccagagtaacactctgaagatcgcgtcc 480
 Db 492 CCACCTCTCCTCTACGACCACTGTACCAAGGAGTGTGGAAGATCTCTCTCC 551
 QY 481 acgctccacccagccaggggacagggcgctggtgcgttattctgcagcgtctggccacc 540
 Db 552 ACCGCTCCAGCCCTCGGACACGGCGTGGCTGCCTCATCTGCATGCTCTGGCCACG 611
 QY 541 gtctgtgctgctgtcctctctctgtgtcatctattgttaagagacagtttatggagaag 600
 Db 612 GTCTGCTCCCTCTGTCTATCTGTGTCTATCTACTGCAAGAGGAGTTCATGGAGAAG 671
 QY 601 aagccagctggtctctgcggtcac 625
 Db 672 AAACCCAGCTGTAGCTCCCATCCC 696

RESULT 8
 AL161422
 LOCUS Homo sapiens chromosome 13 clone RP11-168G12, *** SEQUENCING IN
 DEFINITION
 ACCESSION AL161422
 VERSION
 KEYWORDS HTG: HTGS_PHASE1; HTGS_DRAFT.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 143608)
 Direct Submission
 Submitted (19-SEP-2000) Sanger Centre, Hinxton, Cambridgeshire,
 CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
 requests: clonerequest@sanger.ac.uk
 On Sep 22, 2000 this sequence version replaced gi:10190601.
 ----- Genome Center
 Center: Sanger Centre
 Center code: SC
 Web site: http://www.sanger.ac.uk
 Contact: humquery@sanger.ac.uk
 ----- Project Information
 Center project name: BA168G12
 ----- Summary Statistics
 Assembly program: XGAP4; version 4.5
 Sequencing vector: pBlasmid; L08752; 100% of reads
 Chemistry: Dye-terminator Big Dye; 100% of reads
 Consensus quality: 143007 bases at least Q40
 Consensus quality: 143260 bases at least Q30
 Consensus quality: 143347 bases at least Q20
 Insert size: 143408; sum-of-contigs
 Insert size: 145175; 5.9% error; agarose-fp
 Quality coverage: 8.5x in Q20 bases; sum-of-contigs Quality
 coverage: 8.58x in Q20 bases; agarose-fp

* NOTE: This is a 'working draft' sequence. It currently
 * consists of 3 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.
 * 1
 * 2992: contig of 2992 bp in length
 * 3093: gap of 100 bp
 * 3093 129375: contig of 126283 bp in length
 * 129376 129475: gap of 100 bp
 * 129476 143608: contig of 14133 bp in length.
 Location/Qualifiers
 1. .143608
 /organism="Homo sapiens"

/db_xref="taxon:9606"
 /chromosome="13"
 /clone="Rp11-168G12"
 /clone_lib="RPC1-11.1"
 1. .2992
 /note="assembly_fragment:01799
 fragment_chain:1"
 3093. .129375
 /note="assembly_fragment:02957
 fragment_chain:1
 clone_end:77
 vector_side:left"
 129476. .143608
 /note="assembly_fragment:00106"
 41121 a 29506 c 30419 g 42362 t 200 others
 ORIGIN
 Query Match 33.8%; Score 428.8; DB 67; Length 143608;
 Best Local Similarity 99.5%; Pred. No. 4.9e-105;
 Matches 430; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 838 agaaacgagccagccagggagatggtgcgacttcttgcagtcacgcagtc 897
 Db 84813 AGAAGCCAGCCAGCCAGGGAGATGTCGCCGACTTCTTTCGATCCCTCAGCAGTCC 84872
 QY 898 atctgtggcgagttttcagatgcctggcctctgtagcagaatccatgggtggtgacaac 957
 Db 84873 ATCTGTGGCGAGTTTTCAGATGCTGGCTCTGATGCAATCCCATGGTGGTGACAAC 84932
 QY 958 atctcttttggactcttctgaactgaactcactggagagacattctctcactcca 1017
 Db 84933 ATCTCTTTTGTGACTCTTATCTGAACCTCAGTGGAGAGACATTCTCTCAATCCA 84992
 QY 1018 gaactgaaagcctcaacgtcttggattcaaatagcagtcgaagattggtggtgggct 1077
 Db 84993 GAACTTTGAAAGCTCAACGCTTTTGGATTCAAATAGCAGTCAAGATTGTTGGTGGGGCT 85052
 QY 1078 gtccagtcagctctctctgaaaactttacagcagctactgatttataagataaac 1137
 Db 85053 GTTCCAGTCCAGTCTCATCTGAAAACCTTTACAGCAGCTACTGATTATCTAGATATAAC 85112
 QY 1138 aacacactgtagaatacagcatcaactcaggtgagtgactgaactatgagaagccagctagat 1197
 Db 85113 AACACACTGTGTAGTAATCAGCATCACTCAGGATGCATACTAATATGAGAAGCCAGCTAGAT 85172
 QY 1198 caggagagtggtgctatcatcccccagccactcagcagtcctccctcaggaagagcgca 1257
 Db 85173 CAGGAGAGTGGTGTCTGTCATCCACCCAGCCACTCAGACGCTCCCTCCAGGTAAAGCAGCA 85232
 QY 1258 ctgggttcctcg 1269
 Db 85233 CTGGGTTCCTCGT 85244
 RESULT 9
 AL139080
 LOCUS Homo sapiens chromosome 13 clone RP11-173N17 map q12.11-12.3, ***
 DEFINITION SEQUENCING IN PROGRESS ***, 15 unordered pieces.
 ACCESSION AL139080
 VERSION AL139080.8 GI:10443032
 KEYWORDS HTG: HTGS_PHASE1; HTGS_DRAFT.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 178256)
 Direct Submission
 Submitted (28-SEP-2000) Sanger Centre, Hinxton, Cambridgeshire,
 CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
 requests: clonerequest@sanger.ac.uk

COMMENT

On Oct 1, 2000 this sequence version replaced gi:10129398.
----- Genome Center
Center: Sanger Centre
Center code: SC
Web site: <http://www.sanger.ac.uk>
Contact: humquery@sanger.ac.uk
----- Project Information
Center project name: ba173N17
----- Summary Statistics
Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid; L08752; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 168976 bases at least Q40
Consensus quality: 172107 bases at least Q30
Consensus quality: 173780 bases at least Q20
Insert size: 176856; sum-of-contigs
Insert size: 163577; 8.6% error; agarose-fp
Quality coverage: 3.73x in Q20 bases; sum-of-contigs Quality
coverage: 4.07x in Q20 bases; agarose-fp

* NOTE: This is a 'working draft' sequence. It currently
* consists of 15 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1
* 8224 8223: gap of 100 bp
* 8324 25426: contig of 17103 bp in length
* 25227 25226: gap of 100 bp
* 28264 28263: contig of 2737 bp in length
* 28264 28263: gap of 100 bp
* 28364 34273: contig of 5910 bp in length
* 34274 34373: gap of 100 bp
* 34374 42235: contig of 7862 bp in length
* 42236 42335: gap of 100 bp
* 42336 53917: contig of 11582 bp in length
* 53918 54017: gap of 100 bp
* 54018 71972: contig of 17955 bp in length
* 71973 72072: gap of 100 bp
* 72073 81711: contig of 9639 bp in length
* 81712 81811: gap of 100 bp
* 81812 88644: contig of 6833 bp in length
* 88645 88744: gap of 100 bp
* 88745 95048: contig of 6304 bp in length
* 95049 95148: gap of 100 bp
* 95149 107455: contig of 12307 bp in length
* 107456 107555: gap of 100 bp
* 107556 125465: contig of 17910 bp in length
* 125466 125565: gap of 100 bp
* 125566 140008: contig of 14443 bp in length
* 140009 140108: gap of 100 bp
* 140109 144761: contig of 4653 bp in length
* 144762 144861: gap of 100 bp
* 144862 178256: contig of 33395 bp in length.
Location/Qualifiers
1..178256

FEATURES

source

/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="13"
/map="q12.11-12.3"
/clone="RP11-173N17"
/clone_lib="RPC1-11.1"
1..8223
/note="assembly_fragment:01724
fragment_chain:1"
8324..25426
/note="assembly_fragment:00074
fragment_chain:1"
25527..28263
/note="assembly_fragment:01884

misc_feature
28364..34273
/note="assembly_fragment:00979
fragment_chain:1"
misc_feature
34374..42235
/note="assembly_fragment:00126
fragment_chain:2"
misc_feature
42336..53917
/note="assembly_fragment:00364
fragment_chain:2"
misc_feature
54018..71972
/note="assembly_fragment:01769
fragment_chain:2"
misc_feature
72073..81711
/note="assembly_fragment:00399
fragment_chain:3"
misc_feature
81812..88644
/note="assembly_fragment:01132
fragment_chain:3"
misc_feature
88745..95048
/note="assembly_fragment:01416
fragment_chain:3"
misc_feature
95149..107455
/note="assembly_fragment:00061
fragment_chain:4"
misc_feature
107556..125465
/note="assembly_fragment:00302
fragment_chain:4"
misc_feature
125566..140008
/note="assembly_fragment:01438
fragment_chain:5"
misc_feature
140109..144761
/note="assembly_fragment:01533
fragment_chain:5"
misc_feature
144862..178256
/note="assembly_fragment:01008"
BASE COUNT 52999 a 37393 c 36460 g 49998 t 1406 others
ORIGIN

Query Match 33.8%; Score 428.8; DB 66; Length 178256;
Best Local Similarity 99.5%; Pred. No. 4.9e-105;
Matches 430; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 838 aqaacgcagccgcccgggagatggtgcgactttcttcgagtcctccacgagtc 897
|||||
Db 46631 AGAAACGGAGCCCGCCGAGATGGTGGCGGACTTTCTCGGATCCCTCAGCAGTCC 46690
|||||

QY 898 atctgtgagcttttcagatgcctggcctctgatgcagaatcccatgggtgtgacaac 957
|||||
Db 46691 ATCTGFGGCGAGTTTTCAGATGCTGGCTCTGATGCAGATCCCATGGTGTGACAAAC 46750
|||||

QY 958 atctcttttctgactcttctgaactcactgcagagacattcattctctcaatcca 1017
|||||
Db 46751 ATCTCTTTTGTGACTCTTATCTCTGAACCTCACTGGAGAGACATTCAATTTCTCAATCCA 46810
|||||

QY 1018 gaacttgaagctcaacgtcttttgattcaataagcagctcaagatttgttgagct 1077
|||||
Db 46811 GAACITGAAAGCTCAACGCTTTGGATTCAAATAGCAGTCAAGATTTGGTGGGGCT 46870
|||||

QY 1078 gtccagctcagctctcattctgaaacctttacagagctactgatttattctagataaac 1137
|||||
Db 46871 GTTCCAGTCCAGCTCATCTCTGAAACTTTTACAGCAGCTACTGATTTATCTAGATATAAC 46930
|||||

QY 1138 aacacactggttagaatacagatcaactcaggtgcactaactatgagagccagctagat 1197
|||||
Db 46931 AACACACTGGTAGAAATCAGATCACTCACTGATGCTAACTAATATGAGAAAGCCAGCTAGAT 46990
|||||

QY 1198 caggagagtgagcttatccaccagcactcagagcctccctccagtaaggagcga 1257
|||||
Db 46991 CAGGAGAGTGGTGTCTGTCTCACCAGCCACTCAGACGCTCCCTCCAGGTAAAGGAGCGGA 47050
|||||

QY 1258 ctgggttccctg 1269

[illegible]

* NOTE: This is a 'working draft' sequence. It currently
* consists of 16 contigs, the true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of 'N', but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence,
* as soon as it is available and the accession number will
* be preserved

*	25437	: contig of 25437 bp in length
*	25438	: gap of 100 bp
*	25537	: gap of 100 bp
*	27653	: contig of 2116 bp in length
*	27753	: gap of 100 bp
*	27754	: gap of 100 bp
*	45836	: contig of 18083 bp in length
*	45937	: gap of 100 bp
*	45936	: gap of 100 bp
*	58298	: contig of 12362 bp in length
*	58398	: gap of 100 bp
*	59299	: gap of 100 bp
*	59399	: contig of 5500 bp in length
*	63898	: gap of 100 bp
*	63998	: gap of 100 bp
*	70792	: contig of 6794 bp in length
*	70793	: gap of 100 bp
*	70892	: gap of 100 bp
*	83402	: contig of 12510 bp in length
*	83403	: gap of 100 bp
*	83503	: contig of 29011 bp in length
*	112513	: gap of 100 bp
*	112613	: gap of 100 bp
*	120587	: contig of 7974 bp in length
*	120588	: gap of 100 bp

FEATURES	SOURCE
1. The first two columns are labeled "FEATURES" and "SOURCE".	
2. The third column is labeled "FEATURES".	
3. The fourth column is labeled "SOURCE".	
4. The fifth column is labeled "FEATURES".	
5. The sixth column is labeled "SOURCE".	
6. The seventh column is labeled "FEATURES".	
7. The eighth column is labeled "SOURCE".	
8. The ninth column is labeled "FEATURES".	
9. The tenth column is labeled "SOURCE".	
10. The eleventh column is labeled "FEATURES".	
11. The twelfth column is labeled "SOURCE".	
12. The thirteenth column is labeled "FEATURES".	
13. The fourteenth column is labeled "SOURCE".	
14. The fifteenth column is labeled "FEATURES".	
15. The sixteenth column is labeled "SOURCE".	
16. The seventeenth column is labeled "FEATURES".	
17. The eighteenth column is labeled "SOURCE".	
18. The nineteenth column is labeled "FEATURES".	
19. The twentieth column is labeled "SOURCE".	
20. The twenty-first column is labeled "FEATURES".	
21. The twenty-second column is labeled "SOURCE".	
22. The twenty-third column is labeled "FEATURES".	
23. The twenty-fourth column is labeled "SOURCE".	
24. The twenty-fifth column is labeled "FEATURES".	
25. The twenty-sixth column is labeled "SOURCE".	
26. The twenty-seventh column is labeled "FEATURES".	
27. The twenty-eighth column is labeled "SOURCE".	
28. The twenty-ninth column is labeled "FEATURES".	
29. The thirtieth column is labeled "SOURCE".	
30. The thirty-first column is labeled "FEATURES".	
31. The thirty-second column is labeled "SOURCE".	
32. The thirty-third column is labeled "FEATURES".	
33. The thirty-fourth column is labeled "SOURCE".	
34. The thirty-fifth column is labeled "FEATURES".	
35. The thirty-sixth column is labeled "SOURCE".	
36. The thirty-seventh column is labeled "FEATURES".	
37. The thirty-eighth column is labeled "SOURCE".	
38. The thirty-ninth column is labeled "FEATURES".	
39. The fortieth column is labeled "SOURCE".	
40. The forty-first column is labeled "FEATURES".	
41. The forty-second column is labeled "SOURCE".	
42. The forty-third column is labeled "FEATURES".	
43. The forty-fourth column is labeled "SOURCE".	
44. The forty-fifth column is labeled "FEATURES".	
45. The forty-sixth column is labeled "SOURCE".	
46. The forty-seventh column is labeled "FEATURES".	
47. The forty-eighth column is labeled "SOURCE".	
48. The forty-ninth column is labeled "FEATURES".	
49. The fiftieth column is labeled "SOURCE".	
50. The fifty-first column is labeled "FEATURES".	
51. The fifty-second column is labeled "SOURCE".	
52. The fifty-third column is labeled "FEATURES".	
53. The fifty-fourth column is labeled "SOURCE".	
54. The fifty-fifth column is labeled "FEATURES".	
55. The fifty-sixth column is labeled "SOURCE".	
56. The fifty-seventh column is labeled "FEATURES".	
57. The fifty-eighth column is labeled "SOURCE".	
58. The fifty-ninth column is labeled "FEATURES".	
59. The sixtieth column is labeled "SOURCE".	
60. The sixty-first column is labeled "FEATURES".	
61. The sixty-second column is labeled "SOURCE".	
62. The sixty-third column is labeled "FEATURES".	
63. The sixty-fourth column is labeled "SOURCE".	
64. The sixty-fifth column is labeled "FEATURES".	
65. The sixty-sixth column is labeled "SOURCE".	
66. The sixty-seventh column is labeled "FEATURES".	
67. The sixty-eighth column is labeled "SOURCE".	
68. The sixty-ninth column is labeled "FEATURES".	
69. The seventieth column is labeled "SOURCE".	
70. The seventy-first column is labeled "FEATURES".	
71. The seventy-second column is labeled "SOURCE".	
72. The seventy-third column is labeled "FEATURES".	
73. The seventy-fourth column is labeled "SOURCE".	
74. The seventy-fifth column is labeled "FEATURES".	
75. The seventy-sixth column is labeled "SOURCE".	
76. The seventy-seventh column is labeled "FEATURES".	
77. The seventy-eighth column is labeled "SOURCE".	
78. The seventy-ninth column is labeled "FEATURES".	
79. The eightieth column is labeled "SOURCE".	
80. The eighty-first column is labeled "FEATURES".	
81. The eighty-second column is labeled "SOURCE".	
82. The eighty-third column is labeled "FEATURES".	
83. The eighty-fourth column is labeled "SOURCE".	
84. The eighty-fifth column is labeled "FEATURES".	
85. The eighty-sixth column is labeled "SOURCE".	
86. The eighty-seventh column is labeled "FEATURES".	
87. The eighty-eighth column is labeled "SOURCE".	
88. The eighty-ninth column is labeled "FEATURES".	
89. The ninetieth column is labeled "SOURCE".	
90. The ninety-first column is labeled "FEATURES".	
91. The ninety-second column is labeled "SOURCE".	
92. The ninety-third column is labeled "FEATURES".	
93. The ninety-fourth column is labeled "SOURCE".	
94. The ninety-fifth column is labeled "FEATURES".	
95. The ninety-sixth column is labeled "SOURCE".	
96. The ninety-seventh column is labeled "FEATURES".	
97. The ninety-eighth column is labeled "SOURCE".	
98. The ninety-ninth column is labeled "FEATURES".	
99. The hundredth column is labeled "SOURCE".	
100. The hundred-first column is labeled "FEATURES".	
101. The hundred-second column is labeled "SOURCE".	
102. The hundred-third column is labeled "FEATURES".	
103. The hundred-fourth column is labeled "SOURCE".	
104. The hundred-fifth column is labeled "FEATURES".	
105. The hundred-sixth column is labeled "SOURCE".	
106. The hundred-seventh column is labeled "FEATURES".	
107. The hundred-eighth column is labeled "SOURCE".	
108. The hundred-ninth column is labeled "FEATURES".	
109. The hundred-tenth column is labeled "SOURCE".	
110. The hundred-eleventh column is labeled "FEATURES".	
111. The hundred-twelfth column is labeled "SOURCE".	
112. The hundred-thirteenth column is labeled "FEATURES".	
113. The hundred-fourteenth column is labeled "SOURCE".	
114. The hundred-fifteenth column is labeled "FEATURES".	
115. The hundred-sixteenth column is labeled "SOURCE".	
116. The hundred-seventeenth column is labeled "FEATURES".	
117. The hundred-eighteenth column is labeled "SOURCE".	
118. The hundred-nineteenth column is labeled "FEATURES".	
119. The hundred-twentieth column is labeled "SOURCE".	
120. The hundred-twenty-first column is labeled "FEATURES".	
121. The hundred-twenty-second column is labeled "SOURCE".	
122. The hundred-twenty-third column is labeled "FEATURES".	
123. The hundred-twenty-fourth column is labeled "SOURCE".	
124. The hundred-twenty-fifth column is labeled "FEATURES".	
125. The hundred-twenty-sixth column is labeled "SOURCE".	
126. The hundred-twenty-seventh column is labeled "FEATURES".	
127. The hundred-twenty-eighth column is labeled "SOURCE".	
128. The hundred-twenty-ninth column is labeled "FEATURES".	
129. The hundred-thirtieth column is labeled "SOURCE".	

```
/organism="Homo sapiens"  
/db_xref="taxon:9606"  
/chromosome="17"  
/map="17"
```

```

/misc_feature /clone="Rp11-85120"
/misc_feature /clone_lib="RPC1-11 Human Male BAC"
/misc_feature 1..1267
/misc_feature /note="assembly_fragment"
/misc_feature 1368..2402
/misc_feature /note="assembly_fragment"
/misc_feature 2503..3524
/misc_feature /note="assembly_fragment"
/misc_feature 3625..4913
/misc_feature /note="assembly_fragment"
/misc_feature 5014..6289
/misc_feature /note="assembly_fragment"
/misc_feature 6390..7655
/misc_feature /note="assembly_fragment"
/misc_feature 7756..9267
/misc_feature /note="assembly_fragment"
/misc_feature 9368..11138
/misc_feature /note="assembly_fragment"
/misc_feature 11239..13822
/misc_feature /note="assembly_fragment"
/misc_feature 13923..16968
/misc_feature /note="assembly_fragment"
/misc_feature 17069..20185
/misc_feature /note="assembly_fragment"
/misc_feature 20286..22634
/misc_feature /note="assembly_fragment"
/misc_feature 22735..27012
/misc_feature /note="assembly_fragment"
/misc_feature 27113..29342
/misc_feature /note="assembly_fragment
clone_end.T7
vector_side:right"
/misc_feature 29443..33381
/misc_feature /note="assembly_fragment"
/misc_feature 33482..36562
/misc_feature /note="assembly_fragment"
/misc_feature 36663..40982
/misc_feature /note="assembly_fragment"
/misc_feature 41083..45520
/misc_feature /note="assembly_fragment"
/misc_feature 45621..50623
/misc_feature /note="assembly_fragment"
/misc_feature 50724..55610
/misc_feature /note="assembly_fragment"
/misc_feature 55711..61038
/misc_feature /note="assembly_fragment"
/misc_feature 61139..66159
/misc_feature /note="assembly_fragment"
/misc_feature 66260..73479
/misc_feature /note="assembly_fragment"
/misc_feature 73580..80554
/misc_feature /note="assembly_fragment"
/misc_feature 80655..89313

```

misc_feature /note="assembly_fragment"
89414. .98132
/note="assembly_fragment"

Query Match 5.8%; Score 73; DB 51; Length 205736;
Best Local Similarity 60.2%; Pred.No. 8.3e-09;
Matches 121; Conservative 0; Mismatches 80; Indels 0; Gaps 0;

QY 179 aggaatgtgcttcgctatgggaggatgcacagtggtgacgtgcgcggtgcacaggt 238
||||| ||||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 79395 AGGATGTGTTATGAGAGGGTGGAGATGCTTACTGCACACCTGCGCTCCTCCAGGT 79336
||||| ||||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 239 tcaaggaggactgggctcccaaaatgcacagccctgtctgactgcgcagtggtgaacc 298
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 79335 AAAAAAGCAGCTGGGGCCACCACAGATGTCAGATGTGCATCACCTGTGTCATCAATC 79276
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 299 gcttcagaagcaaatgttcagaccagcagtgatgccatctgcgggactcgttgccac 358
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 79275 GTGTTCAAGAGTCACTGCACAGCTACCTCTAAATGCTGCTGTGGGACTGTTGCCCA 79216
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 359 gattttataggagcgaac 379
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 79215 GGTGACCTGCTTTATGAGAC 79195
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 13

AC023560
LOCUS Homo sapiens chromosome 17 clone RP11-85I20 map 17, WORKING DRAFT
DEFINITION AC023560
SEQUENCE, 34 unordered pieces.
AC023560
VERSION AC023560.2 GI:7229913
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

AUTHORS Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.

TITLE Birren,B., Linton,L., Nusbaum,C. and Lander,E.

JOURNAL Homo sapiens chromosome 17, clone RP11-85I20

REFERENCE 2 (bases 1 to 205736)

Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
Anderson,S., Baldwin,J., Barna,N., Beda,F., Boguslavsky,L.,
Boukhgalter,B., Brown,A., Burkett,G., Campopiano,A., Castle,A.,
Choepe,Y., Colangelo,M., Collins,S., Collymore,A., Cooke,P.,
Dearellano,K., Dewar,K., Dodge,S., Domino,M., Doyle,M., D.,
Fenestor,J., Ferreira,P., FitzHugh,W., Forrest,C., Gage,D.,
Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L.,
Grand-Pierre,N., Grant,G., Hagos,B., Heaford,A., Horton,L.,
Howland,J.C., Iliev,I., Johnson,R., Jones,C., Kann,L., Karatas,A.,
Klein,J., Landers,T., Larcocque,K., Lehoczy,J., Levine,R.,
Lieu,C., Liu,G., Locke,K., Macdonald,P., Marquis,N., McCarthy,M.,
McEwan,P., McGurk,A., McKernan,K., McPheeters,R., Meldrim,J.,
Meneus,L., Mihova,I., Miranda,C., Mlenga,V., Morrow,J., Naylor,J.,
Norman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D., Olivat,T.M.,
Peterson,K., Pierre,N., Pisan,C., Pollara,V., Raymond,C.,
Riley,R., Rogov,P., Rothman,D., Roy,A., Santos,R., Schauer,S.,
Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J., Tirrell,A.,
Travers,M., Triglio,J., Vassiliev,H., Viel,R., Vo,A., Wilson,B.,
Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J., Zimmer,A. and
Zody,M.

Direct Submission

TITLE Submitted (15-FEB-2000) Whitehead Institute/MIT Center for Genome

JOURNAL Research, 320 Charles Street, Cambridge, MA 02141, USA

COMMENT On Mar 12, 2000 this sequence version replaced gi:6978256.

All repeats were identified using RepeatMasker:

Smit, A.F.A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RM/RepeatMasker.html

----- Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIBR

Web site: <http://www-seq.wi.mit.edu>
Contact: sequence.submissions@genome.wi.mit.edu
----- Project Information

Center project name: L6741

Center clone name: 85_I20

----- Summary Statistics

Sequencing vector: M13; M77815; 100% of reads

Chemistry: Dye-terminator Big Dye; 100% of reads

Assembly program: Phrap; version 0.960731

Consensus quality: 178666 bases at least Q40

Consensus quality: 190940 bases at least Q30

Consensus quality: 197088 bases at least Q20

Insert size: 194000; agarose-fp

Insert size: 202436; sum-of-contigs

Quality coverage: 4.2 in Q20 bases; agarose-fp

Quality coverage: 4.0 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
* consists of 34 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

* 1 1267: contig of 1267 bp in length

* 1268 1367: gap of 100 bp

* 1368 2402: contig of 1035 bp in length

* 2403 2502: gap of 100 bp

* 2503 3524: contig of 1022 bp in length

* 3525 3624: gap of 100 bp

* 3625 4913: contig of 1289 bp in length

* 4914 5013: gap of 100 bp

* 5014 6289: contig of 1276 bp in length

* 6290 6389: gap of 100 bp

* 6390 7655: contig of 1266 bp in length

* 7656 7755: gap of 100 bp

* 7756 9267: contig of 1512 bp in length

* 9268 9367: gap of 100 bp

* 9368 11138: contig of 1771 bp in length

* 11139 11238: gap of 100 bp

* 11239 13822: contig of 2584 bp in length

* 13823 13922: gap of 100 bp

* 13923 16968: contig of 3046 bp in length

* 16969 17068: gap of 100 bp

* 17069 20185: contig of 3117 bp in length

* 20186 20285: gap of 100 bp

* 20286 22634: contig of 2349 bp in length

* 22635 22734: gap of 100 bp

* 22735 27012: contig of 4278 bp in length

* 27013 27112: gap of 100 bp

* 27113 29342: contig of 2230 bp in length

* 29343 29442: gap of 100 bp

* 29443 33381: contig of 3939 bp in length

* 33382 33481: gap of 100 bp

* 33482 36562: contig of 3081 bp in length

* 36563 36662: gap of 100 bp

* 36663 40982: contig of 4320 bp in length

* 40983 41082: gap of 100 bp

* 41083 45520: contig of 4438 bp in length

* 45521 45620: gap of 100 bp

* 45621 50623: contig of 5003 bp in length

* 50624 50723: gap of 100 bp

* 50724 55610: contig of 4887 bp in length

* 55611 55710: gap of 100 bp

* 55711 61038: contig of 5328 bp in length

* 61039 61138: gap of 100 bp

* 61139 66159: contig of 5021 bp in length

* 66160 66259: gap of 100 bp

* 66260 73479: contig of 7220 bp in length

* 73480 73579: gap of 100 bp

* 73580 80554: contig of 6975 bp in length

* 80555 80654: gap of 100 bp

*	80655	89313:	contig of 8659 bp in length
*	89413	: gap of	100 bp
*	89314	98132:	contig of 8719 bp in length
*	98133	98232:	gap of 100 bp
*	98233	107469:	contig of 9237 bp in length
*	107470	107569:	gap of 100 bp
*	107570	117873:	contig of 10304 bp in length
*	117874	117973:	gap of 100 bp
*	117974	130973:	contig of 13000 bp in length
*	130974	131073:	gap of 100 bp
*	131074	143236:	contig of 12163 bp in length
*	143237	143336:	gap of 100 bp
*	143337	154478:	contig of 11142 bp in length
*	154479	154578:	gap of 100 bp
*	154579	169567:	contig of 15389 bp in length
*	169568	170067:	gap of 100 bp
*	170068	187347:	contig of 17280 bp in length
*	187348	187447:	gap of 100 bp
*	187448	2057336:	contig of 18289 bp in length

FEATURES

source	1. .20736 /organism="Homo sapiens" /db_xref="taxon:9606" /chromosome="17" /map="17" /clone="RP11-85120" /clone_lib="RPC1-11 Human Male BAC" 1. .1267
misc_feature	/note="assembly_fragment" 1368. .2402
misc_feature	/note="assembly_fragment" 2503. .3524
misc_feature	/note="assembly_fragment" 3625. .4913
misc_feature	/note="assembly_fragment" 5014. .6289
misc_feature	/note="assembly_fragment" 6390. .7655
misc_feature	/note="assembly_fragment" 7756. .9267
misc_feature	/note="assembly_fragment" 9368. .11138
misc_feature	/note="assembly_fragment" 11239. .13822
misc_feature	/note="assembly_fragment" 13923. .16968
misc_feature	/note="assembly_fragment" 17069. .20185
misc_feature	/note="assembly_fragment" 20286. .22634
misc_feature	/note="assembly_fragment" 22735. .27012
misc_feature	/note="assembly_fragment" 27113. .29342
misc_feature	/note="assembly_fragment clone_end.T7 vector_side:right" 29443. .33381
misc_feature	/note="assembly_fragment" 33482. .36562
misc_feature	/note="assembly_fragment" 36663. .40982
misc_feature	/note="assembly_fragment" 41083. .43520
misc_feature	/note="assembly_fragment" 45621. .50623
misc_feature	/note="assembly_fragment" 50724. .55610
misc_feature	/note="assembly_fragment" 55711. .61038
misc_feature	/note="assembly_fragment" 61139. .66159
misc_feature	/note="assembly_fragment"

[illegible]

RESULT

AC034198/c	AC034198	160214 bp	DNA	HTG	19-SEP-2000
LOCUS	Homo sapiens chromosome 3 clone RP11-767C1 map 3p, WORKING DRAFT SEQUENCE, 25 unordered pieces.				
DEFINITION	AC034198				
ACCESSION	AC034198.4				
VERSION	GI:10190766				
KEYWORDS	HTG; HTGS_PHASE1; HTGS_DRAFT.				
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
AUTHORS	1 (bases 1 to 160214)				
	Bao,J., Bao,Q., Bao,W., Bian,X., Cao,T., Chen,C., Chen,J., Ding,H., Dong,W., Fan,H., Feng,X., Guan,Q., Gu,X., Guo,D., He,L., Hu,S., Huang,F., Jin,Y., Kang,N., Li,C., Li,C., Li,G., Li,J., Li,L., Li,S., Li,T., Liu,Y., Liu,N., Liu,B., Liu,Y., Li,W., Li,W., Li,Y., Luo,J., Liu,Y., Qi,Q., Qi,X., Song,S., Sun,M., Sun,W., Sun,Y., Tao,R., Wang,H., Wang,J., Wang,L., Wang,L., Wang,R., Wang,X., Wang,X., Wang,Y., Wu,D., Wu,Q., Xie,F., Xuan,Z., Xue,Y., Yan,C., Yang,X., Yu,B., Zeng,Y., Zhang,G., Zhang,H., Zhang,H., Zhang,L., Zhang,M., Zhang,X., Zhang,X., Zhang,Y., Zhang,Y., Zhang,Z., Zhu,B., Yu,J. and Yang,H.				

TITLE:

JOURNAL
REFERENCE
AUTHORS

Unpublished genome sequence
2 (bases 1 to 160214)
Kang, N., Sun, S., Wu, Q., Wang, J., Zhang, Y., Zhang, C., Wang, Y., Liu, B.,
Bao, W., Hu, Y., Du, Q., Wang, H., Yang, X., Cheng, C., Hong, Y., Niu, Y.,
Qi, X., Li, T., Zhang, H., Liu, N., Wu, D., Yu, B., Fan, H., Liu, Y.,
Li, G., Li, C., Bao, O., Bao, J., Wang, X., Song, L., Zhang, L., Guo, D.,
Huang, F., Zhang, G., Li, J., Bian, X., Zhang, M., Li, L., Feng, X., Yu, J.
and Wang, H.

ПІП'Є

Direct Submission
JOURNAL
Submitted (05-APR-2000) Human Genomic Center, Institute of
Genetics, Chinese Academy of Sciences, Datun Road, Beijing, Beijing
100101, P. R. China
COMMENT On Sep 19, 2000 this sequence version replaced gi:8101278.
-----Genome Center
Center:Beijing Center

```

* 138441 138540: gap of unknown length
* 138541 160214: contig of 21674 bp in length.
FEATURES
    source
        1..160214
            /organism="Homo sapiens"
            /db_xref="taxon:9606"
            /chromosome="3"
            /map="3p"
            /clone="RP11-767C1"
            1..1071
                /note="assembly_name:Contig7"
            1172..2254
                /note="assembly_name:Contig10"
            2355..3851
                /note="assembly_name:Contig12"
            3952..5295
                /note="assembly_name:Contig13"
            5396..6465
                /note="assembly_name:Contig14"
            6566..7857
                /note="assembly_name:Contig15"
            7958..9194
                /note="assembly_name:Contig16"
            9295..11038
                /note="assembly_name:Contig17"
            11139..14420
                /note="assembly_name:Contig18"
            14521..17864
                /note="assembly_name:Contig19"
            17965..21270
                /note="assembly_name:Contig20"
            21371..25050
                /note="assembly_name:Contig21"
            clone_end:T7
            vector_side:right"
            25151..30624
                /note="assembly_name:Contig23"
            30725..37771
                /note="assembly_name:Contig24"
            clone_end:SP6
            vector_side:left"
            37872..42147
                /note="assembly_name:Contig25"
            42248..49752
                /note="assembly_name:Contig26"
            49853..57293
                /note="assembly_name:Contig27"
            57394..63626
                /note="assembly_name:Contig28"
            63727..72520
                /note="assembly_name:Contig29"
            72621..83538
                /note="assembly_name:Contig30"
            83639..95213
                /note="assembly_name:Contig31"
            95314..107621
                /note="assembly_name:Contig32"
            107722..120511
                /note="assembly_name:Contig33"
            120612..138440
                /note="assembly_name:Contig34"
            138541..160214
                /note="assembly_name:Contig35"
BASE COUNT  40339 a 38297 g 38619 c 40533 t 2426 others
ORIGIN
Query Match          3.4%; Score 43.6; DB 54; Length
Best Local Similarity 48.4%; Pred. No. 0.74; Indels
Matches 121; Conservative 0; Mismatches 129; Indels
Qy 637 tacaacgcttcgagcttcgttcgtttgacagaccttcagctccacgaata

```

Db	9589	TCCAAACTCTCTGTGTCGGCGGGGGCAATTCCTTCCCTTGTTGACAGAGATTCCACCCC	9533
QY	697	gcctgtgcagtgccgcctgactcagtgacagactgcggcggtgcctgtgtctccca	756
Db	9529	GCCCTGCCCCACTGTCCCGCCACGGGAAGTGGCCGGGAGTGGAGCGTGGACAGGCA	9470
QY	757	tccatgtgtgtgagagagcctgcagccccaacccgcgcactcttgttgggtgtgcata	816
Db	9469	TCCCGGTGTCTCGAGTCAAGCTGTGGCGCCACGCTGGACACAGCGGCCCGGAGGCGAG	9410
QY	817	tctgcagccagtccttcaggcaagaacacagccagcccgccggggagatgggtgcgactttc	876
Db	9409	ACAGGCGGCACGAGGAGCCCGCCAGGCTCCAGAGACGCCGCTGACAGGCTGTCCAGCTGC	9350
QY	877	ttcggtatccc	886
Db	9349	ATCGGCTCTC	9340
RESULT	15		
LOCUS	AC018836	180511 bp	DNA
DEFINITION	Homo sapiens chromosome 3p clone RP11-588P9, WORKING DRAFT	HTC	03-FEB-2000
ACCESSION	AC018836		
VERSION	AC018836.2	GI:6684178	
KEYWORDS	HTG; HTGS_PHASE1; HTGS_DRAFT.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	1		
AUTHORS	Xuan,Z., Hu,S., Dong,W., Zhang,X., Wang,J., Zhang,Y., Zhang,H., Liu,B., Sun,Y., Wu,Q., Wang,X., Wang,H., Yang,X., Cheng,Qi,X., Li,T., Zhang,H., Liu,N., Wu,D., Yu,B., Fan,H., Yu,B., Li,G., Li,C., Bao,Q., Bao,J., Wang,X., Song,L., Zhang,L., Guo,D., Huang,F., Zhang,G., Li,J., Bian,X., Zhang,M., Li,L., Feng,X., Yu,J. and Yang,H.		
TITLE	Chromosome 3p genomic sequence		
JOURNAL	Unpublished		
REFERENCE	2	(bases 1 to 180511)	
AUTHORS	Cheng,C., Hu,S., Dong,W., Wang,J., Zhang,Y., Zhang,H., Liu,B., Bao,W., Sun,Y., Wu,Q., Wang,H., Yang,X., Cheng,C., Wang,Y., Niu,Qi,X., Li,T., Zhang,H., Liu,N., Wu,D., Yu,B., Fan,H., Liu,Y., Li,G., Li,C., Bao,Q., Bao,J., Wang,X., Song,L., Zhang,L., Guo,D., Huang,F., Zhang,G., Li,J., Bian,X., Zhang,M., Li,L., Feng,X., Wang,X., Yu,J. and Yang,H.		
TITLE	Direct Submission		
JOURNAL	Submitted (21-DEC-1999) Human Genomic Center, Institute of Genetics, Chinese Academy of Sciences, Datun Road, Beijing, Bei100101, P.R.China		
COMMENT	<p>On Jan 9, 2000 this sequence version replaced gi:6623932.</p> <p>* NOTE: This is a 'working draft' sequence. It currently consists of 10 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.</p> <p>* This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.</p>		
	1	3562:	contig of 3562 bp in length
			gap of unknown length
	3563	11714:	contig of 8152 bp in length
			gap of unknown length
	11715	20436:	contig of 8722 bp in length
			gap of unknown length
	20437	29709:	contig of 9273 bp in length
			gap of unknown length
	29710	42278:	contig of 12569 bp in length
			gap of unknown length
	42279	58074:	contig of 15796 bp in length
			gap of unknown length
	58075	72958:	contig of 14884 bp in length

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 2, 2001, 12:42:21 ; Search time 553.05 Seconds
(without alignments)
861.976 Million cell updates/sec

Title: US-09-380-276A-5

Perfect score: 1269

Sequence: 1 atggtttaaagtgtact.....ggcagcgactgggttcctg 1269

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 480022 seqs, 187831343 residues

Total number of hits satisfying chosen parameters: 960044

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_36:*

- 1: /SID56/gcgdata/geneseq/geneseq/NA1980.DAT:*
- 2: /SID56/gcgdata/geneseq/geneseq/NA1981.DAT:*
- 3: /SID56/gcgdata/geneseq/geneseq/NA1982.DAT:*
- 4: /SID56/gcgdata/geneseq/geneseq/NA1983.DAT:*
- 5: /SID56/gcgdata/geneseq/geneseq/NA1984.DAT:*
- 6: /SID56/gcgdata/geneseq/geneseq/NA1985.DAT:*
- 7: /SID56/gcgdata/geneseq/geneseq/NA1986.DAT:*
- 8: /SID56/gcgdata/geneseq/geneseq/NA1987.DAT:*
- 9: /SID56/gcgdata/geneseq/geneseq/NA1988.DAT:*
- 10: /SID56/gcgdata/geneseq/geneseq/NA1989.DAT:*
- 11: /SID56/gcgdata/geneseq/geneseq/NA1990.DAT:*
- 12: /SID56/gcgdata/geneseq/geneseq/NA1991.DAT:*
- 13: /SID56/gcgdata/geneseq/geneseq/NA1992.DAT:*
- 14: /SID56/gcgdata/geneseq/geneseq/NA1993.DAT:*
- 15: /SID56/gcgdata/geneseq/geneseq/NA1994.DAT:*
- 16: /SID56/gcgdata/geneseq/geneseq/NA1995.DAT:*
- 17: /SID56/gcgdata/geneseq/geneseq/NA1996.DAT:*
- 18: /SID56/gcgdata/geneseq/geneseq/NA1997.DAT:*
- 19: /SID56/gcgdata/geneseq/geneseq/NA1998.DAT:*
- 20: /SID56/gcgdata/geneseq/geneseq/NA1999.DAT:*
- 21: /SID56/gcgdata/geneseq/geneseq/NA2000.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1269	100.0	1496	19	V33362
2	1267.4	99.9	1502	20	X08689
3	1256.2	99.0	1489	20	X23415
4	1244.8	98.1	1704	19	V33361
5	1240	97.7	2185	20	X24978
6	835.6	65.8	987	20	X59346
7	729.2	57.5	1678	20	X23413
8	449	35.4	886	20	X23414
9	449	35.4	942	20	X24977
10	449	35.4	981	20	X87394
11	435.4	34.3	893	20	X84622
12	362.6	28.6	538	20	X59345

13	361.6	28.5	371	19	V11422
14	314	24.7	591	20	X23417
15	314	24.7	599	20	X24976
16	314	24.7	623	20	X84623
17	314	24.7	636	21	X2408
18	314	24.7	655	20	X87395
19	154.8	12.2	932	21	X2411
20	121.8	9.6	1133	20	X23416
21	90.4	7.1	791	20	X24979
22	87.4	6.9	181	19	V11423
23	87.4	6.9	201	20	X86655
24	82	6.5	396	20	X23418
25	81.2	6.4	546	21	X2410
26	77.8	6.1	474	21	X2409
27	44	3.5	10732	21	A10594
28	37.4	2.9	1290	20	X23121
29	37.4	2.9	2570	20	X23120
30	37.4	2.9	2703	21	D00061
31	36.4	2.9	1602	15	Q72217
32	36.4	2.9	1978	15	Q72212
33	36.4	2.9	1987	16	T11624
34	36.4	2.9	1997	16	T11600
35	36.4	2.9	1998	15	Q72213
36	36.4	2.9	2004	16	T11599
37	36.4	2.9	2005	15	Q72211
38	36.2	2.9	330	21	A15982
39	36.2	2.9	659	21	A15992
40	36.2	2.9	2485	17	T09866
41	36	2.8	2067	20	V99092
42	36	2.8	19440	20	V99129
43	35.6	2.8	1150	20	Z06928
44	35.2	2.8	1050	21	Z58975
45	35	2.8	326	11	Q05546

ALIGNMENTS

RESULT 1

V33362

ID V33362 standard; cDNA to mRNA; 1496 BP.

XX

AC V33362;

XX

DT 02-DEC-1998 (first entry)

XX

DE Nucleotide sequence of human beta-OAF065.

XX

Human; beta-OAF065; stroma cell; antibody; inflammatory; cytokine-mediated disease; rheumatism; ulcerative colitis; ss.

KW

XX Homo sapiens.

OS

XX

FH Key Location/Qualifiers

FT CDS 45..1316

FT

FT /*tag= a

FT /*product= "human beta-OAF065 protein"

FT sig_peptide 45..119

FT /*tag= b

FT mat_peptide 120..1313

FT /*tag= c

FT /*transl_except= (pos:711..713, aa= Pro)

FT /*transl_except= (pos:714..716, aa= Arg)

XX

W09838304-A1.

XX

03-SEP-1998.

XX

26-FEB-1998; 98WO-JP00799.

XX

27-FEB-1997; 97JP-0043143.

XX

(ONOY) ONO PHARM CO LTD.

Human secreted pro

Mouse MAP04-gamma

Mouse TRAIN-R (sho

Mouse TNFR superfa

CDNA encoding murf

Mouse STRIFE2 (Tan

CDNA encoding huma

Rat rAPO4-alpha DN

Clone GJ156 encodi

Human secreted pro

EST clone AX92. H

Mouse MAP04-beta D

CDNA encoding huma

CDNA encoding huma

Gene encoding a su

Human TANGO 129 (T

Human TANGO 129 (T

Human tumour necro

Human adrenergic r

Truncated human al

Human truncated al

Human alpha-1C adr

Human alpha-1C adr

Human alpha-1C adr

Human protein clon

Human neurotransmi

DNA methyltransfer

DNA methyltransfer

Streptomyces hygro

Human cytoskeletal

Fragment 41-3 of t

XX Fukushima D, Konishi M, Tada H;
PI WPI: 1998-481205/41.
XX P-PSDB; W70387.
PT Membrane polypeptide expressed by human stroma cells, and antibodies
PT recognising it - for treatment of inflammatory and other
PT cytokine-mediated diseases.
XX
XX Disclosure; Pages 40-41; 54pp; Japanese.
XX
CC This is the nucleotide sequence of the human beta-OAF065, used in
CC the method of the invention. The process involves the use of peptides
CC expressed by stroma cells, and its antibodies are used for in the
CC prevention and treatment of inflammatory and other cytokine-mediated
CC diseases such as rheumatism, ulcerative colitis.
XX
SQ Sequence 1496 BP; 388 A; 360 C; 372 G; 376 T; 0 other;

Query Match 100.0%; Score 1269; DB 19; Length 1496;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1269; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 atggcttttaaaagtgctactagacaagagaaaaacgtttttcactcttttagtattacta 60
DB 45 atggcttttaaaagtgctactagacaagagaaaaacgtttttcactcttttagtattacta 104
QY 61 ggctattttgcattgaagtgaactgtgtaaacaggagactgtagacagcaaatcagg 120
DB 105 ggctattttgcattgaagtgaactgtgtaaacaggagactgtagacagcaaatcagg 164
QY 121 gatcgtctggaactgttctcctcaaccagtggtggccaggcaatgagttgtctaaag 180
DB 165 gatcgtctggaactgttctcctcaaccagtggtggccaggcaatgagttgtctaaag 224
QY 181 gaatgtggcttcggctcattggggaggatgacagtggtgacgtgcccgtgcacaggttc 240
DB 225 gaatgtggcttcggctcattggggaggatgacagtggtgacgtgcccgtgcacaggttc 284
QY 241 aaggaggactggggctccagaaatcaagccctgtctggaactgcgcagtggtgaaaccgc 300
DB 285 aaggaggactggggctccagaaatcaagccctgtctggaactgcgcagtggtgaaaccgc 344
QY 301 ttccagaaggcaaatgttcagccaccagtgatgccatctgcgggactgcttgccaggga 360
DB 345 ttccagaaggcaaatgttcagccaccagtgatgccatctgcgggactgcttgccaggga 404
QY 361 ttctataggagaagcaaatgttcgctttcaagacatgagtggtgctctgtggagac 420
DB 405 ttctataggagaagcaaatgttcgctttcaagacatgagtggtgctctgtggagac 464
QY 421 cctctcctctcttcacgaacgcactgtgccagcaaggtcaacctctgaagatcgcgtcc 480
DB 465 cctctcctctcttcacgaacgcactgtgccagcaaggtcaacctctgaagatcgcgtcc 524
QY 481 acggctccagccacgggacacagcgctgctgcgcttatctgacgcctctggccacc 540
DB 525 acggctccagccacgggacacagcgctgctgcgcttatctgacgcctctggccacc 584
QY 541 gtctctgtggccctgtctcctctgtctgtctatctattgtaagagacagtttatggagaag 600
DB 585 gtctctgtggccctgtctcctctgtctgtctatctattgtaagagacagtttatggagaag 644
QY 601 aaacccagctgtgtctgtgggttcacaggacaattcagtaaacggctctgtagctgtcgtgt 660
DB 645 aaacccagctgtgtctgtgggttcacaggacaattcagtaaacggctctgtagctgtcgtgt 704
QY 661 cttagacagacctcagctccacgaatatgccacagagcctgtgcagtgccgcctgtgac 720
DB 705 cttagacagacctcagctccacgaatatgccacagagcctgtgcagtgccgcctgtgac 764

QY 721 tcagtgacagacctgcggccgggtgcgcttgctcccatccatgtgctgtgagagggcctgc 780
DB 765 tcagtgacagacctgcggccgggtgcgcttgctcccatccatgtgctgtgagagggcctgc 824
QY 781 agccccaaaccccgagactcttgggtgtggtgtgcatcttcgcagccagttcttcaggcaaga 840
DB 825 agccccaaaccccgagactcttgggtgtggtgtgcatcttcgcagccagttcttcaggcaaga 884
QY 841 aacgcagggccagccggggagatggtgcgacactttcttcggatccctcagcagtcacc 900
DB 885 aacgcagggccagccggggagatggtgcgacactttcttcggatccctcagcagtcacc 944
QY 901 tgtggcgagtttttcagatgcctggcctctgtatgcagaaatcccatgggtgtgacaaacac 960
DB 945 tgtggcgagtttttcagatgcctggcctctgtatgcagaaatcccatgggtgtgacaaacac 1004
QY 961 tctttttgtgactcttatactgaactcactggagagacattcattctctcaatccagaa 1020
DB 1005 tctttttgtgactcttatactgaactcactggagagacattcattctctcaatccagaa 1064
QY 1021 cttgaaagctcaacgtcttttgattcaaatagcagtcgaagatttggtgtgggctgtt 1080
DB 1065 cttgaaagctcaacgtcttttgattcaaatagcagtcgaagatttggtgtgggctgtt 1124
QY 1081 ccagtcagctctcattctgaaactttacagcagctcactgatttactatagataaacaac 1140
DB 1125 ccagtcagctctcattctgaaactttacagcagctcactgatttactatagataaacaac 1184
QY 1141 acactgtgtagaatcagcatcaactcaggatgcactaactatgagaagccagctagatcag 1200
DB 1185 acactgtgtagaatcagcatcaactcaggatgcactaactatgagaagccagctagatcag 1244
QY 1201 gagagtgccgtctatccaccagccactcagacgtccctccaggaagcagcagctg 1260
DB 1245 gagagtgccgtctatccaccagccactcagacgtccctccaggaagcagcagctg 1304
QY 1261 ggttcacctg 1269
DB 1305 ggttcacctg 1313

RESULT 2
X08689
ID X08689 standard; cDNA: 1502 BP.
XX
AC X08689;
XX
XX 27-SEP-1999 (first entry)
XX
DE Novel nucleotide sequence encoding new protein (Clone AX92_3).
XX
KW Polynucleotide; protein; nutrition; cytokine; cell proliferation;
KW cell differentiation; immunostimulation; immunosuppression;
KW haematopoiesis regulation; tissue growth; activin; inhibin;
KW chemotaxis; chemokinesis; haemostasis; thrombolysis; receptor;
KW ligand; anti-inflammatory; tumour suppression; gene therapy; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
CDS 51..1322
FT /*tag= a
FT /product= "Novel protein"
XX
PN WO9920644-A1.
XX
PD 29-APR-1999.
XX
PF 16-OCT-1998; 98WO-US22034.
XX
PR 18-OCT-1997; 97US-0955557.
XX
PA (GEMY) GENETICS INST INC.

XX Agostino MJ, Bowman MR, Evans C, Jacobs K, Lavallie ER;
 PI McCoy JW, Merberg D, Racie LA, Spaulding V, Treacy M;
 XX
 DR WPI: 1999-288272/24.
 DR P-PSDB; W85724.
 XX

New polynucleotides encoding secreted human proteins

PS Claim 32; Page 116; 136pp; English.

XX The new human secreted proteins are encoded by polynucleotides
 CC obtained from human placenta, adult testes, fetal kidney, fetal
 CC brain, adult brain and adult blood cDNA libraries.
 CC The polynucleotides and proteins are predicted to have biological
 CC activities which would make them suitable for treating, preventing or
 CC ameliorating medical conditions in humans and animals. Suggested
 CC activities include nutritional activity, cytokine and cell
 CC proliferation/differentiation activity, immune stimulating (e.g. as
 CC vaccines) or suppressing activity, haematopoiesis regulating
 CC activity, tissue growth activity, activin/inhibin activity,
 CC chemotactic/chemokinetic activity, haemostatic and thrombolytic
 CC activity, receptor/ligand activity, anti-inflammatory activity,
 CC cadherin/tumour invasion suppressor activity, and tumour inhibition
 CC activity. The polynucleotides are also stated to be useful for gene
 CC therapy. The sequences are identified by a secretory leader
 CC sequence motif in the polynucleotide and it is thought that the
 CC encoded proteins have biological activity by virtue of their secreted
 CC nature. This clone was designated AX92_3. A probe for this clone is
 CC described in X08704.
 XX

SQ Sequence 1502 BP; 388 A; 362 C; 375 G; 377 T; 0 other;

Query Match 99.9%; Score 1267.4; DB 20; Length 1502;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 1268; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 atggtttaaagtgctactagaacagagaaacggttttcaactcttttagtattacta 60
 DB 51 atggtttaaagtgctactagaacagagaaacggttttcaactcttttagtattacta 110
 QY 61 gctatttgctatgaagtgactgtgaacagagagactgtagacagcaagaattcagg 120
 DB 111 ggtatttgctatgaagtgactgtgaacagagagactgtagacagcaagaattcagg 170
 QY 121 gatcggtctggaactgtgttccctgcacaccagtggtggccaggtgaggtgtcctaag 180
 DB 171 gatcggtctggaactgtgttccctgcacaccagtggtggccaggtgaggtgtcctaag 230
 QY 181 gaatggtctcggtatgggagagatgcacagtggtgacgtgcggtgcacaggttc 240
 DB 231 gaatggtctcggtatgggagagatgcacagtggtgacgtgcggtgcacaggttc 290
 QY 241 aaggaggtggtgttcagaaaatgcagccctgtctgagactgcggtgcgagtggaaccgc 300
 DB 291 aaggaggtggtgttcagaaaatgcagccctgtctgagactgcggtgcgagtggaaccgc 350
 QY 301 ttccagaaggcaaatgttccagccaccagtgatgcacatcgcggtgactgctgcagga 360
 DB 351 ttccagaaggcaaatgttccagccaccagtgatgcacatcgcggtgactgctgcagga 410
 QY 361 tttatagaagacgaaactgtcggtcttcaagacatggagtgtgctctgtggagac 420
 DB 411 tttatagaagacgaaactgtcggtcttcaagacatggagtgtgctctgtggagac 470
 QY 421 cctctctctcttagaaccgactgtgcccagcaagggtcaacctgctgaagatcgcgtcc 480
 DB 471 cctctctctcttagaaccgactgtgcccagcaagggtcaacctgctgaagatcgcgtcc 530
 QY 481 acggctctccagccacgggacacgctggtgctgcgtttatctgcagcgtctgcccacc 540
 DB 531 acggctctccagccacgggacacgctggtgctgcgtttatctgcagcgtctgcccacc 590

QY 541 gtctctggccctgtctcatctctgtgtcatctattgttaagagacagtttatgagaag 600
 DB 591 gtctctggccctgtctcatctctgtgtcatctattgttaagagacagtttatgagaag 650
 QY 601 aaaccagctgtctctgtcgggtcagacagacattcagtaacacggctctgagctgctgtg 660
 DB 651 aaaccagctgtctctgtcgggtcagacagacattcagtaacacggctctgagctgctgtg 710
 QY 661 cttagacagacctcagctccagcaaatatgccacagagcctgtgccagtcgcgcgtgac 720
 DB 711 cttagacagacctcagctccagcaaatatgccacagagcctgtgccagtcgcgcgtgac 770
 QY 721 tcagtgcagacctcggcggcgtgctgtgtcccatccatctgtgtgagagagcctgtg 780
 DB 771 tcagtgcagacctcggcggcgtgctgtgtcccatccatctgtgtgagagagcctgtg 830
 QY 781 agccccaacccggcagctctgtgtgtgggtgcattctgcagccagttcttcaggcaaga 840
 DB 831 agccccaacccggcagctctgtgtgtgggtgcattctgcagccagttcttcaggcaaga 890
 QY 841 agcagagcccgagcgggagatggtgcgactttcttcggatccctcagcagtcctc 900
 DB 891 aacgagcggcggcgggagatggtgcgactttcttcggatccctcagcagtcctc 950
 QY 901 tgtggcagttttcagatgcctggtcctctgtgcagaaatcccatgggtgtgacaacatc 960
 DB 951 tgtggcagttttcagatgcctggtcctctgtgcagaaatcccatgggtgtgacaacatc 1010
 QY 961 tcttttctgactctatctgaactcactggaactgagagacattctctcattccatccagaa 1020
 DB 1011 tcttttctgactctatctgaactcactggaactgagagacattctctcattccatccagaa 1070
 QY 1021 ctgaaaactcaactcttttgattcaaatagcagatcagcagattgtgtggtggcgtgt 1080
 DB 1071 ctgaaaactcaactcttttgattcaaatagcagatcagcagattgtgtggtggcgtgt 1130
 QY 1081 ccagtcagctctcattctgaaacttttacagcagctactgatttctctagataaacaac 1140
 DB 1131 ccagtcagctctcattctgaaacttttacagcagctactgatttctctagataaacaac 1190
 QY 1141 acactggttagatcagcactcaactcagagatgcactaactatgagaagcagctagatcag 1200
 DB 1191 acactggttagatcagcactcaactcagagatgcactaactatgagaagcagctagatcag 1250
 QY 1201 gagagtggcgtctatcatccaccagccactcagcgtccctccaggtgaagcagcagctg 1260
 DB 1251 gagagtggcgtctatcatccaccagccactcagcgtccctccaggtgaagcagcagctg 1310
 QY 1261 ggttccctcg 1269
 DB 1311 ggttccctcg 1319

RESULT 3
 X23415
 ID X23415 standard; DNA; 1489 BP.
 XX
 AC X23415;
 XX
 DT 18-JUN-1999 (first entry)
 XX
 DE Human hAPO4-alpha DNA.
 XX
 KW Tumour necrosis factor receptor; signal transducer molecule; TNF; APO4;
 KW developmental abnormality; gestational abnormality; prostate cancer;
 KW APO6; APO8; APO9; TNFR-1; TNFR-3; diagnosis; treatment; therapy; disease;
 KW cytoplasmic domain; immunogen; antibody preparation; breast carcinoma;
 KW apoptosis; human; APO4-alpha; ss.
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers

AC X24978;
 XX 05-JUL-1999 (first entry)
 DT XX Human TRAIN-R cDNA.
 DE
 XX TRAIN-R; receptor; human; tumour necrosis factor receptor;
 KW agonist; antagonist; cancer; immunological disease; therapy;
 KW cytostatic; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT 179..1432
 FT CDS /*tag= a
 FT sig_peptide 179..253
 FT /*tag= b
 FT mat_peptide 254..1429
 FT /*tag= c
 XX
 PN WO9913078-A1.
 XX
 PD 18-MAR-1999.
 XX
 PF 11-SEP-1998; 98WO-US19030.
 XX
 PR 06-MAY-1998; 98US-0084422.
 PR 12-SEP-1997; 97US-0058631.
 XX
 PA (BIOJ) BIOGEN INC.
 XX
 PI Hession C, Tschopp J;
 XX
 XX WPI: 1999-229238/19.
 DR P-PSDB; W98146.
 XX
 PT New cysteine-rich tumor necrosis factor receptor
 XX
 PS Claim 1: Page 27; 30pp; English.
 XX
 CC The present sequence encodes a novel human cysteine-rich tumour
 CC necrosis factor receptor family member termed TRAIN-R (see W98146).
 CC It is a composite of 2 overlapping lambda gt10 clones (GJ159 and
 CC GJ158) from a Clontech human adult lung cDNA library. Human
 CC TRAIN-R was also cloned from a second sequence subclone of a
 CC lambda gt10 cDNA (GJ156, see X24979). Human TRAIN-R is expressed
 CC at low levels in every tissue and cell line tested thus far, with
 CC higher expression detected in heart, prostate, ovary, testis,
 CC peripheral blood lymphocytes, thyroid and adrenal gland.
 CC Cell death can be induced by administering an agent capable of
 CC inhibiting the binding of TRAIN-R to its ligand. A claimed method
 CC of treating, or reducing, the advancement, severity or effects of
 CC an immunological disease in a mammal comprises administering a
 CC pharmaceutical composition which comprises a TRAIN-R blocking agent,
 CC e.g. soluble TRAIN-R. TRAIN-R can be fused to an immunoglobulin to
 CC produce a fusion protein which may be targeted to various sites.
 CC It can be used in binding assays, and to identify antagonists and
 CC agonists. Anti-TRAIN-R antibodies can be used to reduce the
 CC severity of an immune response or to treat cancer. TRAIN-R
 CC blocking agents can also be used to reduce the severity or effects
 CC of an immunological disease (all claimed).
 XX
 SQ Sequence 2185 BP; 546 A; 551 C; 550 G; 538 T; 0 other;

Query Match 97.7%; Score 1240; DB 20; Length 2185;
 Best Local Similarity 99.6%; Pred. NO. 0;
 Matches 1243; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 atggctttaaagtgtactagacaagagagaaacgttttttactcttttagtattacta 60
 DB 179 atggctttaaagtgtactagacaagagagaaacgttttttactcttttagtattacta 238

QY 61 ggctattgtcatgtaaagtgaactgtgaacacaggagagactgtagacagcaagaattcagg 120
 DB 239 ggctattgtcatgtaaagtgaactgtgaacacaggagagactgtagacagcaagaattcagg 298
 QY 121 gatcggctcggaaaactgtgttccctgcgaaccagtggtggccagggaatgagttgtctaag 180
 DB 299 gatcggctcggaaaactgtgttccctgcgaaccagtggtggccagggaatgagttgtctaag 358
 QY 181 gaatgtggtctcggtctatggggagagatcacagtggtgacgtgcgggtgcacaggttc 240
 DB 359 gaatgtggtctcggtctatggggagagatcacagtggtgacgtgcgggtgcacaggttc 418
 QY 241 aaggaggactggggtccagaaaatcgaagccctgtctggaactgcgcagtggggaaccgc 300
 DB 419 aaggaggactggggtccagaaaatcgaagccctgtctggaactgcgcagtggggaaccgc 478
 QY 301 ttccagaaggaataatgtttcagccaccagtgatgccatctgcggggactgcttgccagga 360
 DB 479 ttccagaaggaataatgtttcagccaccagtgatgccatctgcggggactgcttgccagga 538
 QY 361 ttttatagaagaacaaactgtcggtttcaagacatggaagtgtgtccttctgtgagagac 420
 DB 539 ttttatagaagaacaaactgtcggtttcaagacatggaagtgtgtccttctgtgagagac 598
 QY 421 cctcctcctcttaacgaacgcactgtgccagcaaggtcaacctctgaagaatcggtctc 480
 DB 599 cctcctcctcttaacgaacgcactgtgccagcaaggtcaacctctgaagaatcggtctc 658
 QY 481 acggcctccagcccaacgggacacggcgctgggtgcgcttatctgcagcgctctggccacc 540
 DB 659 acggcctccagcccaacgggacacggcgctgggtgcgcttatctgcagcgctctggccacc 718
 QY 541 gtctgtggcctgctcatctctgtgcatactatgttaagagacagtttatggagaag 600
 DB 719 gtctgtggcctgctcatctctgtgcatactatgttaagagacagtttatggagaag 778
 QY 601 aaaccagctggtctctgcggtcacaggacattcagataacggctctgagctgctggt 660
 DB 779 aaaccagctggtctctgcggtcgaaggacattcagataacggctctgagctgctggt 838
 QY 661 cttagacacacctcagctccacgaataatgccacagagcctgtctgcagtcgcgcctgac 720
 DB 839 tttagacacacctcagctccacgaataatgccacagagcctgtctgcagtcgcgcctgac 898
 QY 721 tcaagtcaacacctgcggcggtgcgcttgcctccatgctgctgagagagcctgc 780
 DB 899 tcaagtcaacacctgcggcggtgcgcttgcctccatgctgctgagagagcctgc 958
 QY 781 agcccaacccggcgactcttgggtgggtgcatcttcgagccagctcttcaggcaaga 840
 DB 959 agcccaacccggcgactcttgggtgggtgcatcttcgagccagctcttcaggcaaga 1018
 QY 841 aacgcggcccccagccgggagatggtgcgcactttcttcggatccctcagcagtcacc 900
 DB 1019 aacgcggcccccagccgggagatggtgcgcactttcttcggatccctcagcagtcacc 1078
 QY 901 tggggcgaagtttcagatccctgcctctgagtcagaatcccatgggtggtacacatc 960
 DB 1079 tggggcgaagtttcagatccctgcctctgagtcagaatcccatgggtggtacacatc 1138
 QY 961 tcttttttgactcttctatcctgaactcactggagagacattctctcctcaatccagaa 1020
 DB 1139 tcttttttgactcttctatcctgaactcactggagagacattctctcctcaatccagaa 1198
 QY 1021 cttgaagctcaacgtcttttgattcaaatagcagtcgaagatttgggtgggtggtgtt 1080
 DB 1199 cttgaagctcaacgtcttttgattcaaatagcagtcgaagatttgggtgggtggtgtt 1258
 QY 1081 ccagtcagct 1140
 DB 1259 ccagtcagct 1318
 QY 1141 acactggttagaatcagcatcaactcaggatgcactaactatgagaagccagctagatcag 1200

Db 1319 acatggttagaatcagcatcaactcaggatgcactaactatgagaaagccagctagatcag 1378
QY 1201 gagagtggcgtatcatccaccacccagccactcagcagctccctccaggtta 1248
Db 1379 gagagtggcgtatcatccaccacccagccactcagcagctccctccaggtta 1426
RESULT 6
X59346
ID X59346 standard; cDNA; 987 BP.
AC X59346;
XX
DT 20-SEP-1999 (first entry)
XX
DE Human NTR-5 cDNA.
XX
KW NTR-5; human; receptor; signal transduction; bone; muscle;
KW diagnosis; therapy; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT sig_peptide 1..57
FT /*tag= a
FT mat_peptide 58..987
FT /*tag= b
XX
PN W09933967-A2.
XX
PD 08-JUL-1999.
XX
PF 28-DEC-1998; 98WO-US27688.
XX
PR 29-DEC-1997; 97US-0068925.
XX
PA (REGE-) REGENERON PHARM INC.
XX
PI Valenzuela DM;
XX
DR WPI; 1999-419102/35.
XX
PT P-PSDB; Y06400.
XX
PS New mammalian receptor NTR-5 polypeptides
Claim 2a; Page 21-22; 27pp; English.
XX
CC This is the claimed coding region of human cDNA encoding a novel
CC receptor, designated NTR-5 (see Y06400), that shows homology to
CC osteoprotegerin and tumour necrosis factor receptor. The cDNA was
CC isolated from a heart cDNA library using mouse NTR-5 cDNA (see
CC X59345) as probe. Homology to osteoprotegerin suggests that NTR-5
CC is involved in the regulation of bone mass, and may be useful for
CC regulating development, proliferation and death of osteoblast or
CC osteoclast cells or for regulating muscle metabolism, and that it
CC may be implicated in muscle diseases or disorders. A host-vector
CC system for production of NTR-5 is claimed. NTR-5 polypeptides can
CC be used as immunogens and in screening assays to identify NTR-5
CC ligands, agonists and antagonists. The NTR-5 polynucleotide is
CC useful as a diagnostic tool, and as a source of probes and primers.
CC The invention also provides for diagnostic and therapeutic methods
CC based on the interaction of NTR-5 and agents that initiate signal
CC transduction through binding to NTR-5.
XX
SQ Sequence 987 BP; 220 A; 251 C; 278 G; 238 T; 0 other;

Query Match 65.8%; Score 835.6; DB 20; Length 987;
Best Local Similarity 99.5%; Pred. No. 7.1e-247;
Matches 838; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 1 atggccttaaaagtgcactagaacagagaaaaacgtttttcactcttttagtattacta 60

Db 1 atggccttaaaagtgcactagaacagagaaaaacgtttttcactcttttagtattacta 60
QY 61 ggctatttgcctatgataaagtgcactgtgaaacagagagactgtagacagcaagaattcagg 120
Db 61 ggctatttgcctatgataaagtgcactgtgaaacagagagactgtagacagcaagaattcagg 120
QY 121 gatcggtctgaaactgtgttccctgcacacagtggtggccagcagcatgagttgtcttaag 180
Db 121 gatcggtctgaaactgtgttccctgcacacagtggtggccagcagcatgagttgtcttaag 180
QY 181 gaatgtggtctcggtatggtgggagatgcacagtgtgtgacgtgccggtcacagggttc 240
Db 181 gaatgtggtctcggtatggtgggagatgcacagtgtgtgacgtgccggtcacagggttc 240
QY 241 aaggagactggggtctccagaaaatgaagccctgtctggaactgcgaagtgtgaaccgc 300
Db 241 aaggagactggggtctccagaaaatgaagccctgtctggaactgcgaagtgtgaaccgc 300
QY 301 ttccagaagcacaattgttccagccaccagtgtgccatctgcgggactgcttgcaccaga 360
Db 301 ttccagaagcacaattgttccagccaccagtgtgccatctgcgggactgcttgcaccaga 360
QY 361 ttttataggaagacgaacattgtcggtcttccaagacatggagtggtgtgccttggagac 420
Db 361 ttttataggaagacgaacattgtcggtcttccaagacatggagtggtgtgccttggagac 420
QY 421 cctcctcctcttaagaaacgcgaactgtgccaagaaggtcaacctctgtaaatgcgctcc 480
Db 421 cctcctcctcttaagaaacgcgaactgtgccaagaaggtcaacctctgtaaatgcgctcc 480
QY 481 acggcctccagccacagggacacggcgtgctgccgttatctgcagcgtcttgccacc 540
Db 481 acggcctccagccacagggacacggcgtgctgccgttatctgcagcgtcttgccacc 540
QY 541 gtctgtgtggcctgtcctcctctgtgtcatttattgttaagagacagttttatggagaag 600
Db 541 gtctgtgtggcctgtcctcctctgtgtcatttattgttaagagacagttttatggagaag 600
QY 601 aaaccagctgtctctgcgttcacaggaattcagatacaaacggtctgcagctgtcgtgt 660
Db 601 aaaccagctgtctctgcgttcacaggaattcagatacaaacggtctgcagctgtcgtgt 660
QY 661 cttgacagacctcagctccacgaatattgccacagagcctgtgccagtcgcgcgtgac 720
Db 661 cttgacagacctcagctccacgaatattgccacagagcctgtgccagtcgcgcgtgac 720
QY 721 tcaagtgcagacctcggggccggtgctgtgtcccatccatcctgtgtgagagagcctgac 780
Db 721 tcaagtgcagacctcggggccggtgctgtgtcccatccatcctgtgtgagagagcctgac 780
QY 781 agccccaaacccgcgactcttggtgtgggtgcatcttcgagcagctcttcaggcaaga 840
Db 781 agccccaaacccgcgactcttggtgtgggtgcatcttcgagcagctcttcaggcaaga 840
QY 841 aa 842
Db 841 aa 842
RESULT 7
X23413
ID X23413 standard; DNA; 1678 BP.
XX
AC X23413;
XX
DT 18-JUN-1999 (first entry)
XX
DE Mouse mAP04-alpha (long) DNA.
XX
KW Tumour necrosis factor receptor; signal transducer molecule; TNF; APO4;
KW developmental abnormality; gestational abnormality; prostate cancer;
KW APO6; APO8; APO9; TNRL-1; TNRL-3; diagnosis; treatment; therapy; disease;

X23414
 ID X23414 standard; DNA; 886 BP.
 XX
 AC X23414;
 XX
 DT 18-JUN-1999 (first entry)
 XX
 DE Mouse mAPO4-alpha (short) DNA.
 XX
 KW Tumour necrosis factor receptor; signal transducer molecule; TNF; APO4;
 KW developmental abnormality; gestational abnormality; prostate cancer;
 KW APO6; APO8; APO9; TNRL-1; TNRL-3; diagnosis; treatment; therapy; disease;
 KW cytoplasmic domain; immunogen; antibody preparation; breast carcinoma;
 KW apoptosis; mouse; mAPO4-alpha; ss.
 XX
 OS Mus sp.
 XX
 FH Key Location/Qualifiers
 CDS 72..716
 FT /*tag= a
 FT /product= "mAPO4-alpha short"
 XX
 PN W09911791-A2.
 XX
 PD 11-MAR-1999.
 XX
 PF 04-SEP-1998; 98WO-US18393.
 XX
 PR 05-SEP-1997; 97US-0924634.
 XX
 PA (UNIW) UNIV WASHINGTON.
 XX
 PI Chaudhary PM;
 XX
 DR WPI: 1999-205191/17.
 DR P-PSDB; W93580.
 XX
 PT New Tumor Necrosis Factor family receptor polypeptides and ligands -
 PT useful for diagnosis and treatment of prostate cancer and
 PT developmental or gestational abnormalities
 XX
 PS Example IV; Fig 7B; 156pp; English.
 XX
 CC This invention describes isolated Tumor Necrosis Factor (TNF) family
 CC receptor polypeptides: APO4, APO6, APO8 and APO9 or their active
 CC fragments, and isolated TNF related ligands 1 and 3 (TNRL1 and TNRL3) or
 CC their active fragments. APO4 is useful for diagnosing prostate cancer
 CC by determining levels of APO4 in an individual. Prostate cancer can also
 CC be treated using APO4 selective binding agents linked to a therapeutic
 CC moiety. APO4 polypeptides are also useful for identifying selective
 CC binding agents, useful in diagnosis/treatment of disease by binding of
 CC agents to the polypeptide/active fragment which is extracellular, or
 CC expressed on the cell surface. The binding is preferably performed in
 CC vivo. APO4 polypeptides/active fragments are also useful for screening
 CC for agonists and antagonists by binding and observing the change in APO4
 CC activity. Effective pharmacological agents useful in diagnosis or
 CC treatment of disease are also identified using APO4 polypeptides/active
 CC fragments and APO4 signal transducer molecules that specifically interact
 CC with a cytoplasmic domain of APO4 and detecting a change in level of APO4
 CC activity. The method is performed in vivo or in vitro. APO polypeptides
 CC are all useful as immunogens for preparing antibodies. APO4 is also
 CC useful for diagnosis/treatment of developmental or gestational
 CC abnormalities. APO8 was transfected to human breast carcinoma cell line
 CC MCF-7, and induced apoptosis.
 XX
 SQ Sequence 886 BP; 204 A; 245 C; 247 G; 190 T; 0 other;

Query Match 35.4%; Score 449; DB 20; Length 886;
 Best Local Similarity 82.4%; Pred. NO. 4.9e-128;
 Matches 515; Conservative 0; Mismatches 110; Indels 0; Gaps 0;
 QY 1 atggttttaaaagtctactagaacaagaaagcgtttttcactcttttagtattacta 60

Db	72	atggcaactcaaggctcctacctacacagcggtgctcttcgcgtccattcttctocta	131
QY	61	ggctattgtcatgtaaagtactgtgaacacagagagacttagacacagaagaattcagg	120
Db	132	ctccacctggcatgtaaaagtgtgcaaacccgagattgcaggcagcaggaaattcaag	191
QY	121	gacggctctggaactgtgtccctgcacacagtgaggccagcgcatggagtgtctaaag	180
Db	192	gatcatgtgaaactgtgtcctctgcaaacagtgccgacctggcatggagtgtccaaag	251
QY	181	gaatgtgcttcggctatggggagatgcacagtggtgacgtgcccgtgcacaggttc	240
Db	252	gaatgtgcttcggctatggggagatgcacagtggtgacgtgcccgtgcacaggttc	311
QY	241	aaggagagctgggctctccagaaatgcaagccctgtctggaactgcgcagtggtgaaccgc	300
Db	312	aaggagagctgggctctccagaaatgcaagccctgtctggaactgcgcagtggtgaaccgc	371
QY	301	tttcagaaggcaaatgttcagccaccagtgatgcacatctgcgggagctgcttgccagga	360
Db	372	tttcagaaggcaaatgttcagccaccagtgatgcacatctgcgggagctgcttgccagga	431
QY	361	ttttatggaagacgaaactgtcgctttcaagacatggagtggtgcttctgtggagac	420
Db	432	ttttaccggaagacaaactgtggttttcaagacatggagtggtgcttctgtggagac	491
QY	421	ctctctctcttaccgaaccgcaactgtgccagcaaggtcaacctgtgaagatcgctcc	480
Db	492	ccacctctctctacgaaccacactgtaccagcaaggtgaacctgtgaagatctctccc	551
QY	481	acggctctcagccacgggacacgctgctgccttatctgcagcgctctgcccacc	540
Db	552	accgtctcagccctcgggacacgctgctgccttatctgcagcgctctgcccacc	611
QY	541	gtcctgtgcccctgctcctctctgtcatctatttgaagacagactttatggagaag	600
Db	612	gtgctgtgcccctgctcctctctgtcatctactcaagagcagtgctatggagaag	671
QY	601	aaaccacagctgtctctggtgtcac	625
Db	672	aaaccacagctgtgaagctccatccc	696

RESULT 9
 X24977
 ID X24977 standard; CDNA; 942 BP.
 XX
 AC X24977;
 XX
 DT 05-JUL-1999 (first entry)
 XX
 DE Mouse TRAIN-R (long form) CDNA.
 XX
 KW TRAIN-R; receptor; mouse; tumour necrosis factor receptor;
 KW agonist; antagonist; cancer; immunological disease; therapy;
 KW cytosolic; ss.
 OS Mus musculus.
 FH Key Location/Qualifiers
 CDS 101..745
 FT /*tag= a
 XX
 PN W09913078-A1.
 XX
 PD 18-MAR-1999.
 XX
 PF 11-SEP-1998; 98WO-US19030.
 XX
 PR 06-MAY-1998; 98US-0084422.
 PR 12-SEP-1997; 97US-0058631.
 XX

BEST LOCAL SIMILARITY 82.16; PRED. NO. 7.4E-124;
Matches 513; Conservative 0; Mismatches 111; Indels 1; Gaps 1;


```

ID V11422 standard; cDNA; 371 BP.
XX V11422;
AC
XX
XX
DT 23-JUL-1998 (first entry)
XX
DE Human secreted protein clone AX92_3 cDNA 5'-end.
XX
XX Secreted protein; prevention; treatment; gene therapy; ds.
XX
XX Homo sapiens.
XX
XX W09801554-A2.
XX
XX 15-JAN-1998.
XX
XX 07-JUL-1997; 97WO-US11876.
XX
XX 09-JUL-1996; 96US-0677231.
XX
XX (GEMY ) GENETICS INST INC.
XX
XX Bowman M, Evans C, Jacobs K, Lavallie ER, McCoy JM;
XX Merberg D, Racie LA, Spaulding V, Treacy M;
XX WPI; 1998-110230/10.
XX
XX P-PSDB; W58844.
XX
XX Secreted proteins and polynucleotides encoding them - useful to
XX prevent, treat and ameliorate medical conditions
XX
XX Claim 15; Page 57; 93pp; English.
XX
XX V11422-V11424 encode fragments of a novel secreted protein derived from
XX clone AX92_3 which was isolated from a human adult testes cDNA library.
XX The protein can be used to prevent, treat or ameliorate a medical
XX condition, while the polynucleotides can be used for gene therapy.
XX
XX Sequence 371 BP; 83 A; 96 C; 107 G; 82 T; 3 other;

Query Match 28.5%; Score 361.6; DB 19; Length 371;
Best Local Similarity 98.1%; Pred. NO. 2.2e-101;
Matches 364; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Oy 128 ctggaaactgtgttcctgcaaccagtggtggccagcatgagtggtcttaaggaaatgtg 187
Db 1 ctggaaactgtgttcctgcaaccagtggtggccagcatgagtggtcttaaggaaatgtg 60
Oy 188 gcttcggctatgggaggatgcacagtggtgacgtgcggcggtgcacagggttcaaggagg 247
Db 61 gcttcggctatgggaggatgcacagtggtgacgtgcggcggtgcacagggttcaaggagg 120
Oy 248 actggggttcagaatacgaagccctgtctgactgcgagtggtgaaccgctttcaga 307
Db 121 actggggttcagaatacgaagccctgtctgactgcgagtggtgaaccgctttcaga 180
Oy 308 aggcgaattgttcagccaccagtgatgccatctgcgggactgcttgccaggaattata 367
Db 181 aggcgaattgttcagccaccagtgatgccatctgcgggactgcttgccaggaattata 240
Oy 368 ggaagacgaatacttcgggctttcaagacatgagtggtgcttctgtggagacctcttc 427
Db 241 ggaagacgaatacttcgggctttcaagacatgagtggtgcttctgtggagacctcttc 300
Oy 428 ctccttacgaaccgactgtgcagcaaggtcaacctgctgaagatcgctccacggcct 487
Db 301 ctccttacgaaccgactgtgcagcaaggtcaacctgctgaagatcgctccacggcct 360
Oy 488 ccagccacgg 498
Db 361 ccagccacgg 371
```

RESULT 14

```

X23417
ID X23417 standard; DNA; 591 BP.
XX
XX X23417;
AC
XX
XX
DT 18-JUN-1999 (first entry)
XX
XX Mouse mAPO4-gamma DNA.
DE
XX
XX Tumour necrosis factor receptor; signal transducer molecule; TNF; APO4;
XX developmental abnormality; gestational abnormality; prostate cancer;
XX APO6; APO8; APO9; TNRL-1; TNRL-3; diagnosis; treatment; therapy; disease;
XX cytoplasmic domain; immunogen; antibody preparation; breast carcinoma;
XX apoptosis; mouse; APO4-gamma; ss.
XX
XX Mus sp.
OS
XX
XX Key Location/Qualifiers
XX CDS 95..547
XX FT /*tag= a
XX FT /product= "mAPO4-gamma"
XX
XX W09911791-A2.
XX
XX 11-MAR-1999.
XX
XX 04-SEP-1998; 98WO-US18393.
XX
XX 05-SEP-1997; 97US-0924634.
XX
XX (UNIW ) UNIV WASHINGTON.
XX
XX Chaudhary PM;
XX
XX WPI; 1999-205191/17.
XX
XX P-PSDB; W93583.
XX
XX New Tumor Necrosis Factor family receptor polypeptides and ligands -
XX useful for diagnosis and treatment of prostate cancer and
XX developmental or gestational abnormalities
XX
XX Disclosure; Fig 7E; 156pp; English.
XX
XX This invention describes isolated Tumor Necrosis Factor (TNF) family
XX receptor polypeptides: APO4, APO6, APO8 and APO9 or their active
XX fragments, and isolated TNF related ligands 1 and 3 (TNRL1 and TNRL3) or
XX their active fragments. APO4 is useful for diagnosing prostate cancer
XX by determining levels of APO4 in an individual. Prostate cancer can also
XX be treated using APO4 selective binding agents linked to a therapeutic
XX moiety. APO4 polypeptides are also useful for identifying selective
XX binding agents, useful in diagnosis/treatment of disease by binding of
XX agents to the polypeptide/active fragment which is extracellular, or
XX expressed on the cell surface. The binding is preferably performed in
XX vivo. APO4 polypeptides/ active fragments are also useful for screening
XX for agonists and antagonists by binding and observing the change in APO4
XX activity. Effective pharmacological agents useful in diagnosis or
XX treatment of disease are also identified using APO4 polypeptides/active
XX fragments and APO4 signal transducer molecules that specifically interact
XX with a cytoplasmic domain of APO4 and detecting a change in level of APO4
XX activity. The method is performed in vivo or in vitro. APO polypeptides
XX are all useful as immunogens for preparing antibodies. APO4 is also
XX useful for diagnosis/treatment of developmental or gestational
XX abnormalities. APO8 was transfected to human breast carcinoma cell line
XX MCF-7, and induced apoptosis.
XX
XX Sequence 591 BP; 148 A; 145 C; 175 G; 123 T; 0 other;

Query Match 24.7%; Score 314; DB 20; Length 591;
Best Local Similarity 78.9%; Pred. No. 1.2e-86;
Matches 374; Conservative 0; Mismatches 100; Indels 0; Gaps 0;
```


GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 2, 2001, 09:59:02 ; Search time 4027.99 Seconds
(without alignments)
2207.677 Million cell updates/sec

Title: US-09-380-276A-5
Perfect score: 1269
Sequence: 1 atgctttaaaagtctact.....ggcagcgactgggtccctg 1269

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 7991742 seqs, 3503743858 residues
Total number of hits satisfying chosen parameters: 15983484

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_est4:*
5: gb_est5:*
6: gb_est6:*
7: gb_est7:*
8: gb_est8:*
9: gb_est9:*
10: gb_est10:*
11: gb_est11:*
12: gb_est12:*
13: gb_est13:*
14: gb_est14:*
15: gb_est15:*
16: gb_est16:*
17: gb_est17:*
18: gb_est18:*
19: gb_est19:*
20: gb_est20:*
21: gb_est21:*
22: gb_est22:*
23: gb_est23:*
24: gb_est24:*
25: gb_est25:*
26: gb_est26:*
27: gb_est27:*
28: gb_est28:*
29: gb_est29:*
30: gb_est30:*
31: gb_est31:*
32: gb_est32:*
33: gb_est33:*
34: gb_est34:*
35: gb_est35:*
36: gb_est36:*
37: gb_est37:*
38: gb_est38:*
39: gb_est39:*
40: gb_est40:*
41: em_estba:*
42: em_estfun:*
43: em_esthum1:*
44: em_esthum2:*
45: em_esthum3:*
46: em_esthum4:*
47: em_esthum5:*
48: em_esthum6:*
49: em_esthum7:*
50: em_esthum8:*
51: em_esthum9:*
52: em_esthum10:*
53: em_esthum11:*
54: em_esthum12:*
55: em_esthum13:*
56: em_esthum14:*
57: em_esthum15:*
58: em_esthum16:*
59: em_esthum17:*
60: em_esthum18:*
61: em_esthum19:*
62: em_esthum20:*
63: em_estin1:*
64: em_estin2:*
65: em_estin3:*
66: em_estin4:*
67: em_estov1:*
68: em_estov2:*
69: em_estpl1:*
70: em_estpl2:*
71: em_estpl3:*
72: em_estpl4:*
73: em_estpl5:*
74: em_estro1:*
75: em_estro2:*
76: em_estro3:*
77: em_estro4:*
78: em_estro5:*
79: em_estro6:*
80: em_estro7:*
81: em_estro8:*
82: em_estro9:*
83: em_estro10:*
84: em_estro11:*
85: em_estro12:*
86: em_estro13:*
87: gb_est41:*
88: gb_est42:*
89: gb_est43:*
90: gb_est44:*
91: gb_est45:*
92: gb_est46:*
93: gb_est47:*
94: gb_est48:*
95: gb_est49:*
96: gb_est50:*
97: gb_est51:*
98: gb_est52:*
99: gb_est53:*
100: gb_est54:*
101: gb_est55:*
102: gb_est56:*
103: gb_est57:*
104: gb_est58:*
105: gb_est59:*
106: gb_est60:*
107: gb_est70:*
108: gb_est71:*
109: gb_est72:*
110: gb_est73:*
111: gb_est74:*
112: em_esthum21:*
113: em_esthum22:*
114: em_esthum23:*
115: em_estom1:*
116: em_estom2:*

117: em_estpl6:*
 118: em_estpl7:*
 119: em_estpl8:*
 120: em_estpl9:*
 121: em_estpl10:*
 122: em_estpl11:*
 123: em_estpl12:*
 124: em_estpl13:*
 125: em_estpl14:*
 126: em_estpl15:*
 127: em_estpl16:*
 128: em_estpl17:*
 129: em_estpl18:*
 130: em_estpl19:*
 131: em_estpl20:*
 132: em_estpl21:*
 133: em_estpl22:*
 134: em_estpl23:*
 135: em_estpl24:*
 136: em_estpl25:*
 137: em_estpl26:*
 138: em_estpl27:*
 139: em_estpl28:*
 140: em_estpl29:*
 141: em_estpl30:*
 142: em_estpl31:*
 143: em_estpl32:*
 144: em_estpl33:*
 145: em_estpl34:*
 146: em_estpl35:*
 147: em_estpl36:*
 148: em_estpl37:*
 149: em_estpl38:*
 150: em_estpl39:*
 151: em_estpl40:*
 152: em_estpl41:*
 153: em_estpl42:*
 154: em_estpl43:*
 155: em_estpl44:*
 156: em_estpl45:*
 157: em_estpl46:*
 158: em_estpl47:*
 159: em_estpl48:*
 160: em_estpl49:*
 161: em_estpl50:*
 162: em_estpl51:*
 163: em_estpl52:*
 164: em_estpl53:*
 165: em_estpl54:*
 166: em_estpl55:*
 167: em_estpl56:*
 168: em_estpl57:*
 169: em_estpl58:*
 170: em_estpl59:*
 171: em_estpl60:*
 172: em_estpl61:*
 173: em_estpl62:*
 174: em_estpl63:*
 175: em_estpl64:*
 176: em_estpl65:*
 177: em_estpl66:*
 178: em_estpl67:*
 179: em_estpl68:*
 180: em_estpl69:*
 181: em_estpl70:*
 182: em_estpl71:*
 183: em_estpl72:*
 184: em_estpl73:*
 185: em_estpl74:*
 186: em_estpl75:*
 187: em_estpl76:*
 188: em_estpl77:*
 189: em_estpl78:*

190: gb_gss25:*
 191: gb_gss26:*
 192: gb_gss27:*
 193: gb_gss28:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	302.2	23.8	395	106	BE306459 601103459
2	296.4	23.4	454	147	W56629 zd16a11.r1
3	274.8	21.7	282	28	AL036000 DKFp3584K
4	241.2	19.0	534	135	BE757704 212225 MA
5	203	16.0	401	1	AA003356 mg49a01.r
6	192.8	15.2	369	91	AA478317 19558 MAR
7	174.8	13.8	358	1	AA036247 m17a03.r
8	157.6	12.4	258	133	BB542020 BB542020
9	155	12.2	643	159	AQ563354 HS-5335-B
10	125.8	9.9	646	159	AQ544065 RPTI-11-3
11	124.4	9.8	275	31	AV111112 AV111112
12	120.8	9.5	404	8	AA495217 fa04d10.r
13	113.8	9.0	450	158	AQ514075 HS-5184-A
14	95	7.5	1110	193	CNS0507C
15	91.2	7.2	414	91	AW527025 UI-R-B01-
16	80.2	6.3	381	21	AI551729 vfl1e02.y
17	67.4	5.3	442	109	BE554624 ur48c11.y
18	59	4.6	405	150	AQ173919 HS-3204-A
19	42.6	3.4	443	11	AA759377 ah5a10.s
20	41.4	3.3	551	12	AA814296 nz07d08.s
21	39.4	3.1	397	13	AA860208 ak48c10.s
22	39.4	3.1	465	147	W47341 zc34h02.s1
23	39.2	3.1	266	128	BB350382 BB350382
24	39	3.1	407	146	W32428 zc05c12.s1
25	39	3.1	559	3	AA161105 zc58c05.s
26	38.8	3.1	706	109	BE535395 601058548
27	38.8	3.1	925	190	CNS0091P
28	38	3.0	391	21	AI522266 t184f06.x
29	38	3.0	597	97	AW968349 EST380424
30	37.8	3.0	458	88	AA303441 xv19b01.x
31	37.8	3.0	482	139	BF018062 uw95a06.x
32	37.6	3.0	510	29	AU060928 AU060928
33	37.4	2.9	319	103	BB219800 BB219800
34	37.4	2.9	343	96	AW877284 MR4-PT005
35	37.4	2.9	472	7	AA417295 zu18c03.s
36	37.4	2.9	968	193	CNS056T4
37	37.4	2.9	1002	191	CNS0206F
38	37.2	2.9	344	37	AV630854
39	37.2	2.9	372	89	AW312781
40	37	2.9	910	190	CNS0060N
41	36.8	2.9	366	8	AA542636
42	36.8	2.9	447	17	AI217695 qh26d07.x
43	36.8	2.9	465	38	AAQ015051 UI-H-B10-
44	36.8	2.9	465	87	AW181919 xj68d07.x
45	36.8	2.9	689	109	BE532858 601234740

ALIGNMENTS

RESULT 1
 BE306459
 LOCUS 601103459F1 NCI_CGAP_Lu29 Mus musculus cdna clone IMAGE:3495566 5',
 DEFINITION mRNA sequence.
 BE306459
 ACCESSION BE306459
 VERSION EST.
 KEYWORDS house mouse.
 SOURCE

ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Chordata; Sciurognathi; Muridae; Mus.
REFERENCE 1 (bases 1 to 395)
AUTHORS NH-MGC <http://www.ncbi.nlm.nih.gov/MGC/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: L14M8546 row: f column: 15
High quality sequence stop: 395.
Location/Qualifiers
source
1. .395
/organism="Mus musculus"
/strain="C57BL/6J (f129)"
/db_xref="taxon:10090"
/clone="IMAGE:3495566"
/tissue_type="spontaneous tumor, metastatic to mammary."
Stem cell origin.
/lab_host="DH10B"
/note="Organ: lung; Vector: pCMV-SPORT6; Site: 1: SalI;
Site: 2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
BASE COUNT 88 a 101 c 120 g 86 t
ORIGIN
Query Match 23.8%; Score 302.2; DB 106; Length 395;
Best Local Similarity 85.3%; Pred. No. 2.8e-78;
Matches 337; Conservative 0; Mismatches 58; Indels 0; Gaps 0;
Qy 56 tactaggctattgtcattgaagtgcctgtgaacaggagactgtagacagcaagaat 115
Db 1 TCCTACTCCACTTGGCATGTAAGTGTGCTGCGAAACCGAGATTGCGAGCAGGAAT 60
Qy 116 tcaggatcgctgtgaacgtgttccctgaacacagtggtggccaggaatgagttgt 175
Db 61 TCAGAGTCGATCGGAACGTGTGCTCTGCAACACGTGGCGACCTGGCATGGAGTTGT 120
Qy 176 ctaaggaatgtgcttcgctatggggaggtgacagtggtgacgtgcccgtgcaca 235
Db 121 CCAAGGATGTGGCTTCGGCTATGGGAGGATGCACAGTGTGCGCTGCAGGCGCAC 180
Qy 236 ggttcaggagactggggcttcagaaatgaagccctgtctggaactgcagtggtga 295
Db 181 GGTTCAGGAAGACTGGGGTGTCCAGAAAGTGTAAAGCCGTGTGCGGACTGTGCGTGA 240
Qy 296 accgtttcagaagcaaatgttcagccaccagtgatgccatctcggggactgttgc 355
Db 241 ACCGCTTCAGAGGCGCAACTGCTCACACACAGTGTGCTGTGCGGGGACTGCCCTGC 300
Qy 356 caggattttataggaagcaaatgttcgcttcagagacatgagtggtgcttgtg 415
Db 301 CAGGATTTACGGAGAACCAACTGGTGTGTTTCAGAGACATGGAGTGTGCGCTCG 360
Qy 416 gagaccctctctcttcacgaacgcactgtgc 450
Db 361 GAGACCCACCTCCTCCCTACGAACACACACTGTACC 395

RESULT 2

W56629

LOCUS

W56629

454 bp

mRNA

EST

15-OCT-1996

DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

zdl6ell.r1 Soares fetal_heart_NbHL19W Homo sapiens cDNA clone
IMAGE:340844 5', mRNA sequence.
W56629
W56629.1 GI:1358487
EST.
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 454)
AUTHORS Hallier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman,
M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J.,
Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston,
R., Williamson, A., Wohlmann, P. and Wilson, R.
The WashU-Merck EST Project
Unpublished (1995)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (image.llnl.gov) for further information.
Insert Length: 1373 Std Error: 0.00
Seq primer: mob.REGA+ET.

LOCATION/Qualifiers

1. .454

/organism="Homo sapiens"

/db_xref="GDB:1266219"

/db_xref="taxon:9606"

/clone="IMAGE:340844"

/clone_lib="Soares_fetal_heart_NbHL19W"

/sex="unknown"

/dev_stage="19 weeks"

/lab_host="DH10B (ampicillin resistant)"

/note="Organ: heart; Vector: pT73D (Pharmacia) with a
modified polylinker; Site: 1: Not I; Site: 2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5',
TGTTACCAATCTGAAGTGGAGGCGCCGATCTTTTTTTTTTTTTTTT 3'], RI
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT73 vector
(Pharmacia). Library went through one round of
normalization to a Cot = 5. Library constructed by
M.Fatima Donaldo. This library was constructed from the
same fetus as the fetal lung library, Soares fetal lung
NbHL19W."

BASE COUNT 132 a 96 c 88 g 138 t
ORIGIN

Query Match 23.4%; Score 296.4; DB 147; Length 454;
Best Local Similarity 99.7%; Pred. No. 1.5e-76;
Matches 297; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 972 ctcttattcctgaactcactgagagacattcattctctcaatccagactgaagctc 1031
Db 1 CTCATTATCTGAACCTACTGGAGAGACATTCATTCTCTCAATCCAGAACTTGAAGCTC 60
Qy 1032 aacgtctttgattcaaatagcagtcacagatttggttggtgggctgtccagtcagtc 1091
Db 61 AACGCTTTGGATCAATAGCAGTCAAGATTGGTGGTGGGGCTGTTCAGTCCAGTC 120
Qy 1092 tcatttgaaactttacagcagctactgtatttatctagatatacaaacacactggtaga 1151
Db 121 TCATTCTGAAAACTTTACAGCAGCTACTGATTATCTAGATATATAACAACACACTGCTAGA 180
Qy 1152 atcagcatcaactcaggatgcactaactatgagaagccagctagatcaggagtggtgc 1211
Db 181 ATCAGCTCAACTCAGGTGCTCACTAACTATGAGAAAGCCAGCTAGATCAGGAGTGCGC 240
Qy 1212 tatcatccaccagcactcagactccctccagtcacagtcacagtcacagtcacagtc 1269


```
QY 796 actctgtgttggtggtcattctgcagccagtccttcaggcaagaacacgagccagcc 855
Db 86 ACTCTGGTGTGTCAGGGGCACACTGCAAGGCGCACACTTCAGGACAGAAACACAGGTCCAGCG 145
QY 856 gggagagatggtgccgacttcttcgagatccctcagcagcagtcacatctgtggcagatttca 915
Db 146 GGGAGGCGGATTCCTCTTCTTGGTGCCTCTGCAAGGTCCTCTGTGGCGAGTTCTCA 205
QY 916 gatcgctgcccctctgagcagatcccatgggtggtgagcaacatctcttttgaactct 975
Db 206 GACGCTGGCCCTGTATGAGAGATCCCGGTGGTGGTGGAGATGCTCTCTCCCTGCCGACTCC 265
QY 976 tatcctgaactcactgagaagacattctctcctaaccagaacttgaaagctcaacg 1035
Db 266 TGCCCTGAGCTCCCTCGAGAGAGCGCTCACTCTCTCGACCCAGAGACACAAGCTTGGCT 325
QY 1036 tctttgattcaaatgacagtcagatttgggtgggtgggg 1075
Db 326 TCCTCGACTCAGACAGCAGTCGGGCTCGTGGTGGGG 365

RESULT 7
AA036247 358 bp mRNA EST 26-AUG-1996
LOCUS mi174a03.r1 Soares mouse p3NMF19.5 Mus musculus cDNA clone
DEFINITION IMAGE:472300 5', mRNA sequence.
ACCESSION AA036247.1 GI:1509376
VERSION AA036247
KEYWORDS house mouse.
SOURCE Mus musculus
ORGANISM Mus musculus

REFERENCE
AUTHORS Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Willson,R. and
Waterston,R.
TITLE The WashU-HMI Mouse EST Project
JOURNAL Unpublished (1996)
COMMENT Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LBNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:283044
Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 347.
FEATURES
source
1..358
Location/Qualifiers
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="IMAGE:472300"
/clone_lib="Soares mouse p3NMF19.5"
/dev_stage="19.5 dpc total fetus"
/lab_host="DH10B (ampicillin resistant)"
/note="Vector: pT7T3D (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer [5'
TCTTACCATCTGAGTGGGAGCGCGCGCATTTTCTTTTCTTTT 3']
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT7T3 vector
(Pharmacia). Library went through one round of
normalization to a Cot = 5. Library constructed by Bento
Soares and M.Fatima Bonaldo. RNA was kindly provided by
Dr. Minoru Ko (Wayne State University)."
```

BASE COUNT

81 a

98 c

110 g

69 t

ORIGIN

Query Match 13.8%; Score 174.8; DB 1; Length 358;

Best Local Similarity 78.6%; Pred. No. 1.3e-40;

Matches 209; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

QY 1 atgggttttaaaagtcctagacaagaagaaaagtttttccactcttttagtattacta 60

Db 92 ATGGCACTCAAGTCTACTCTACACAGGAGGGTCTCTTCGCTGCCATTCTCTTCTTA 151

QY 61 ggctatttgcattgaaagtgtgaaacagagactgtagacagcaagaattcagg 120

Db 152 CTCCACCTGGCATGTAAAGTGAGTTGCGAAACCGGAGATTGCGAGCAGCAAGTAATCAAG 211

QY 121 gatcggtctggaaaactgtgttccctcgaaccagtggtggcaggcaatggtctctaaag 180

Db 212 GATCGATCTGGAAACTGTCTCTCTGCAACAGTGGCGACCTGGCATGAGTTGTCCTCAAG 271

QY 181 gaatgtggtctcggtctatgggagatgcacagtgctgacgtgctgcagcgtgcacaggttc 240

Db 272 GAATGTGGCTTCGGCTATGGGAGGATGCACACTGTCTCCCTGCGAGCGCCGACCGGTTTC 331

QY 241 aaggagactgggtgttccagaaatg 266

Db 332 AAGGAAGACTGGGGTTTCCAGAAGTG 357

RESULT 8

BB542020

LOCUS BB542020

DEFINITION BB542020 RIKEN full-length enriched, 0 day neonate eyeball Mus

musculus cDNA clone El30118G08 3', mRNA sequence.

ACCESSION BB542020

VERSION BB542020.1 GI:9613243

KEYWORDS EST.

SOURCE house mouse.

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

AUTHORS Konno,H., Aizawa,K., Akahira,S., Akiyama,J., Arakawa,T., Carninci

P., Endo,T., Fukuda,S., Fukunishi,Y., Hara,A., Hayatsu,N.,

Hirozane,T., Hori,F., Ishii,Y., Ishikawa,J., Ishikawa,T., Itoh,M.,

Izawa,M., Kadota,K., Kagawa,I., Kai,C., Kawai,J., Kikuchi,N.,

Kiyosawa,H., Kojima,Y., Kondo,S., Koya,S., Kurihara,C., Kusakabe,M.

, Matsuyama,T., Miki,R., Mizuno,Y., Nakamura,M., Oda,H., Okazaki,Y.

, Ono,T., Owa,C., Saito,H., Sakai,C., Sato,K., Shibata,K., Shibata

, Y., Shigemoto,Y., Shinagawa,A., Shiraki,T., Sogabe,Y., Sugahara,Y.

, Suzuki,H., Suzuki,H., Tagawa,A., Takahashi,F., Tomimaga,N., Toya

, T., Tsunoda,Y., Watahiki,A., Watanabe,S., Yamamura,T., Yamanaka,I.

, Yano,R., Yasunishi,A., Yokota,T., Yoshida,K., Yoshiki,A., Yoshino

, M., Muramatsu,M. and Hayashizaki,Y.

RIKEN Mouse ESTs (Konno,H., et al.)

Unpublished (2000)

Contact: Yoshihide Hayashizaki

Genome Exploration Research Group, Life Science Tsukuba Center,

Genome Science Laboratory

The Institute of Physical and Chemical Research (RIKEN), Genomic

Sciences Center

3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan

Tel: +81-298-36-9013

Fax: +81-298-36-9098

Email: genome-res@rtc.riken.go.jp/

URL:http://genome.rtc.riken.go.jp/

N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.

Thermotransformation and thermostabilization of the molibdenum enzymes by

trehalose and its application for the synthesis of full length

cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)

Itoh,M., Kitsuina,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,

Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki

, Y. and Hayashizaki,Y.

Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)
 Carninci, P. and Hayashizaki, Y.
 High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)
 Please visit our web site (<http://genome.rtc.riken.go.jp>) for further details.

FEATURES

source
 1. .258
 /organism="Mus musculus"
 /db_xref="taxon:10090"
 /clone_lib="RIKEN full-length enriched, 0 day neonate eyeball"
 /tissue_type="eyeball"
 /dev_stage="0 day neonate"
 /lab_host="DH10B"
 /note="Site_1: SalI; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5'
 GAGAGAGAGCGCGCAACTCGAGTGTTCCTTTTTCCTTTTNN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5'
 GAGAGAGAGATTCGAGTTAAATTAATCCCGCCCCCCCC 3']. cDNA was cleaved with BamHI and XhoI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I."
 55 a 77 C 66 g 60 t

BASE COUNT
 ORIGIN

Query Match 12.4%; Score 157.6; DB 133; Length 258;
 Best Local Similarity 80.7%; Pred. No. 1.4e-35;
 Matches 184; Conservative 0; Mismatches 44; Indels 0; Gaps 0;
 Qy 221 cgtgccggtcacaggttcaggagactggggttcagaaatgaagccctgtctgg 280
 Db 1 CCTGAGCCCCCGGTTCTTAAGAAGACTGGGCTTTCAGAAAGTGAAGCATGTGGCG 60
 Qy 281 actgcgagtgtaacgcgttcagaaaggcaaatgttcagccacagtgatgccatc 340
 Db 61 ACTTTGCCCTGGTGNACCGCTTTAGAGCGCCCACTGCTCACACCACTGATGCTTTT 120
 Qy 341 gcggggactgttgccaggtttataggaagacgaactgtcggtttcaagacatgg 400
 Db 121 GCGGGACTGCTGCCAGGATTTTACCGGAAGACCAAACTGGTTGTTTCAAGACATGG 180
 Qy 401 agtgtgtcctgtgagaacctctcctcctctctctctctctctctctctctctgtg 448
 Db 181 AGTGTGTCCTCCGCGGAGACCACTCCTCCTCTCTCTCTCTCTCTCTCTCTCTCTG 228

RESULT 9
 AQ563354 AQ563354 643 bp DNA GSS 29-MAY-1999
 LOCUS HS_5335_B2_B03_77A RPCI-11 Human Male BAC Library Homo sapiens
 DEFINITION genomic clone Plate=911 Col=6 Row=D, DNA sequence.
 ACCESSION AQ563354
 VERSION AQ563354.1 GI:4922825
 KEYWORDS GSS.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 643)
 AUTHORS Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and Hood,L.

TITLE

JOURNAL Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
 MEDLINE Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
 COMMENT 99380589
 Contact: Mahairas GG, Wallace JC, Hood L
 High Throughput Sequencing Center
 University of Washington
 401 Queen Anne Avenue North, Seattle, WA 98109, USA
 Tel: (206) 616-3618
 Fax: (206) 616-3887
 Email: jwallace@u.washington.edu
 Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm) or from Research Genetics (info@resgen.com). BAC end Web Server: <http://www.htsc.washington.edu>
 Plate: 911 row: D column: 6
 Seq primer: T7
 Class: BAC ends
 High quality sequence stop: 643.
 Location/Qualifiers
 1. .643

FEATURES

source
 1. .643
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_plate="911 Col=6 Row=D"
 /clone_lib="RPCI-11 Human Male BAC Library"
 /sex="male"
 /note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRI methylase. Size selected DNA was cloned into the pBACe3.6 vector at EcoRI sites"
 151 a 154 c 158 g 167 t 13 others

BASE COUNT
 ORIGIN

Query Match 12.2%; Score 155; DB 159; Length 643;
 Best Local Similarity 85.9%; Pred. No. 1.1e-34;
 Matches 170; Conservative 0; Mismatches 28; Indels 0; Gaps 0;
 Qy 445 tgtgccagcaaggttcacacctgctgaagatcgctccacgctccacgccccgagacacg 504
 Db 315 TGTGCCAACAAAGGTCAACCTCGTGAAGATCGGTNACAGGGCTCCAGCCACGGGACAG 374
 Qy 505 gcctgtgctgcgttatctgcagcgctctggccaccgctcctgctgctgctcctcctc 564
 Db 375 GCGCTGTGCTGCCGTATCTGCAGCGCTCTGGCCACCGCTCTGCTGCTCATCTC 434
 Qy 565 tgtgtcatctattgtaagagacagtttatgagagaacccacagctgtctctcggtca 624
 Db 435 TGTGTCTCTATTGTAGAGACAGTNTATGAGAGAACCCAGCTGTGAAGTGTGAGCT 494
 Qy 625 caggacattcagtaaac 642
 Db 495 CATTACATNTCTTATCAC 512

RESULT 10
 AQ544065 AQ544065 646 bp DNA GSS 19-MAY-1999
 LOCUS RPCI-11-315F10.TV RPCI-11 Homo sapiens genomic clone RPCI-11-315F10
 DEFINITION DNA sequence.
 ACCESSION AQ544065
 VERSION AQ544065.1 GI:4869459
 KEYWORDS GSS.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 646)
 AUTHORS Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and Venter,J.C.

TITLE Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready Map Building

JOURNAL Unpublished (1997)

COMMENT Other_GSSs: RPCI-11-315F10.T3
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0208
Email: hbeet@ig.org
Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from Research Genet cs (info@resgen.com). BAC end search page: http://www.tigr.org/tldb/hungen/bac_end_search/bac_end_search.html.
Seq primer: T7
Class: BAC ends.

FEATURES

Location/Qualifiers
1. .646
/organism="Homo sapiens"
/db_xref="GDB:7620705"
/db_xref="taxon:9606"
/clone="RPCI-11-315F10"
/clone_lib="RPCI-11"
/sex="Male"
/cell_type="Lymphocytes"
/note="Vector: pBAC3.6; Site_1: EcoRI; Site_2: EcoRI; RPCI11 Human Male BAC Library"

BASE COUNT 175 a 135 c 145 g 191 t

ORIGIN

Query Match 9.9%; Score 125.8; DB 159; Length 646;
Best Local Similarity 94.9%; Pred. No. 4.8e-26;
Matches 130; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 611 ggtctctcggtcacaggacattcagtaacacggctctgagctgtgtctgttgacagac 670
|||||
Db 263 GGTCTCTCGGTCACAGGACATTCAGTACACGGCTCTGAGCTGTGTGTGACAGAC 322
|||||
QY 671 cttagctccacgaatagccccacagagctgtgctgacagtcggtgacgtgacgtgacga 730
|||||
Db 323 CTCAGCTCAGCAATATGCCACAGAGCCTGCTGCCAGTGCCCGCTGACTCAGTGCAGA 382
|||||
QY 731 cctgcgggcgggtgcgc 747
|||||
Db 383 CTTGCGGTAAAGTTCAGC 399

RESULT 11

AV111112 275 bp mRNA EST 29-JUN-1999

LOCUS AV111112 Mus musculus C57BL/6J 10-day embryo Mus musculus cDNA clone 2600016N17, mRNA sequence.

ACCESSION AV111112

VERSION AV111112.1 GI:5265192

KEYWORDS EST.

SOURCE house mouse.

ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 275)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

AUTHORS Carninci, P., Shibata, K., Ozawa, Y., Konno, H., Itoh, M., Aizawa, K., Akahira, S., Akiyama, J., Fukuda, S., Fukunishi, Y., Funayama, T., Hara, A., Hayatsu, N., Hori, F., Ishikawa, T., Itoh, M., Izawa, M., Kawai, J., Kikuchi, N., Kojima, Y., Matsuyama, T., Naitsuma, H., Oda, H., Owa, C., Sato, K., Shibata, Y., Shigemoto, Y., Shiraki, T., Sogabe, Y., Sugahara, Y., Suzuki, H., Suzuki, H., Tateno, M., Tomaru, Y., Tomimaga, N., Watanabe, S., Yagame, M., Yamamura, T., Yokota, Y., Yoshino, M., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y.

TITLE Riken Mouse ESTs

JOURNAL COMMENT

Unpublished (1999)
Contact: Chie Owa
Genome Science Laboratory
RIKEN
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-9145
Fax: 81-298-36-9098
Email: genome-res@rtc.riken.go.jp
Thermostabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA (Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))
Transcriptional sequencing: A method for DNA sequencing using RNA polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
Please visit our web site (http://genome.rtc.riken.go.jp) for further details.

FEATURES

Location/Qualifiers
1. .275
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="2600016N17"
/clone_lib="Mus musculus C57BL/6J 10-day embryo"
/sex="mixed"
/dev_stage="10-day embryo"

BASE COUNT 77 a 86 c 55 g 57 t

ORIGIN

Query Match 9.8%; Score 124.4; DB 31; Length 275;
Best Local Similarity 71.3%; Pred. No. 9.1e-26;
Matches 164; Conservative 0; Mismatches 66; Indels 0; Gaps 0;

QY 245 aggactggggtccagaaatgcaggccgtctggaactgcgcagtggtgaaccgtttc 304
|||||
Db 43 AGAAAGTGGTTTCCAGAGTAAAGCCCATTCGCCCAACCTGCCCTGTAGAACCCCTATC 102
|||||
QY 305 agaagsgcaattgttcagccaccagtgatgccatctgcgggagctctgcccagggatttt 364
|||||
Db 103 TGAGGACCCATGCTCACACACCACCTGATGCTCTGCGGGGACTGCTGCCAAGATTTT 162
|||||
QY 365 ataggagacgaataatgttcggctttcgaagacatggagtgtgtccttggagaccctc 424
|||||
Db 163 ACCAGAAAGACCAACCTGGTTGGTTTCAAGACATGTAGTGTGTGCGCTCGGAGACCCAC 222
|||||
QY 425 ctctctcttacaacgcgcactgtgccagcaaggtcaacctgtgaagatc 474
|||||
Db 223 CTCCTCCCTACCAACCAACACAGTGTGATGTGCCCAAGTGGCGAGCAGACC 272

RESULT

AA495217 404 bp mRNA EST 27-JUN-1997

LOCUS fa04d10.r1 zebrafish ICRFzfls Danio rerio cDNA clone 10E17 5', mRNA sequence.

ACCESSION AA495217

VERSION AA495217.1 GI:2225645

KEYWORDS EST.

SOURCE zebrafish.

ORGANISM Danio rerio

REFERENCE 1 (bases 1 to 404)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi; Cypriniformes; Cyprinidae; Rasbora; Danio.

AUTHORS Clark, M., Lebrach, H., Appel, B., Eisen, J., Johnson, S., Marra, M., Jody, S., Hillier, L., Allen, M., Bowles, L., Dubuque, P., Geisel, G., Jost, S., Kucaba, T., Lacy, M., Le, N., Lennon, G., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R.

TITLE WashU Zebrafish EST Project

JOURNAL Unpublished (1997)

COMMENT Contact: Steve Johnson
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Search completed: March 2, 2001, 09:59:07
Job time: 28932 sec

THIS PAGE BLANK (USPTO)

Db 1227 GCCCAAGAGGGAGAGCCGGGGCTCAAGTC

;
; CORRESPONDENCE ADDRESS:
; ADDRESS: CARFELIA RYRNE BAIN GILFILLIAN

db 1227 GGCCAAGAGGGAGAGCCGGGGCTCAAGTC 1256

```

RESULT      7
US-08-334-698-5
; Sequence 5, Application US/08334698
; Patent No. 5556753
; GENERAL INFORMATION:
; APPLICANT: Jonathan A. Bard et al.
; TITLE OF INVENTION: DNA Encoding Human Alpha 1 Adrenergic
; TITLE OF INVENTION: Receptors and Uses Thereof
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESS: COOPER & DUNHAM
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24

```

PATENT NO.: 0578011
 GENERAL INFORMATION:
 APPLICANT: Charles Gluchowski, Carlos C. Furray, George Chlu,
 APPLICANT: Theresa A. Brancheck, John M. Wetzel and Paul R. Hartig
 TITLE OF INVENTION: USE OF ALPHA-1C SPECIFIC COMPOUNDS TO TREAT BENIGN
 TITLE OF INVENTION: PROSTATIC HYPERPLASIA
 NUMBER OF SEQUENCES: 6
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: COOPER & DUNHAM
 STREET: 30 Rockefeller Plaza
 CITY: New York
 STATE: New York
 COUNTRY: U.S.A.
 ZIP: 10112
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.24
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/228,932
 FILING DATE: 13-APR-1994

CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 41878-B/JPW/TEP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 977-9550
TELEFAX: (212) 664-0525
TELEX: (212) 422523 COOP UI
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1639 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: N
ANTI-SENSE: N
FEATURE:
NAME/KEY: CDS
LOCATION: 126..1523
OTHER INFORMATION:
US-08-228-932-5

Query Match 2.7%; Score 34.8; DB 1; Length 1639;
Best Local Similarity 52.0%; Pred. No. 0.59;
Matches 78; Conservative 0; Mismatches 72; Indels 0; Gaps 0;

QY 474 cgcgtccacggcctccagccacgggacacggcgctggtcggttatctgcagcgctct 533
DB 635 CGAGGACGAGACCATCTGCCAGATCAACGAGGAGCGGGCTACGTCTTCTCAGCGCT 694
QY 534 ggcacccgtcctgtggcctctcatctctgtgtcatctattgttaagagacagttat 593
DB 695 GGGCTCTTCTACCTTGCCTCTGGCCATCATCTGCTGCTACTGCTGCTGCTGCTGCT 754
QY 594 ggaagaagaacccagctggtctcggctc 623
DB 755 GGCCAAGAGGAGAGCGGGGCTCAAGTC 784

RESULT 9
US-08-468-939-5
Sequence 5, Application US/08468939
Patent No. 5714381
GENERAL INFORMATION:
APPLICANT: Jonathan A. Bard et al.
TITLE OF INVENTION: DNA Encoding Human Alpha 1 Adrenergic
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: COOPER & DUNHAM LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,939
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 41337-1B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400

TELEFAX: (212) 391-0526
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1639 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: N
ANTI-SENSE: N
FEATURE:
NAME/KEY: CDS
LOCATION: 126..1523
OTHER INFORMATION:
US-08-468-939-5

Query Match 2.7%; Score 34.8; DB 1; Length 1639;
Best Local Similarity 52.0%; Pred. No. 0.59;
Matches 78; Conservative 0; Mismatches 72; Indels 0; Gaps 0;

QY 474 cgcgtccacggcctccagccacgggacacggcgctggtcggttatctgcagcgctct 533
DB 635 CGAGGACGAGACCATCTGCCAGATCAACGAGGAGCGGGCTACGTCTTCTCAGCGCT 694
QY 534 ggcacccgtcctgtggcctctcatctctgtgtcatctattgttaagagacagttat 593
DB 695 GGGCTCTTCTACCTTGCCTCTGGCCATCATCTGCTGCTACTGCTGCTGCTGCTGCT 754
QY 594 ggaagaagaacccagctggtctcggctc 623
DB 755 GGCCAAGAGGAGAGCGGGGCTCAAGTC 784

RESULT 10
US-08-406-855A-5
Sequence 5, Application US/08406855A
Patent No. 5861309
GENERAL INFORMATION:
APPLICANT: Jonathan A. Bard et al.
TITLE OF INVENTION: DNA Encoding Human Alpha 1 Adrenergic
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/406,855A
FILING DATE: 21-AUG-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 41337-A-PCT-US/JPW/KDB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0526
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1639 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)

RESULT 15

```

5386025-5
; Patent No. 5386025
; APPLICANT: JAY, SCOTT D.; ELLIS, STEVEN B.; HARPOLD, MICHAEL
; M.; CAMPBELL, KEVIN P.
; TITLE OF INVENTION: CALCIUM CHANNEL COMPOSITIONS AND METHODS
; NUMBER OF SEQUENCES: 9
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/482,384
; FILING DATE: 20-FEB-1990
; SEQ ID NO: 5
; LENGTH: 5962
5386025-5

Query Match      2.7%; Score 34.6; DB 5; Length 5962;
Best Local Similarity 48.7%; Pred. NO. 1.5;
Matches 94; Conservative 0; Mismatches 99; Indels 0; Gaps 0;

QY 462 cctcgtgaagatcgctccacgagcctccacgcccacacgagcgcgcgtgctgctgttat 521
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 3177 ccagctgctgtacagggccatagactccacacgagggagacatggcccccgtttacaacaa 3236

QY 522 ctgcagcgcctctggccaccgctcctgctggccctgctcctcctctgtgtcatctatgttaa 581
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 3237 cagcgtggagatggccatctcttctcatcctcctcatcctcctcatgctcttctcatgat 3296

QY 582 gagacagttttatggagaagaacccagcgtggtctctgcgggtcacagggacattcagtaacaa 641
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 3297 gaactactttgtgggtttgtgtcatcctccagggagcagggggagacgaggtacaa 3356

QY 642 cggctctgagctg 654
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 3357 gaactgcgagctg 3369
  
```

Search completed: March 2, 2001, 12:33:29
 Job time: 31298 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 2, 2001, 12:41:42 ; Search time 8955.7 Seconds
(without alignments)
2608.160 Million cell updates/sec

Title: US-09-380-276A-2
Perfect score: 1704
Sequence: 1 gggaacgtagaactctccaa.....gaccacagagtatacttttc 1704

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1118133 seqs, 6853842396 residues
Total number of hits satisfying chosen parameters: 2236266

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl:*

- 1: gb_bal:*
- 2: gb_ba2:*
- 3: gb_om:*
- 4: gb_ov:*
- 5: gb_ph:*
- 6: gb_pl1:*
- 7: gb_pl2:*
- 8: gb_pr1:*
- 9: gb_pr2:*
- 10: gb_pr3:*
- 11: gb_ro:*
- 12: gb_sy:*
- 13: gb_un:*
- 14: em_fun:*
- 15: em_hum1:*
- 16: em_hum2:*
- 17: em_in:*
- 18: em_om:*
- 19: em_or:*
- 20: em_ov:*
- 21: em_pat:*
- 22: em_ph:*
- 23: em_pl:*
- 24: em_ro:*
- 25: em_sts:*
- 26: em_sy:*
- 27: em_un:*
- 28: em_vi:*
- 29: gb_htg1:*
- 30: gb_htg2:*
- 31: gb_in1:*
- 32: gb_in2:*
- 33: em_ba1:*
- 34: em_ba2:*
- 35: em_hum3:*
- 36: em_hum4:*
- 37: gb_pr4:*
- 38: gb_htg3:*
- 39: gb_htg4:*
- 40: gb_htg5:*
- 41: gb_htg6:*
- 42: gb_htg7:*
- 43: em_htg1:*

- 44: em_htg2:*
- 45: em_htg3:*
- 46: em_hum5:*
- 47: gb_pl3:*
- 48: gb_pr5:*
- 49: gb_htg8:*
- 50: gb_htg9:*
- 51: gb_htg10:*
- 52: gb_htg11:*
- 53: gb_htg12:*
- 54: gb_htg13:*
- 55: gb_htg14:*
- 56: gb_in3:*
- 57: gb_htg15:*
- 58: gb_htg16:*
- 59: gb_htg17:*
- 60: em_htg4:*
- 61: em_htg5:*
- 62: em_htg6:*
- 63: em_htg7:*
- 64: em_hum6:*
- 65: gb_htg18:*
- 66: gb_htg19:*
- 67: gb_htg20:*
- 68: gb_htg21:*
- 69: gb_htg22:*
- 70: gb_htg23:*
- 71: gb_vil:*
- 72: gb_vl2:*
- 73: gb_ba3:*
- 74: em_htg8:*
- 75: em_htg9:*
- 76: em_htg10:*
- 77: gb_pr6:*
- 78: gb_pr7:*
- 79: gb_sts1:*
- 80: gb_sts2:*
- 81: gb_pat1:*
- 82: gb_pat2:*
- 83: em_htg0:*
- 84: gb_htg24:*
- 85: gb_pr8:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1277.6	75.0	1364	8	AB040434 Homo sapi
2	1270	74.5	1489	37	AF167555 Homo sapi
3	830.4	48.7	3964	11	AB040432 Mus muscu
4	823	48.3	1678	11	AF167552 Mus muscu
5	692.6	40.6	1075	11	AF173166 Mus muscu
6	460.8	27.0	744	11	AB040433 Mus muscu
7	460.8	27.0	886	11	AF167553 Mus muscu
8	420.2	24.7	143608	67	AL161422 Homo sapi
9	420.2	24.7	178256	66	AL139080 Homo sapi
10	326.6	19.2	591	11	AF167554 Mus muscu
c 11	73	4.3	188351	67	AL353136 Homo sapi
c 12	73	4.3	205736	51	AC023560 Homo sapi
c 13	65.4	3.8	205736	51	AC023560 Homo sapi
c 14	43.6	2.6	160214	54	AC034198 Homo sapi
c 15	43.6	2.6	180511	42	AC018836 Homo sapi
c 16	43.6	2.6	209876	10	AC011599 Homo sapi
c 17	42.6	2.5	98218	59	AC074232 Oryza sat
c 18	42.6	2.5	196312	42	AC020616 Mus muscu
c 19	42	2.5	207166	42	AC018843 Homo sapi
c 20	41.4	2.4	147001	68	AL355986 Homo sapi
c 21	41.2	2.4	186797	49	AC021965 Homo sapi

```

c 22 40.2 2.4 217422 59 AC073747 AC073747 Mus muscu
23 40.2 2.4 236195 59 AC073713 AC073713 Mus muscu
24 39.2 2.3 178715 68 AL359536 AL359536 Homo sapi
25 38.8 2.3 188714 48 CNS01DMR AL138478 Human chr
26 38.8 2.3 200948 38 AC010331 AL010331 Homo sapi
27 38.8 2.3 204573 41 AC016589 AC016589 Homo sapi
28 38.4 2.3 145934 67 AL353611 AL353611 Homo sapi
29 38.4 2.3 148018 67 AL159992 AL159992 Homo sapi
30 38.4 2.3 171491 50 AC022606 AC022606 Homo sapi
31 38.4 2.3 173767 8 AC002449 AC002449 Human PAC
32 38.4 2.3 259474 78 HUAC004605 AC004605 Homo sapi
33 38.2 2.2 141675 69 AF000405 AP000405 Homo sapi
34 38.2 2.2 202047 70 AP001271 AP001271 Homo sapi
35 38 2.2 166704 70 AP001559 AP001559 Homo sapi
36 38 2.2 189199 9 AC006566 AC006566 Homo sapi
37 37.8 2.2 108774 70 AP001862 AP001862 Homo sapi
38 37.8 2.2 177014 8 AC004063 AC004063 Homo sapi
39 37.8 2.2 189239 53 AC026557 AC026557 Homo sapi
40 37.6 2.2 38532 73 SCE94 AL049628 Streptomy
41 37.6 2.2 188351 67 AL353136 AL353136 Homo sapi
42 37.6 2.2 189841 57 AC068802 AC068802 Homo sapi
43 37.4 2.2 32354 73 SCD84 AL353816 Streptomy
44 37.4 2.2 73868 55 AC055762 AC055762 Homo sapi
45 37.2 2.2 128200 84 CNS01DMN AL137785 Homo sapi

```

ALIGNMENTS

```

RESULT 1
AB040434 1364 bp mRNA PRI 22-JUL-2000
LOCUS AB040434 Homo sapiens mRNA for hTROY, complete cds.
DEFINITION AB040434 hTROY.
VERSION AB040434.1 GI:9392329
KEYWORDS hTROY.
SOURCE Homo sapiens cDNA to mRNA.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (sites) Morikawa, Y., Copeland, N.G., Gilbert, D.J., Jenkins, N.A.,
AUTHORS Senba, E. and Kitamura, T.
TITLE TROY, a newly identified member of the tumor necrosis factor
receptor superfamily, exhibits a homology with Edar and is
expressed in embryonic skin and hair follicles
J. Biol. Chem. 275 (27), 20742-20747 (2000)
20347167
2 (bases 1 to 1364)
Kojima, T. and Kitamura, T.
Direct Submission
Submitted (23-MAR-2000) to the DDBJ/EMBL/GenBank databases, Tetsuo
Kojima, Chugai Research Institute for Molecular Medicine, Inc.,
CytoKine Research Program; 153-2 Nagai, Niihari, Ibaraki 300-4101,
Japan (E-mail: kojima@ci.medicom.com, Tel:81-298-306211,
Fax:81-298-306270)
COMMENT Sequence updated (06-Apr-2000).
FEATURES
Source
1..1364
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
37..1308
/gene="hTroy"
37..1308
/gene="hTroy"
/codon_start=1
/product="hTROY"
/protein_id="BAB03269.1"
/db_xref="GI:9392330"
/translacion="WALKVLLRQKTFFTLLVLLGVLSCKVTCESDCRQOFFRDRSG
NCVPCNOCSPGHELSKECGFYGEDAQCVTCRLHRFKEDWGFQKCPCLDCAVNRFQ
KANCATSDAICGDLCPYFRKTKLVGFQDMCEVPCGDPDPPEPHPCASKVNLVIAIS
TASSPRDTALAAVICSALATVLLALLILCVIYCKRQFMKPKPSWLSRSDIYNGSEL

```

```

SCFDRPOLHEVAHRAACCCRRDSVOTGVPVRLLLPSMCCCEACSPNPATLGCCVHSAAS
LQARNAGPAGEMVPTFFGSLTQSGICGEFSDAPMLQNPMDGDNISFCDSYRELGTEDI
HSLNLESGSTSLDSNSODLVGGAVPVQSHSENFTAAATDLRSYNNTLVSQATQDAL
TMRSDQDESGAVIHPTATQTSLOVQRQLGSL"
BASE COUNT 325 a 351 c 358 g 330 t
ORIGIN
Query Match 75.0%; Score 1277.6; DB 8; Length 1364;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1280; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 9 agaactctccaacaataatacatattgataaagaagaatggctttaaaagtactactagaa 68
DB 1 AGAACTCTCCAAACAATAATACATTTGATAAGAAAGATGGCTTTAAAGCTGCTACTAGAA 60
QY 69 caagagaagaacgtttttcactctcttttagtattactaggctatttgcataagagtgact 128
DB 61 CAAGAGAAACCGTTTTCATCTCTTTTAGTATTACTAGGCTATTGTGTCATGTAAGTGACT 120
QY 129 tgtgaacacaggagactgtagacagcaagaattccagagatcggtctggaacatgtgtccc 188
DB 121 TGTGAATCAGGAGACTGTAGACAGCAAGAATTCAGGGATCGGTCTGGAACCTGTGTTC 180
QY 189 tgaacacagtgaggccagggcatggagttgtctaaagaatgtggcttcggctatggggag 248
DB 181 TGCAACCCAGTGTGGGCCAGGCATGGAGTTGTCTAAGAAATGTGGCTTCGGCTATGGGAG 240
QY 249 gatgcacagtgatgacgtgcccggctgcacaggttcaaggagagactggggcttccagaaa 308
DB 241 GATGACACAGTGTGTGACGTGCCGGCTGCACAGGTTCAAGGAGGACTGGGGCTTCCAGAA 300
QY 309 tgaacacccctctctgagactgcacagtggtgaaacgcctttcagaagcaaatgttcagcc 368
DB 301 TGCAACCCCTCTCTGACTCGGCAGTGGTGAACCGCTTTCAAGAGCAAAATGTGTTCAGCC 360
QY 369 accagtgatgccatctgcgggagctcttgccaggattttataggagagcgaactgtc 428
DB 361 ACCAGTGATGCCATCTGCGGGGACTGCTTGCACAGGATTTTATAGGAAGACGAAACTTGT 420
QY 429 ggccttcaagacatggagtgatgctctgtggagaccctctctctcttcaagaacggac 488
DB 421 GGCTTTCAAGACATGGAGTGTGTGCTTGTGGAGACCCCTCTCTCTTACGAACCCGAC 480
QY 489 tgtgcacgaaggtcaacctcgtgaagatcggtccacgcctcccagccacgggagacg 548
DB 481 TGTGCCCAAGCAAGGTCAACCTCGTGAAGATCGCGTCCACGGCTCCACAGCCACGGGACG 540
QY 549 ggcgtggctgcggttatctgcagcgctctggccacgcgtcgtggtgacctgtcactc 608
DB 541 GCCTGGCTGCCTGTTATCTGCAGCGCTCTGGCCACCGTCTGCTGCTGCTGCTATCTTC 600
QY 609 tgtgcatctattgtaagagacagtttatggagaagaacccagctgggtctctgaggtca 668
DB 601 TGTGTCTATCTATTGTGAAGACAGTATTATGGAGAAGAAACCCAGCTGGTCTCTCGCGG 660
QY 669 caggacattcagtacaaacgctctgagctgtcgtgtcttgacagacctcagctccacgaa 728
DB 661 CAGGACATTCAGTACACACCGCTCTGAGCTGTCTGTGTTTTTACAGAGACCTCAGCTTCCAG 720
QY 729 tatgcccacagagcctgctgacgtgcccgcgtgactcagtgacagacctgcgggcccgtg 788
DB 721 TATGCCACACAGAGCCCTGCTGCCAGTCCCGCGTGACTCAGTCAGTCAGACACCTGCGGG 780
QY 789 cgcttctccatccatgtgctgtgaggagcctgagagcccaaacccggcgactcttgg 848
DB 781 CGCTTCTCCCATCCATGTGCTGTGAGGAGGCGCTGCAGCCCCAACCCGCGGACTCTTGGT 840
QY 849 tgtggggtgcattctgcagcagctcttcaggcaagaacacgcagggcccgaggagatg 908
DB 841 TGTGGGGTGCATTCTGCAGCCAGTCTTTCAGGCAAGAAACGACGCCACCCGGGAGATG 900
QY 909 gtgcccagactttctcggtatccctccacgcagtgccatctgtggcgagttttcagatg 968

```

||||| 901 GTGCGGACTTTCTTGGATCCCTCAGCAGTCCATCTGTGGGAGTTTTCAGATGCCCTGG 960
Qy 969 cctctgatgcagaatcccatgggtgagtcacacatctcttttttgactcttactctgaa 1028
Db 961 CTTCTGATGCAGAAATCCCATGGGTGGTGACAAATCTCTTTTGGACTCTTATCCTGAA 1020
Qy 1029 ctcaatgagagacattcattctctcaatccagaaacttgaaagctcaacgtctttgat 1088
Db 1021 CTCACGTGAGAGACATTCATTTCTCAATCCAGAACTTGAAGCTCAACGCTTTGGAT 1080
Qy 1089 tcaatagcagtcagattggttgggtgagtcacacatctcttcagtcacatctcagaaac 1148
Db 1081 TCAAAATAGCAGTCAAGATTTGGTGTGGTGGGCTGTTCAGTCCAGTCTCATTTCTGAAAC 1140
Qy 1149 ttacagcagctactgatttcttagatataacacacacactggttagaatcagcatcaact 1208
Db 1141 TTTACAGCAGCTACATTTATTTCTAGATATAACACACACTGTTAGAAATCAGATCAAACT 1200
Qy 1209 caggatgcactaactatgagaagccagctagatcaggagagtgccgctatcatccacca 1268
Db 1201 CAGGATGCACCTAACTATGAGAAGCCAGCTAGATCAGGAGTGGCGCTGTCTATCCACCCA 1260
Qy 1269 gccactcagacgtccctccaggaa 1292
Db 1261 GCCACTCAGACGTCCCTCCAGGTA 1284

RESULT 2
AF167555 AF167555 1489 bp mRNA PRI 25-MAY-2000
LOCUS Homo sapiens TAJ-alpha mRNA, complete cds.
DEFINITION AF167555
ACCESSION AF167555
VERSION AF167555.1 GI:8071643
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1489)
AUTHORS Eby,M.T., Jasmin,A., Kumar,A., Sharma,K. and Chaudhary,P.M.
TITLE TAJ, a Novel Member of the Tumor Necrosis Factor Receptor Family,
Activates the c-Jun N-terminal Kinase Pathway and Mediates
Caspase-Independent Cell Death
J. Biol. Chem. 275 (20), 15336-15342 (2000)
10809768
REFERENCE 2 (bases 1 to 1489)
AUTHORS Chaudhary,P.M.
TITLE Direct Submission
JOURNAL Submitted (12-JUL-1999) Internal Medicine, UT Southwestern Medical
Center, 5323 Harry Hines Blvd., Dallas, TX 75235-8593, USA
FEATURES
source 1..1489
/organism="Homo sapiens"
/db_xref="taxon:9606"
65..1336
/codon_start=1
/product="TAJ-alpha"
/protein_id="AA71828.1"
/db_xref="GI:8071644"
translation="MAKLVLEQEKFTFTLLVLGLYLSCKVTCESGDCRQOEFRDRSG
NCVPCNOGPMGELSKEGFGYGEDACVACRLHRFKEDWGFKCKPLCDCAVYVNRFO
KANGSATSDATCGDCLPGFYRKTKLVGFQDMCEVPCGDPPEPPHPCASKVNLVKIAS
TASSPRDPAALAVTCSALATVLLALLILCVLYCKRQMEKKPKPSLSRSDILOYNTEL
SCFQRPOLHEVHARCCOCRRDSVQTCGPVRLPSMCCEEACSPNPATLGGVVSAAAS
LQARNAGPAGEMVPTFFGSLTQSGFSDAWPLMNPMPGMDNISFCDSYBELTGEDI
HSLNPESSSTLSNDSQDLVGAVPVQSHSENPTAATDLSRYNNLTLSASQDAL
TMSQLODESGAVIHPATQTSLOVRQLGSL"
BASE COUNT 361 a 366 c 380 g 382 t

Query Match

74.5% Score 1270; DB 37; Length 1489;

Best Local Similarity 99.2%; Pred. No. 0;
Matches 1276; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
Qy 7 gtagaacctctccacaataaatacatatttgataagaagaatggcttttaaaagtgtactag 66
Db 27 GAAGAACACTCTCCAAACATAAATACATTTGATAAAGAAGATGCTTTAAAAAGTGCTAC 86
Qy 67 aacaagagaacaacgtttttcactctcttttagtattactaggctatttgcattgtaaaag 126
Db 87 AACAGAAGAAACGTTTTTCACTCTTTTAGTATTAAGGCTATTGTTCATGTAAGTGA 146
Qy 127 ctttgaaacaggagactgttagacagcaagaattcagggtatcggtctggaactgtgttc 186
Db 147 CTTGTGAATCAGGAGACTGTAGACAGCAAGAATTCAGGGATCGGTCTCGAAACTGTGTTC 206
Qy 187 cctgcaaacagtggtggccaggatgagtgctctaagaagaatgtgcttcggctatgggg 246
Db 207 CCTGCAACAGTGTGGCCAGCATGGAGTTGTCTPAAGGAATGTGGCTTCGGCTATGGGG 266
Qy 247 aggatgcacagtggtgacgtgcccggctgcacaggttcaaggaggaactggggctccaga 306
Db 267 AGGATGCACAGTGTGGCGTCCGGCTGCACAGGTTCAAGGAGACTTGGGGCTTCCAGA 326
Qy 307 aatgcaagccctgtctggactgcgcagtggtgaaacgcgttttcagaaggaatgtgttcag 366
Db 327 AATGCAAGCCCTGTCTGGACTGCGCAGTGGTCAACCCGCTTTCAGAAGGCAAAATGTTCA 386
Qy 367 ccaccagtgaatgcattctgcggggactcttgcaaggattttataggaaagacgaacttg 426
Db 387 CCACAGTGAATGCCATCTGCGGGGACTGCTTGCCAGGATTTTATAGGAAGACGAAACTTG 446
Qy 427 tcggctttcaagacatgagtggtgctctgtggagacccctcctcctcttactacgaacgc 486
Db 447 TCGGCTTTCAAGACATGAGTGTGTGCCTGTGGAGACCCCTCTCTCTTCTTACGAACCGC 506
Qy 487 actgtgcagcaaggtcaacctctgtgaagatgcgtgccagcgtccacggcctccagccacgg 546
Db 507 ACTGTGCAGCAAGGTCAACCTCGTGAAGATCGCGTCCACGGCTCCACGCCACCGGACA 566
Qy 547 cggcgctgctgcctgtatctgcagcgtctgcgcacgtcctgcgtgccctgcctcatcc 606
Db 567 CGGCGCTGGCTGCCGTTATCTGACAGCGCTTGGCCACCGTCTGTGTCCTCTGCTCTCTCC 626
Qy 607 ctctgtcatctattgtaagacagatttatgagaagaacccagctggctctgcggt 666
Db 627 TCTGTGTCATCTATTGTAAGACAGATTATGGAAGAAACCCAGCTGGTCTCTCGGCT 686
Qy 667 cacaggacattcagtaacaagcgtctgagctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 726
Db 687 CACAGGACATTCAGTACACAGAGACTGAGTGTGCTGTGTTTGACAGAGCTCAGCTCCACG 746
Qy 727 aatatgccacagacgtctgcagtcgccgctgcagtcagtcagtcagtcagtcagtcagtcag 786
Db 747 AATATGCCACAGAGCCCTGCTGCCAGTGGCCCGCTGACTCAGTCAGTCAGACCTCGCGG 806
Qy 787 tgcgctgtctccatccatgctgtgtgagagagcctgcagccccacccggcgactcttg 846
Db 807 TCGGCTTGTCTCCATCCATGTCTGTGAGGAGCCCTGCAGCCCCCAACCCGGGACTCTTG 866
Qy 847 gttgtggggtgctattctgcagccagtcttcagggtcgaagaacagcagccagccagccagc 906
Db 867 GTTGTGGGTGTCATTCTGCAGCCAGTCTTCAGGCAAGAAACAGCGCCAGCGCGGGAGA 926
Qy 907 tgggtccagactttctcagatccctcagcactccatctgtgtgagagttttcagatgct 966
Db 927 TGGTCCCGACTTTCTTCGATCCCTCAGCAGTCCATCTGTGCGGAGTTTTCAGATGCT 986
Qy 967 ggcctctgatgcagaatcccaatgggtggtgacaacatctctttttgtgactcttatctcg 1026
Db 987 GGCTCTGATGCAGAAATCCCATGGGTGGTGACAAACATCTCTTTTGTGACTCTTATCTCG 1046
Qy 1027 aactcactggagaagacattctctcaatccagaactgaaagctcaacgctcttgg 1086

Db 1047 AACTCACTGGAGAGACATTCATTCTCTCAATCAGAACTTGAAGCTCAACGCTCTTTGG 1106
QY 1087 attcaaatagcagtcagatttggttggtggcgtgtccagtcagtcattctgaaa 1146
Db 1107 ATTCAATACAGTCAGATTGTTGGTGGGGCTGTTCAGTCCAGTCATCTGAAA 1166
QY 1147 actttacagcagtcactgatttatctagatatacaacacactggtagaatcagatcaa 1206
Db 1167 ACTTACAGCAGCTACTGATTATCTAGATATAACACACACTGGTAGAATCAGATCAA 1226
QY 1207 ctacagatgcactaatatgagagccagctagatcagcagagtggtgcctatcatccacc 1266
Db 1227 CTCAGATGCACCTAACTATGAGAGCCAGCTAGATCAGGAGTGGCGCTGTATCCACC 1286
QY 1267 cagccactagcagctccctccaggaa 1292
Db 1287 CAGCCACTCAGACGTCCTCCAGGTA 1312

RESULT 3
AB040432 3964 bp mRNA ROD 22-JUL-2000
LOCUS Mus musculus mRNA for TROY, complete cds.
DEFINITION AB040432
ACCESSION AB040432
VERSION AB040432.1 GI:9392325
KEYWORDS TROY.
SOURCE Mus musculus cDNA to mRNA.
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Cranial; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS Kojima,T., Morikawa,Y., Copeland,N.G., Gilbert,D.J., Jenkins,N.A.,
Senba,E. and Kitamura,T.
TITLE TROY, a newly identified member of the tumor necrosis factor
receptor superfamily, exhibits a homology with Edar and is
expressed in embryonic skin and hair follicles
J. Biol. Chem. 275 (27), 20742-20747 (2000)
20347167
2 (bases 1 to 3964)
Kojima,T.
Direct Submission
Submitted (23-MAR-2000) to the DDBJ/EMBL/GenBank databases. Tetsuo
Kojima, Chugai Research Institute for Molecular Medicine, Inc.,
Cytokine Research Program; 153-2 Nagai, Niihari, Ibaraki 300-4101,
Japan (E-mail:kojimat@climmed.com, Tel:81-298-306211,
Fax:81-298-306270).

FEATURES
Location/Qualifiers
source 1..3964
/organism="Mus musculus"
/db_xref="taxon:10090"
gene 127..1377
/gene="Troy"
CDS 127..1377
/gene="Troy"
/note="a member of TNFR superfamily exhibits a homology
with Edar"
/codon_start=1
/product="TROY"
/protein_id="BAB03267.1"
/db_xref="GI:9392326"
/translation="NALKVLPLHRTVLFNAILLHLACKVSCETGDCRQBFKDRSG
NCVLKQCGPMELSKCEGFGYGEDAQVPCPRHFKEDWGFQKPCADCALVNRFO
RANCSTSDAVGDCDLPGFYRTKLGVFODMECVPGDPPPEPHCTSKVLNVLKSS
TVSSPDTLAAVICSALATVLLALLILCVYCKRQFMKKPSWSLRSDIOYNGSEL
SQFDQPLRHCRACQYHRSDAPYMGVPHLIPSLCCCEARSSARAVLGCGRSPPT
LQERNPASVGTWMPAFVGSRSICAEFSDAWPLMQLPGGDSISLSDSTPELUTDPTN
SLNPENSAASLDSGGDLAGTALESNGVNSESTDSRPHGDTGTVWRQTIAQDAQR
TPSQGWEDRENILNAMPFAQDA"

BASE COUNT 984 a 958 c 980 g 1041 t 1 others
ORIGIN

Query Match 48.7%; Score 830.4; DB 11; Length 3964;

Best Local Similarity 71.9%; Pred. No. 6.9e-219;
Matches 1195; Conservative 0; Mismatches 431; Indels 36; Gaps 7;

QY 22 aataaatatattgataaagaagatggcttttaaaagtctactagaaagaagaacgt 81
Db 104 AATAAATACAGCTTTGGTGAGAGCATGACCTCAAGTCTCCTACCTACACAGCAGGTGC 163
QY 82 ttttactcttttagtatattactaggtctattgtcatgtaaaagtactttgaaacagag 141
Db 164 TCTTCCTGCTCCATCTCTTCTTACTCCACTGGCATGTAAAGTGAGTTGGAAACCGGAG 223
QY 142 actgtagacagcaagaattcagggtatcggtctggaactgtgttccctgcacacacgtg 201
Db 224 ATTGCAGGCAGCAGGAATTCAGGATCGATCTGGAACCTGTGTCTCTGCAACAGTCGG 283
QY 202 ggcagggcatggagttgtctaaaggaatgtggtctcggctatggggaggatgcacagtgt 261
Db 284 GACCTGGCATGGAGTTGTCCAGGAATGTGGCTTCGGCTATGGGGAGGATGCACAGTGTG 343
QY 262 tgacgtgcccgtgcaggttcaaggaggaactgggcttccagaataatgcagccctgtc 321
Db 344 TGGCCTGACAGCCGCGACCGGTTCAAGGAAGACTGGGGTTTCCAGAACTGTAAAGTGTG 403
QY 322 tgacgtgcagtggttgaaacgcgtttcagaaggaactgttcagccacacagtgatgcca 381
Db 404 CGGACTGTGCGCTGGTGAACCGCTTTTTCAGAGGGCCAACTGCTCACACACAGTGTGCTG 463
QY 382 tctgcccggagactgctgacaggttttataggaagcagaactgtcggttttcaagaca 441
Db 464 TCTGCGGGGACTGCTCCGTCAGGATTTTTCGGAAGACCAAACTGGTGGTTTCAAGACA 523
QY 442 tggagtgtgctctgtgagaccctcctcctcttaccgaacgcactgtgccagcaag 501
Db 524 TGGAGTGTGTGCGCTGCGGAGACCCACTCTCTCCCTACGAACACACACTGTACCCAGCAAG 583
QY 502 tcaacctgtgaaagatcgcggtccacggcctccagcccacgggacacggcgctggtgcg 561
Db 584 TGAACCTTGTGAAGATCTCTCTCCACGCTGTCCAGCGCTCGGGACACGGCGCTGGCTGCCG 643
QY 562 ttatctgcagcgctctggccacgcgtcctggtgacctgtcctctgtgtgactatt 621
Db 644 TCATCTGCAAGTGTCTGCGCACCGTGTCTGCGCCCTGCTCAATCTCTGTGTGTCATCTACT 703
QY 622 gtaagagacagatttatggagaagaaacccagctggtctctgcggttcacaggaacatcag 681
Db 704 GCAAGAGGAGTTCATGGAGAGAAACCCAGCTGGTCTCTGCGGTTCACAGGACATTCAGT 763
QY 682 acaacggctctgagctgtcgtgtcttgacagacctcagctccacgaataatgccacagag 741
Db 764 ACAATGGCTCTGAGCTGTCTATGCTTTGACCAAGCTCGGGCTCCGCCACTGTGCCCATAGAG 823
QY 742 cctgctgcagtgcccgctgactcagtgacagacctgcggcggtgcgctgtctcccat 801
Db 824 CATGCTGTCTGATATACACCGGACTACGCCCAATGTATGGGCTGTTCACCTGATTTCCGT 883
QY 802 ccatgtgctgtgagggcgctgcagcccccaacccggcgactctgtgtggtgggtgcatt 861
Db 884 CTTTGTGTGTGAAGAGGCCCGCAGGCTTCGCCGAGCTGTGCTTGGCTGTGGGCTCGGTT 943
QY 862 ctgacgccagcttctcaggcaagaacgcagccagcccggggagatggttgcgactttct 921
Db 944 CTCCCACTACCTCCAGGAGAGAAACCCGGCTTCTGTGGGGACACGATGCCACGCTTCT 1003
QY 922 tcggtatccctcagcagtcacatgtgtggagagtttcagatgcctgacctgtatcagaga 981
Db 1004 TCGGGTGTGTTTCCCGTTCATCTCGCTGAAATTTTCTGATGCTGGCTTCTGATGCAGA 1063
QY 982 atcccatgggtgtgacaacatctctttttgtgactcttactcactgaactcactggagag 1041
Db 1064 ATCCTCTGGGTGGTG---ACAGCTCTCTGTGACTCTTATCTGAACTCCTGAGAGAG 1120
QY 1042 acattcattctcattccagaaactgaaagctcaacgtcttttggattcaaatagcagtc 1101

Db	1121	ATACCAATTCCCTCANTCCCGAAACGAGCGCAGCATCTCTGGATTCCAGTGGCGGCC	1180
Qy	1102	aagatttggttggtggggctgtccagtcacgctctctcattctgaaaaactttacacgacgcta	1161
Db	1181	AGGATCTGGCTGGGACAGCTGCTAGAGTCTTCTTGGGAATGTTTCAGAAATCTACTGACT	1240
Qy	1162	ctgatttctatagataaacaacacactggtagaatcagcatcaactcagatgacactaa	1221
Db	1241	CACCTAGACATGTTGACATGGTACAGTCTGGGACGACAGCTAGCTCAGAGATGCTCAAA	1300
Qy	1222	ctatgagaagccagctagatcagagagatggcgctctatcatccaccacgacctcagacgt	1281
Db	1301	GGACTCCAAGCCCAAGGAGGCTGGGAAGACAGGGAACCTGAATCTAGCCATGCCACAG	1360
Qy	1282	ccctccagaagcttaaaagaactgcttcttctcagtagaagcgtgtgctggaaccca	1341
Db	1361	CTTTCCAGGATGCTGAAG-----GCCATCTCTGACGTGGAGGTGGGGCTG-----	1410
Qy	1342	aagagtactcttctgttagcttattggactgagcagctctgaccttgcattgctctctggg	1401
Db	1411	--GACAAGCCTGTGATGAGGCCTACAGACTGAGCAGTCTTG-----GTGTCTGGAA	1459
Qy	1402	gcataataaatctgaaccacaaactgacggcatttggaagcctttcagccagttgcttctga	1461
Db	1460	GCAAAATAAATCTGAACCAAACTGACAAACATTTCCATCTCTTCAGCCACTAGCTTCTGA	1519
Qy	1462	gccagaccagcttaagctgaacctcaatgaataacaagaaaagact---ccaagccga	1518
Db	1520	GCCAGACCAGCTTAGCTGAAACCCCAAGAACGAGAGAGACTGACTGATGGCGG	1579
Qy	1519	ctcatgatactctgcatcttctctacatgagagcttctctgcacacaaagtgcattcaa	1578
Db	1580	CTTTGGACATGTGCTTCTTCCTTAAGCGAGAACCTTAGCTGGGGCCA-----ATTGAA	1634
Qy	1579	agacgagtggttgagctgcagcctatgagatttgacatatataacaagaacagaaat	1638
Db	1635	GGACCCATGGGTGGATGTGTCGCTGTGAGCTTTGGGACAGCA-----GGACCCAGCC	1690
Qy	1639	gcctcatgctcttcttctggtgattggttggttttacaagac	1680
Db	1691	TGGCTCCTCTTATGTCCACGGTGAATGTGGTTTCACAAGAC	1732
RESULT	4		
AF167552			
LOCUS	AF167552	1678 bp mRNA ROD	25-MAY-2000
DEFINITION	Mus musculus TAJ-alpha long mRNA, complete cds.		
ACCESSION	AF167552		
VERSION	AF167552.1	GI:8071637	
KEYWORDS	mouse mouse.		
SOURCE	Mus musculus		
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus; Mus.		
REFERENCE	1 (bases 1 to 1678)		
AUTHORS	Eby M.T., Jasmin A., Kumar A., Sharma K. and Chaudhary P.M.		
TITLE	TAJ, a Novel Member of the Tumor Necrosis Factor Receptor Family, Activates the c-Jun N-terminal Kinase Pathway and Mediates Caspase-independent Cell Death		
JOURNAL	J. Biol. Chem. 275 (20), 15336-15342 (2000)		
PUBLISHED	10809768		
REFERENCE	2 (bases 1 to 1678)		
AUTHORS	Chaudhary P.M.		
TITLE	Direct Submission		
JOURNAL	Submitted (12-July-1999) Internal Medicine, UT Southwestern Medical Center, 5323 Harry Hines Blvd., Dallas, TX 75235-8593, USA		
FEATURES	Location/Qualifiers		
source	1..1678		
	/organism="Mus musculus"		
	/db_xref="taxon:10090"		
CDS	72..1322		
	/codon_start=1		
	/product="TAJ-alpha long"		

		/protein_id="AAF71825.1"			
		/db_xref="GI:8071638"			
		/translation="MALVKLPLRLHTVLFAAILFLHLACKVSCETGDCROOEKFKDRSS			
		NCVLCQCGPGMELSSGKGYGEDAQVPCRPHRKEDWGFQKCPKCPADCALVNRFO			
		RANCSHTSDAVCGDCLPGFYKTKLVGFQDMECVPCGDPDPPEYFICTSKVNLVKLSS			
		TVSSPRDTALAANVCISALATYKLRQFMEKKRPSWSRSQDIQTNGSEL			
		SCEDQPSRHCIAHRCAQHRSDAPFVPHLIPSLCCEARSARAVLGCGLURSPPT			
		LQERNPAGTNTWPAFGYSRSICAFESDAPLMQNLPGDSSLDSDVPELTGEDTN			
		SLNPENESTASLDSSQCDIAGTAALSSGNVSESTDSPRHGDTGTWVEQTLQAQAR			
		TPSQGWEDRENILNLAQPTAFQDA"			
BASE COUNT	371 a	467 c	466 g	374 t	
ORIGIN					
Query Match	48.3%	Score 823:	DB 11:	Length 1678:	
Best Local Similarity	71.6%	Pred. No. 7.2e-217:			
Matches 1191:	Conservative 0:	Mismatches 435:	Indels 37:	Gaps 7:	
Qy	22	aataaatacattgataagaagaatggtctttaaagtgtctactagaacaagagaaaaacgt	81		
Db	49	AATAAACACGTTTGGTGAGAGCCATTGGCACAAGGTCTTACCTCTACACAGGACGGTGC	108		
Qy	82	ttttcaactcttttagtattactaaggctatttggcatgtaaagtgaacttgtgaacaacagag	141		
Db	109	TCMTTCGGCTGCCATTCTCTCTTACTCCACCTGGGATGTAAAGTAGTGTCCGAACCCGGAG	168		
Qy	142	actgtagacacaagaattcaggatcggtctgaaactgtgttccctgcgaaccagatgtg	201		
Db	169	ATTGCAGCACACAGATTCAAGGATCGATCTGGAACCTGTCTCTGCAAAACAGTGGC	228		
Qy	202	ggccaggcatggagtgtgtctaaggaattggtgcttcgcgctatggggagagatgcacagtggtg	261		
Db	229	GACCTGGCATGGAGTGTGCCAAGGAATGTGCTTCGGCTATGGGAGGATGCACAGTGTG	288		
Qy	262	tgaagtcgcgctgcacaggttcaaggaggactggggcttccagaaatgcaagccctgtctc	321		
Db	289	TGCCCTCGAGCCGCCACCGGTTCAAGGAAGACTGGGGTTTCCAGAAGTGTAAAGCCATGTG	348		
Qy	322	tggactgcgagtggtgaaccgcttcaagaaggcaaatgttccagcaccacagtgatgccca	381		
Db	349	CGGACTGTGCCCTGGTGAACCGCTTTACAGAGGGCCAAGTGTCTACACACCACTGATGCTG	408		
Qy	382	tctcgggggactgcttgcaggattttataggaagacgaacttgcggcttttcaagaca	441		
Db	409	TCTCGGGGACTGCGTGCACGAGATTTTACCGGAAGACCAAACTGTTGGTGTTCGAAGACA	468		
Qy	442	tggagtggtgcctgttgagaaacctctctcttaacgaacgcgactgtgccagcaagg	501		
Db	469	TGGAGTGTGTCCTCTCGGAGACCCACCTCTCTCCTACGAACCACTGTACCAAGCAAGG	528		
Qy	502	tcaacctcgtaagaatcgctccagcgctccagccacggaacagcgctgactctccg	561		
Db	529	TGAACCTTGTGAAGATCTCTCCACCGTCTCCAGCCCTCGGGACACGCGCTGCTGCCG	588		
Qy	562	ttatctgagcgctctgtggccaccgtctctgtcggcctgtctatctctgtgtcatctatt	621		
Db	589	TCATCTGCAGTGTCTGSCCAACGGTGTGCTGCTGCCCTGCTCATCTGTGTGTCTATCTACT	648		
Qy	622	gtaaagacagtttatgagagaagaataccacgctgggtctctcggttcaagagacattcaagt	681		
Db	649	GCAAGAGCAGTTTATGAGAGAAGAAACCAACCTGCTCTCGGCTTCACAGGACATTCAGT	708		
Qy	682	acaacggtctgaactgtcggtcttaacagacctcagctccagcaaatatgccacagag	741		
Db	709	ACAATGGCTCTGAGGTGTCTATGCTTTTGACCAAGCTCTGGCTCCGGCACTGTGCCCATAGAG	768		
Qy	742	cctgctgcagtgccgcgctgactcagtgagaaacctgcggcggtgcgcttgcctcccat	801		
Db	769	CATGCTGTCACTATCACCGGCACTCAGCCCCAATGATATGGGCCCTGTTACACTGATTCGCT	828		
Qy	802	ccatgtgctgtgaggaggcctgcagccccaaccccgcgactcttgggttggggtgcatt	861		
Db	829	CCTTGTGCTGTGAAGAGCCCGCAGCTCTGCCAGAGTGTCTGTGGTGTGGCGTGGCGTT	888		

Qy	862	ctgagccagctcttcaggcaagaacacgagcccgagccgggagatgggtgcgcagattctt	921
Db	889	CTCCCACTACCTCTCCAGGAGAAAACCGGCTTCTGTGGGAAACACGATGCCAGCCTTCT	948
Qy	922	tcggatccctcagcagtcacatctgtggtgagattttcagatgcctggcctctgatcgaga	981
Db	949	TTGGGTCGTTCCTCCGCTCCATCTCGCGGAGTTTCTGATGCCCTGGCCTCTGATGAGA	1008
Qy	982	atcccatgggtggatgaacacatctcttttggactcttatacctgaactcaactgagaga	1041
Db	1009	ATCCTCTGGGGGTG---ACAGCTCTCTCTGTGACTCTTATCCTGAATCACTGTGAGAAG	1065
Qy	1042	acattctctctcaatccagaaactgaaagctcaacgtcttctggattcctaaatagcagtc	1101
Db	1066	ATACCAATTCCTCAATCCGAAACGAAAGACACAGCATCTCTGGATTCAGATCTACTGACT	1125
Qy	1102	aagatttggtggggggtgttccagtcacgtctcattcttgaaaaactttacagcagcta	1161
Db	1126	AGGATCTGGCTGGGACAGCTGCTCTAGAGTCTCTCGGAATGTTTCAGAACTTACTGACT	1185
Qy	1162	ctgattattctagatataaacaacacactggtagaatcagcatcaactcagcagatgcactaa	1221
Db	1186	CACCTAGACATGCTGACACTGGTACAGCTGGGAGCACACGCTAGCTCAGGATGCTCAAA	1245
Qy	1222	ctatgagaagcagctagatcaggagatggcgctctatcatccacccagcactcagacgt	1281
Db	1246	GGACTCCAAGCCAAAGGAGGCTGGGAAGACAGGGAACCTGAATCTAGCCATGCCACAG	1305
Qy	1282	ccctcagaagacttaagaacactgctcttcttcagtagaagcgtgtgcgtgaaccca	1341
Db	1306	CCTTCCAGGATGCTCTGAAG---GCCATCTTCTCAGCTGGAGGTGTGGTCTGGACAC-	1360
Qy	1342	aagagtactcttctgttagcttctgagctgagcagctggaacctgcatgctctctggg	1401
Db	1361	-----GCCTGTGATGAGCCTACAGACTGAGCAGTCTTG-----GTGTCTGGAA	1404
Qy	1402	gcataataaactgcacaaactgacgcatattgaagcctttcagccagctgtgctctga	1461
Db	1405	GCAAAATAAATCTGAACCAAACTGACAACATTTCCATCTTTTCAGCCACTAGCTACTGA	1464
Qy	1462	gcagaccagctgtaagctgaaacctcaatgaataacaagaaaaagactcca---ggcgg	1517
Db	1465	GCCAGACCAGCTGTAACTGTAAACCCCAAGCAAGAACAGAGAGAGACTGTACTGTAGCG	1524
Qy	1518	actcatgatactctgcatcttctccatagagaagctctctgccaaaaagtgacttca	1577
Db	1525	GCCTTGGGACATGCTCTTCTCCCTAAGCGAAACCTTAGCTGGGGCA-----ATTGA	1579
Qy	1578	aagacggatgggttgagctggcagcctatgagattgtggacatatcaagaacacagaaa	1637
Db	1580	AGGACCATGGGTGGAATGCTGCTGTGAACTTGTGGCACAGCA---GGACCCAGC	1635
Qy	1638	tgcctcctgcttatttcatggatgattggttttacaagac	1680
Db	1636	CTGGCTCCTTCTTATGCTCCAGGTGAATGTGGTTTTCACAAGAC	1678

RESULT

5

AF173166

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

1075 bp

mus musculus TNFRSF19 mRNA, complete cds.

GI:6635354

house mouse.

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 1075)

Hu,S., Tamada,K., Nt,J., Vincenz,C. and Chen,L.

Characterization of TNFRSF19, a novel member of the tumor necrosis factor receptor superfamily.

26-DEC-1999

Genomics 62 (1), 103-107 (1999)
20054362
2 (bases 1 to 1075)
Hu.S.
Direct Submission
Submitted (29-JUL-1999) Department of Immunology, Mayo Clinic and
Foundation, 200 First Street SW, Rochester, MN 55905, USA
Location/Qualifiers
source 1..1075
/organism="Mus musculus"
/db_xref="taxon:10090"
28..1074
/codon_start=1
/product="TNFRSF19"
/protein_id="AAFL19795.1"
/db_xref="GI:6635365"
/translation="MALKVLPLHRTVLFAAILFLHLACKVSCFAGDCRQEPFKDRSG
NCVLKQCQPGMBELSECEGYGEDAQVCPRHREKEDWGCFQKCPKPCADCALVNRPQ
RANCSHSDAVAGDCILPGFYRTKLGVQDMECVCPGPPPYEPHCTSKVNLVLISS
TVSSPRLTAAAYISALATVLIALLILCYIKRQFMKKPKWSLRPODIQVNGSEL
SCFDQPLRHCARACQVHRDSAPMYGPVHLIPLSCCEARSARAVLGCGLRSPPT
LQDRNPASVGNTHPAFFGVSRSICAEFSDAWPLMQNPLGGSSLCDSYPELTTCEDTN
SLNPEMLCFRFDLI"
BASE COUNT 211 a 308 c 296 g 259 t 1 others
ORIGIN
Query Match 40.6%; Score 692.6; DB 11; Length 1075;
Best Local Similarity 78.7%; Pred. No. 9.4e-181;
Matches 840; Conservative 0; Mismatches 224; Indels 3; Gaps 1;
Qy 22 aataatacatattgataagaagaatggcttttaaagtgtctactagaacaagaagaaacgt 81
Db 5 AATAAACACGTTTGGTGAGAGCCATGGCACTCAAGTCTTACCCTACACAGGACGGTGC 64
Qy 82 tttaactcttttagtattactaggctatttgcattgtaagtgaactgtgaaacagag 141
Db 65 TCTTTCGCTGGCATTCTCTTCTACTCCACCTGGCATGTAAAGTCAGTTCGGAAGCCGAG 124
Qy 142 actgtagacagcaagaattcaaggatcggctggaactgtgtccctgcaacacagtg 201
Db 125 ATTGACGGACAGGAATTCAGGATCGATCTGAAACTGTGTCTCTGCAAAACAGTCCG 184
Qy 202 ggccaggcatggagtgtctaaagaaatgggcttcggctatggggagatgcacagtg 261
Db 185 GACCTGCATGGAGTTGTCCAAGGAATGGCTTCGCCTATGGGAGGATGCACAGTGTG 244
Qy 262 tgaactgcggctgcacaggttcaagagagactgggcttcacagaaatgcaagccctgtc 321
Db 245 TGCCCTCGAGCCGCACCGGTTCAAGGAAGACTGGGGTTTCCAGAAGTGTAAAGCATGTG 304
Qy 322 tgaactgcagtggtgaacgccttcagaagcgaatgttcagaccacagtgatgcc 381
Db 305 CGGACTGTGGCTGGTGAACCGCTTTCAGAGGGCCAACTGCTCACACACCACTGATGCTG 364
Qy 382 tctcggggagctgcttgccaggatttatagaagaagcgaactgtcggctttcaagaca 441
Db 365 TCTCGGGGACTGCTGCCAGGATTTACCGGAGAGACCAACTGGTTGGTTTTCAGACA 424
Qy 442 tggagtgtgtcccttgyagaccctctctctcttaagaaacgcactgtgcgaagcagg 501
Db 425 TGGAGTGTGTGCCCTGGCGAGACCCAGCTCTCCCTACGAAACCACTGTACCAGCAAGG 484
Qy 502 tcaacctcgtgaagatcgctccacggcctccagcccaacgggacacggcgtgctgccg 561
Db 485 TGAACCTTGTGAAGATCTCTCCACCGCTCTCCAGCCCTCGGGACACGGCGTGGCTGCCG 544
Qy 562 ttactgcagcgtctggcaccgctctctctggccctgctcatctctctgtgtcatctatt 621
Db 545 TCATCTGCAGTGTCTTGCCACAGGTGTGCTCGCCCTGCTCATCTCTGTGTCATCTACT 604
Qy 622 gtaagagacagatttatggagaagaaacccagctggtctgtcagtcagacattcagt 681

Db 605 GCAAGAGCAGTTCATGAGAGAGAAACCCAGCTGGTCTCTCGGCCACAGACATTCAGT 664
Qy 682 acaacggctctgagctgctgtcttgacagacactcaagctcacgaataatccacacagag 741
Db 665 ACAATGGCTCTGAGCTGTCATGCTTTGACACAGAGCTCGCTCCGCCACTGTGCCATAGAG 724
Qy 742 cctgtgcagctgcgcgcgtgactcagtcagagacctgcggccggtgcgcttctcccat 801
Db 725 CATGCTGTGACATATACCGGGACTCAGCCCAATGATGATGGGCCCTGTTCACCTGATTCGGT 784
Qy 802 ccatgtctgagagagcctgcagcccaacccggcgagactcttggtgtgaggtgcaatt 861
Db 785 CTTGTGCTGTGAGAGAGCCGCGACTCTGCCGAGCTGTGCTGGCTGTGGGTGGCTGGT 844
Qy 862 ctgcagcagctcttcaggagaaagacagcagccagccgagagatggtgcgacttct 921
Db 845 CTCCACTACCTCCAGGAGAGAAACCGGCTTCTGTGGGGAACACAGATGCCAGCTTCT 904
Qy 922 tcggatccctcagcagtcctctgtggtgagcttcttcagatgctggtcctctgagcaga 981
Db 905 TTGGGTCTGTTCCTCCATCTCGCGGAGGTTTCTGTATGCTGCTGGCTCTGTATGCAGA 964
Qy 982 atcccatgggtgagcaacatctctttttgtgactcttaccgaaactcaactcaggaag 1041
Db 965 ATCCTCTGGGCGGTG---ACAGCTCTCTCTGTGACTCTTATCCTGAACCTCACTGGAGA 1021
Qy 1042 acattcattctcctcaatccagaaacttgaagctcaagctcttctgag 1088
Db 1022 ATACCAATTCCTCAATCCAGAGATGCTGTGCTTCTGTTTCGGGAT 1068

RESULT 6
LOCUS AB040433 744 bp mRNA ROD 22-JUL-2000
DEFINITION Mus musculus mRNA for dTROY, complete cds.
ACCESSION AB040433
VERSION AB040433.1 GI:9392327
KEYWORDS dTROY.
SOURCE Mus musculus
ORGANISM Mus musculus

REFERENCE
AUTHORS Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (sites)
Kojima,T., Morikawa,Y., Copeland,N.G., Gilbert,D.J., Jenkins,N.A.,
Senba,E. and Kitamura,T.
TROY, a newly identified member of the tumor necrosis factor
receptor superfamily, exhibits a homology with Edar and is
expressed in embryonic skin and hair follicles
J. Biol. Chem. 275 (27), 20742-20747 (2000)
20347167

JOURNAL
MEDLINE 2 (bases 1 to 744)
REFERENCE Kojima,T. and Kitamura,T.
AUTHORS Direct Submission
TITLE Submitted (23-MAR-2000) to the DDBJ/EMBL/GenBank databases. Tetsuo
Kojima, Chugai Research Institute for Molecular Medicine, Inc.,
Cytochrome Research Program; 153-2 Nagai, Niihari, Ibaraki 300-4101,
Japan (E-mail:kojimat@ciimed.com, Tel:81-298-306211,
Fax:81-298-306270)

FEATURES
Location/Qualifiers
1..744
/organism="Mus musculus"
/db_xref="taxon:10090"
/chromosome="14"
67..711
/gene="dTroy"
67..711
/gene="dTroy"
/note="a member of TNFR superfamily exhibits a homology
with Edar"
/codon_start=1
/product="dTROY"
/protein_id="BAB03268.1"
/db_xref="GI:9392328"

/translation="MALKVLPLHRTVLFAAILFLHLIAKVSCTGDCRQOEKDRSG
NCVLCKQCGPMELSKCEGYGEDAOCVCPRHPRKEDWGFQKCKPCADCAVLNRFO
RANCSHTSDAVCGDCLPGFYRKTKLGVQDMECVPCGDPPEYEPHCTSKVLVKISS
TVSPRDTALAAVICSALATVLLALLLLLCVLYKRPQMEKKPSCKLPSLCITVK"

BASE COUNT 162 a 208 c 211 g 163 t
ORIGIN

Query Match 27.0%; Score 460.8; DB 11; Length 744;
Best Local Similarity 81.9%; Pred No. 1.5e-116;
Matches 531; Conservative 0; Mismatches 117; Indels 0; Gaps 0;

Qy 22 aataaatacatattgataaagaagatggcttttaaagtgctactactagaacaagagaacagt 81
Db 44 AATAAACAGCTTTGGTGAGAGCCATGGCACATCAAGGTCCTACCTCTACACAGGACGGTGC 103
Qy 82 ttttcaactcttttagtattactaggctatttgcattgtaaaagtgaacttgtgaaacagag 141
Db 104 TCTTTCGCTGCCATTTCTTCTCTACTCCACCTGGCATGTAAAGTGAGTTGCCAAACCGGAG 163
Qy 142 actgtacacagaagaattcaggatcggtctgaaactgttctccctgcaaccagtg 201
Db 164 ATTGAGGACGACGAAATTCAGGATCGATCTGGAACCTGTCTCTGCAACAGTGC 223
Qy 202 ggccagggcatggagtgttctaaggaatggtctcggtatgggagagatgcacagtg 261
Db 224 GACCTGGCATGGAGTGTCCAAGGAATGTGGCTTGGGCTATGGGAGGATGCACAGTGTG 283
Qy 262 tgaagtcgcggctgcacaggttcaagggaggtggggtcttcagaaaatgcgaagccctgtc 321
Db 284 TGCCCTGCAGCGCCGACCGGTTCAAGGAAGACTGGGGTTTCCAGAAGTGTGAAGCATGTG 343
Qy 322 tggactgcagtggtgtaaccgctttcagaaggcaaatgttccagccaccagtgatgcca 381
Db 344 CGGACTGTGCGCTGTGTGAACCGCTTTACAGAGGCCCACTGCTCACACACAGTGTGTG 403
Qy 382 tctgcggggactgcttgcaggattttatagaagacgaaactgtcggctttcaagaca 441
Db 404 TCTCGGGGACTGCCTGCCAGGATTTTACCGGAAGACCAAACTGTTGGTTTTCAGACA 463
Qy 442 tggagtgtgcttgcagagacctctctctctctctctctctctctctctctctctctctc 501
Db 464 TGGAGTGTGTGCTCCCTGCGGAGACCCACCTCTCCCTACGAAACCACTGTACCCAGG 523
Qy 502 tcaactcgtgaagatcgctccacggtccagcccgagcccgagacagcgctggctgcgcg 561
Db 524 TGAACCTGTGAAGATCTCCTCCACCGCTCCAGGCCCTCGGGACACAGCGGCTGGCTGCCG 583
Qy 562 ttatctgcagcgtctgtggccacggtctctgtcggccctgctcctctctctctctctctct 621
Db 584 TCATCTGCAGTGTCTTGCCACGGTGTCTGCGCCCTGCTCATCTGTGTGTCTACTACT 643
Qy 622 gtaagagacagtttatgagagaagaacccagcgtggtctctctcgtcagtcac 669
Db 644 GCAAGAGCAGTTTCATGTGAGAGAAGAAACCCAGCTGTGAAGCTCCCATCCC 691

RESULT 7
AF167553
LOCUS AF167553 886 bp mRNA ROD 25-MAY-2000
DEFINITION Mus musculus TAJ-alpha short mRNA, complete cds.
ACCESSION AF167553
VERSION AF167553.1 GI:8071639
KEYWORDS house mouse.
SOURCE Mus musculus
ORGANISM Mus musculus

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 886)
Eby,M.T., Jasmin,A., Kumar,A., Sharma,K. and Chaudhary,P.M.
TAJ, a Novel Member of the Tumor Necrosis Factor Receptor Family,
Activates the c-Jun N-terminal Kinase Pathway and Mediates
Caspase-Independent Cell Death

[illegible]


```
Query Match      24.7%; Score 420.2; DB 67; Length 143608;
Best Local Similarity 86.4%; Pred. No. 4.1e-105;
Matches 464; Conservative 0; Mismatches 73; Indels 0; Gaps 0;

Qy 1168 tatctagatatacaacacactggttagaatacagatcaactcagagtgacataactatga 1227
Db 89373 TATTATTATCCATCTACTACTAGTAAAGATTATGCATATAATATCTTTTACCATTTGA 89432

Qy 1228 gaagccagctagatcagagagtgcgctatcatccaccagccagccagagctccctcc 1287
Db 89433 AATTAGCAGATTTAACTGTGAAGACATATTCTTAAGCTTCCCTTCTGTGCTGTTTT 89492

Qy 1288 aggaagcttaagaacctgctctcttcttcagtgagaagcgtgtgctggaaccccaaaagagt 1347
Db 89493 AGGAAGCTTAAGAACCTGCTTCTTCGTCAGTAGAAGCGGTGCTGGAACCCAAAGAGT 89552

Qy 1348 actcctttgttagcttagctagcagtgagcagctctggacccttcagtgctctcggggcaaaa 1407
Db 89553 ACTCCTTTGTTAGGCTTATGAGCTTAGCAGTCTGACCTTGCACCTTGCATGGCTTCGGGGCAAAA 89612

Qy 1408 ataaatctgaacaaactgacgcaattggaagcctttcagccagttgcttctctgagccaga 1467
Db 89613 ATAAATCTGAACAACTGACGGCATTTGAAGCCTTTGAGCCAGTTGCTTCTGAGCCAGA 89672

Qy 1468 ccagctgtaagctgaacactcaatgaataacaagaagactccagggccgactcatgata 1527
Db 89673 CCAGCTGTAAGCTGAACCTCAATGAATAACAAGAAGAACTCCAGGCGGACTCATGATA 89732

Qy 1528 ctctgcatcttctctacatgagaagctctctcgcacaaaagtgacttcaagacggatg 1587
Db 89733 CTCTGCACTCTTCTACATGAGAAGCTTCTCTGCCACAAAAGTACTTCAAGACGGATG 89792

Qy 1588 ggttgagctgcagcctatgagattgtgacataatacaagaacacagaaatgcctcatg 1647
Db 89793 GGTTCAGCTGCAGCCTATGAGATTGTGGACATATAACAAGAAACAGAAATGCCCTCATG 89852

Qy 1648 cttatttctcgttgattgtgttttacaagactgaagaccagagtagtatacttttc 1704
Db 89853 CTTATTTCCTGCTGATTGTGTTTACAAAGCTGAAGACCCAGAGTACTACTTTTTC 89909

RESULT 9
AL139080 178256 bp DNA HTG 29-SEP-2000
LOCUS Homo sapiens chromosome 13 clone RP11-173N17 map q12.11-12.3, ***
DEFINITION SEQUENCING IN PROGRESS ***, 15 unordered pieces.
ACCESSION AL139080
VERSION AL139080.8 GI:10443032
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 178256)
Direct Submission
Submitted (28-SEP-2000) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK E-mail enquiries: humquery@sanger.ac.uk Clone
requests: clonerequest@sanger.ac.uk
On Oct 1, 2000 this sequence version replaced gi:10129398.
-----
Center: Sanger Centre
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
-----
Center project name: bA173N17
-----
Summary Statistics
Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid; L08752; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 168976 bases at least Q40
```

Consensus quality: 172107 bases at least Q30
Consensus quality: 173780 bases at least Q20
Insert size: 176856; sum-of-contigs
Insert size: 163577; 8.6% error; agarose-fp
Quality coverage: 3.73x in Q20 bases; sum-of-contigs Quality
coverage: 4.07x in Q20 bases; agarose-fp

* NOTE: This is a 'working draft' sequence. It currently
* consists of 15 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

* 1 8223: contig of 8223 bp in length
* 8224 8323: gap of 100 bp
* 8324 25426: contig of 17103 bp in length
* 25427 25526: gap of 100 bp
* 25527 28263: contig of 2737 bp in length
* 28264 28363: gap of 100 bp
* 28364 34273: contig of 5910 bp in length
* 34274 34373: gap of 100 bp
* 34374 42235: contig of 7862 bp in length
* 42236 42335: gap of 100 bp
* 42336 53917: contig of 11582 bp in length
* 53918 54017: gap of 100 bp
* 54018 71972: contig of 17955 bp in length
* 71973 72072: gap of 100 bp
* 72073 81711: contig of 9639 bp in length
* 81712 81811: gap of 100 bp
* 81812 88644: contig of 6833 bp in length
* 88645 88744: gap of 100 bp
* 88745 95048: contig of 6304 bp in length
* 95049 95148: gap of 100 bp
* 95149 107455: contig of 12307 bp in length
* 107456 107555: gap of 100 bp
* 107556 125465: contig of 17910 bp in length
* 125466 125565: gap of 100 bp
* 125566 140008: contig of 14443 bp in length
* 140009 140108: gap of 100 bp
* 140109 144761: contig of 4653 bp in length
* 144762 144861: gap of 100 bp
* 144862 178256: contig of 33395 bp in length.

FEATURES

Location/Qualifiers
1. 178256
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="13"
/map="q12.11-12.3"
/clone="RP11-173N17"
/clone.lib="RPC1-11.1"
1..8223
/note="assembly_fragment:01724
fragment_chain:1"
8324..25426
/note="assembly_fragment:00074
fragment_chain:1"
25527..28263
/note="assembly_fragment:01884
fragment_chain:1"
28364..34273
/note="assembly_fragment:00979
fragment_chain:1"
34374..42235
/note="assembly_fragment:00126
fragment_chain:2"
42336..53917
/note="assembly_fragment:00364
fragment_chain:2"
54018..71972
/note="assembly_fragment:01769
fragment_chain:2"

misc_feature

misc_feature

misc_feature

misc_feature

misc_feature

misc_feature

misc_feature

----- Summary Statistics -----
 Sequencing vector: M13; M77815; 100% of reads
 Chemistry: Dye-terminator Big Dye; 100% of reads
 Assembly program: Phrap; version 0.960731
 Consensus quality: 178666 bases at least Q40
 Consensus quality: 190940 bases at least Q30
 Consensus quality: 197088 bases at least Q20
 Insert size: 194000; agarose-fp
 Insert size: 202436; sum-of-contigs
 Quality coverage: 4.2 in Q20 bases; agarose-fp
 Quality coverage: 4.0 in Q20 bases; sum-of-contigs

 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 34 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

```

1      1267: contig of 1267 bp in length
*      1268 1367: gap of 100 bp
*      1368 2402: contig of 1035 bp in length
*      2403 2502: gap of 100 bp
*      2503 3524: contig of 1022 bp in length
*      3525 3624: gap of 100 bp
*      3625 4913: contig of 1289 bp in length
*      4914 5013: gap of 100 bp
*      5014 6289: contig of 1276 bp in length
*      6290 6389: gap of 100 bp
*      6390 7655: contig of 1266 bp in length
*      7656 7755: gap of 100 bp
*      7756 9267: contig of 1512 bp in length
*      9268 9367: gap of 100 bp
*      9368 11138: contig of 1771 bp in length
*      11139 11238: gap of 100 bp
*      11239 13822: contig of 2584 bp in length
*      13823 13922: gap of 100 bp
*      13923 16968: contig of 3046 bp in length
*      16969 17068: gap of 100 bp
*      17069 20185: contig of 3117 bp in length
*      20186 20285: gap of 100 bp
*      20286 22634: contig of 2349 bp in length
*      22635 22734: gap of 100 bp
*      22735 27012: contig of 4278 bp in length
*      27013 27112: gap of 100 bp
*      27113 29342: contig of 2230 bp in length
*      29343 29442: gap of 100 bp
*      29443 33381: contig of 3939 bp in length
*      33382 33481: gap of 100 bp
*      33482 36562: contig of 3081 bp in length
*      36563 36662: gap of 100 bp
*      36663 40982: contig of 4320 bp in length
*      40983 41082: gap of 100 bp
*      41083 45520: contig of 4438 bp in length
*      45521 45620: gap of 100 bp
*      45621 50623: contig of 5003 bp in length
*      50624 50723: gap of 100 bp
*      50724 55610: contig of 4887 bp in length
*      55611 55710: gap of 100 bp
*      55711 61038: contig of 5328 bp in length
*      61039 61138: gap of 100 bp
*      61139 66159: contig of 5021 bp in length
*      66160 66259: gap of 100 bp
*      66260 73479: contig of 7220 bp in length
*      73480 80554: contig of 6975 bp in length
*      80555 80654: gap of 100 bp
*      80655 89313: contig of 8659 bp in length
*      89314 89413: gap of 100 bp
*      89414 98132: contig of 8719 bp in length
*      98133 98232: gap of 100 bp
*      98233 107469: contig of 9237 bp in length

```

```

*      107470 107569: gap of 100 bp
*      107570 117873: contig of 10304 bp in length
*      117874 117973: gap of 100 bp
*      117974 130973: contig of 13000 bp in length
*      130974 131073: gap of 100 bp
*      131074 143236: contig of 12163 bp in length
*      143237 143336: gap of 100 bp
*      143337 154478: contig of 11142 bp in length
*      154479 154578: gap of 100 bp
*      154579 169967: contig of 15389 bp in length
*      169968 170067: gap of 100 bp
*      170068 187347: contig of 17280 bp in length
*      187348 187447: gap of 100 bp
*      187448 205736: contig of 18289 bp in length.
*
*      Location/Qualifiers
*      1..205736
*      /organism="Homo sapiens"
*      /db_xref="taxon:9606"
*      /chromosome="17"
*      /map="17"
*      /clone="RP11-85I20"
*      /clone_lib="RPC1-11 Human Male BAC"
*      1..1267
*      /note="assembly_fragment"
*      1368..2402
*      /note="assembly_fragment"
*      2503..3524
*      /note="assembly_fragment"
*      3625..4913
*      /note="assembly_fragment"
*      5014..6289
*      /note="assembly_fragment"
*      6390..7655
*      /note="assembly_fragment"
*      7756..9267
*      /note="assembly_fragment"
*      9368..11138
*      /note="assembly_fragment"
*      11239..13822
*      /note="assembly_fragment"
*      13923..16968
*      /note="assembly_fragment"
*      17069..20185
*      /note="assembly_fragment"
*      20286..22634
*      /note="assembly_fragment"
*      22735..27012
*      /note="assembly_fragment"
*      27113..29342
*      /note="assembly_fragment"
*      clone_end=T7
*      vector_side:right"
*      29443..33381
*      /note="assembly_fragment"
*      33482..36562
*      /note="assembly_fragment"
*      36663..40982
*      /note="assembly_fragment"
*      41083..45520
*      /note="assembly_fragment"
*      45621..50623
*      /note="assembly_fragment"
*      50724..55610
*      /note="assembly_fragment"
*      55711..61038
*      /note="assembly_fragment"
*      61139..66159
*      /note="assembly_fragment"
*      66260..73479
*      /note="assembly_fragment"
*      73580..80554
*      /note="assembly_fragment"
*      80655..89313

```

```
misc_feature      /note="assembly_fragment"
                  89414..98132
                  /note="assembly_fragment"

Query Match      3.8%; Score 65.4; DB 51; Length 205736;
Best Local Similarity 38.6%; Pred. No. 8.4e-07;
Matches 114; Conservative 0; Mismatches 181; Indels 0; Gaps 0;

QY 223 aggaatgtgctcgctgggaggtgagagtgacagtggtgacgtgcgcggtgcacaggt 282
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 154301 AGGAGAGTGTATGGAGAGGGTGGAGATGCCCTACTGTGCACACTGTCTCTCAGGT 154360

QY 283 tcaaggagagctggggtcccaagaatgcagccctgtctgtgactgcgcagtggtgaacc 342
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 154361 AACACAGCAGCTGGGGCCACCACACATGTCAGAGATGCATCACCTGTGTCATCAATC 154420

QY 343 gcttcagaagcgaatgttcagccaccagtcagtcacatctgcgggactcgtgcgac 402
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 154421 GCGTTCAAGAGTGAAGTCGCGACATACCTCTAAATGCTGTGTGGGGACTGTGTGCCNN 154480

QY 403 gatttataggagcgaactctgcgcgtttcaagacatggagtgtgtgccttggag 462

Db 154481 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 154540

QY 463 accctctctcttcacgaacgcactgtgccagcaggtcaacctcgtgaagat 517
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 154541 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 154595

RESULT 14
AC034198/c
LOCUS
DEFINITION      Homo sapiens chromosome 3 clone RP11-767C1 map 3p, WORKING DRAFT
ACCESSION      AC034198
VERSION         AC034198.4
KEYWORDS        HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE          human.
ORGANISM        Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 160214)
Bao,J., Bao,Q., Bao,W., Bian,X., Cao,T., Chen,C., Chen,J., Ding,H.,
Dong,W., Fan,H., Feng,X., Guan,Q., Gu,X., Guo,D., He,L., Hu,S.,
Huang,F., Jin,Y., Kang,N., Li,C., Li,G., Li,J., Li,L.,
Li,S., Li,T., Liu,Y., Liu,N., Liu,B., Liu,Y., Li,W., Li,Y.,
Luo,J., Niu,Y., Qi,Q., Qi,X., Song,S., Sun,M., Sun,W., Sun,X.,
Tao,R., Wang,H., Wang,J., Wang,J., Wang,L., Wang,L., Wang,R.,
Wang,X., Wang,X., Wang,Y., Wu,D., Wu,Q., Xie,F., Xuan,Z., Xue,Y.,
Yan,C., Yang,X., Yu,B., Zeng,Y., Zhang,G., Zhang,H., Zhang,H.,
Zhang,L., Zhang,M., Zhang,X., Zhang,X., Zhang,Y., Zhang,Y.,
Zhang,Z., Zhu,B., Yu,J. and Yang,H.
Chromosome 3p genomic sequence
Unpublished
2 (bases 1 to 160214)
Kang,N., Hu,S., Dong,W., Wang,J., Zhang,Y., Zhang,H., Liu,B.,
Bao,W., Sun,Y., Wu,Q., Wang,H., Yang,X., Cheng,C., Wang,Y., Niu,Y.,
Qi,X., Li,T., Zhang,H., Liu,N., Wu,D., Yu,B., Fan,H., Liu,Y.,
Li,G., Li,C., Bao,Q., Bao,J., Wang,X., Song,L., Zhang,L., Guo,D.,
Huang,F., Zhang,G., Li,J., Bian,X., Zhang,M., Li,L., Feng,X., Yu,J.
and Yang,H.
Direct Submission
Submitted (05-APR-2000) Human Genomic Center, Institute of
Genetics, Chinese Academy of Sciences, Datun Road, Beijing, Beijing
100101, P.R.China
On Sep 19, 2000 this sequence version replaced gi:8101278.
-----Genome Center
Center:Beijing Center
Center code:Beijing
Website:http://hgsc.igtp.ac.cn
http://www.genomics.org.cn
Contact:hgscigtp.ac.cn
----- Project Information

Center project name:il% project
Center clone name: RP11-767C1
----- Summary Statistics
Sequencing vector: pUC18; 100% of reads
Chemistry: Dye-terminator; ET 55% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 155354 bases at least Q40
Consensus quality: 160750 bases at least Q30
Consensus quality: 164545 bases at least Q20
Insert size: 150147; sum-of-contigs
Quality coverage: 4.62x in Q20 bases; sum-of-contigs
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 25 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
* 1071: contig of 1071 bp in length
* 1171: gap of unknown length
* 1172: contig of 1083 bp in length
* 2255: gap of unknown length
* 2355: contig of 1497 bp in length
* 3852: gap of unknown length
* 3952: contig of 1344 bp in length
* 5295: gap of unknown length
* 5396: contig of 1070 bp in length
* 5396: gap of unknown length
* 6466: contig of 1292 bp in length
* 6566: gap of unknown length
* 7858: gap of unknown length
* 7958: contig of 1237 bp in length
* 9195: gap of unknown length
* 9295: contig of 1744 bp in length
* 11039: gap of unknown length
* 11139: contig of 3282 bp in length
* 14421: gap of unknown length
* 14521: contig of 3344 bp in length
* 17865: gap of unknown length
* 17965: contig of 3306 bp in length
* 21271: gap of unknown length
* 21371: contig of 3680 bp in length
* 25051: gap of unknown length
* 25151: contig of 5474 bp in length
* 30625: gap of unknown length
* 30725: contig of 7047 bp in length
* 37725: gap of unknown length
* 37871: contig of 4276 bp in length
* 42148: gap of unknown length
* 42248: contig of 7505 bp in length
* 49753: gap of unknown length
* 49853: contig of 7441 bp in length
* 57294: gap of unknown length
* 57394: contig of 6233 bp in length
* 63627: gap of unknown length
* 63727: contig of 8794 bp in length
* 72521: gap of unknown length
* 72621: contig of 10918 bp in length
* 83539: gap of unknown length
* 83639: contig of 11575 bp in length
* 95214: gap of unknown length
* 95314: contig of 12308 bp in length
* 107622: gap of unknown length
* 107722: contig of 12790 bp in length
* 120512: gap of unknown length
* 120612: contig of 17829 bp in length
* 138441: gap of unknown length
* 138541: contig of 21674 bp in length.
Location/Qualifiers
1..160214
/organism="Homo sapiens"
```

FEATURES

source

* 132824 180511: contig of 47688 bp in length.

FEATURES

Location/Qualifiers
1..180511
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="3p"
/clone="RP11-588P9"

BASE COUNT 43759 a 46432 c 47713 g 42605 t 2 others
ORIGIN

Query Match 2.6%; Score 43.6; DB 42; Length 180511;
Best Local Similarity 48.4%; Pred. No. 0.91;
Matches 121; Conservative 0; Mismatches 129; Indels 0; Gaps 0;
QY 681 tacaacggtctcgtgctgtcgtcttgacagacctcagctccacgaatatgcccacaga 740
Db 114940 TCCNAACTCTCTGTGCCCCGGGGGCAATTCCTTCCTGCTTGCACGAGATTCACACCCC 114999
QY 741 gctgtgcccagtgccgcggtgactcagtgacagacctgcggccggtgcgcttgcctcca 800
Db 115000 GCCCTGCCCACTGCCCGCCCCCAGCGGGAAGTGGCCCGGAGTGGAGGCGTGGACAGGCA 115059
QY 801 tccatgtgctgtgaggaagcctgcagcccccaaccgagactcttggttgtgggtgcat 860
Db 115060 TCCCGGTGTCTCGAGTCAAGGCTGTGCGGCCAGCCTGGACAGCACCGGCCCGCGGAGGCGAG 115119
QY 861 tctgcagccagctctcaggaagaacgcagccagccagccgggagatggtgccgactttc 920
Db 115120 ACAGGGCGACGAGCAGGCGCCCGCAGGCTCCAGAGCAGCCGCTGACAGGCTGTCCAGCTGC 115179
QY 921 ttcggatccc 930
Db 115180 ATCGGCTCTC 115189

Search completed: March 2, 2001, 12:59:17
Job time: 32956 sec

THIS PAGE BLANK (10/70)

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 2, 2001, 12:41:53 ; Search time 553.05 Seconds
(without alignments)
1157.453 Million cell updates/sec

Title: US-09-380-276A-2

Perfect score: 1704

Sequence: 1 ggaacgtagaactccaa.....gaccagagtatacttttc 1704

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 480022 seqs, 18781343 residues

Total number of hits satisfying chosen parameters: 960044

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_36.*

1: /SID56/gcgdata/geneseq/geneseq/NA1980.DAT.*
2: /SID56/gcgdata/geneseq/geneseq/NA1981.DAT.*
3: /SID56/gcgdata/geneseq/geneseq/NA1982.DAT.*
4: /SID56/gcgdata/geneseq/geneseq/NA1983.DAT.*
5: /SID56/gcgdata/geneseq/geneseq/NA1984.DAT.*
6: /SID56/gcgdata/geneseq/geneseq/NA1985.DAT.*
7: /SID56/gcgdata/geneseq/geneseq/NA1986.DAT.*
8: /SID56/gcgdata/geneseq/geneseq/NA1987.DAT.*
9: /SID56/gcgdata/geneseq/geneseq/NA1988.DAT.*
10: /SID56/gcgdata/geneseq/geneseq/NA1989.DAT.*
11: /SID56/gcgdata/geneseq/geneseq/NA1990.DAT.*
12: /SID56/gcgdata/geneseq/geneseq/NA1991.DAT.*
13: /SID56/gcgdata/geneseq/geneseq/NA1992.DAT.*
14: /SID56/gcgdata/geneseq/geneseq/NA1993.DAT.*
15: /SID56/gcgdata/geneseq/geneseq/NA1994.DAT.*
16: /SID56/gcgdata/geneseq/geneseq/NA1995.DAT.*
17: /SID56/gcgdata/geneseq/geneseq/NA1996.DAT.*
18: /SID56/gcgdata/geneseq/geneseq/NA1997.DAT.*
19: /SID56/gcgdata/geneseq/geneseq/NA1998.DAT.*
20: /SID56/gcgdata/geneseq/geneseq/NA1999.DAT.*
21: /SID56/gcgdata/geneseq/geneseq/NA2000.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1702.4	99.9	1704	V33361	Nucleotide sequenc
2	1690	99.2	2185	20 X24978	Human TRAIN-R cdna
3	1290.4	75.7	1496	19 V33362	Nucleotide sequenc
4	1288.8	75.6	1502	20 X08689	Novel nucleotide s
5	1270	74.5	1489	20 X23415	Human hAPO4-alpha
6	835.6	49.0	987	20 X59346	Human NTR-5 cdna.
7	823	48.3	1678	20 X23413	Mouse MAP04-alpha
8	460.8	27.0	886	20 X23414	Mouse MAP04-alpha
9	460.8	27.0	942	20 X24977	Mouse TRAIN-R (lon
10	460.8	27.0	981	20 X87394	Mouse STRIFE1 (ran
11	447.2	26.2	893	20 X84622	Human TNFR superfa
12	362.6	21.3	538	20 X59345	Mouse NTR-5 cdna.

13	361.6	21.2	371	19	V11422	Human secreted pro
14	326.6	19.2	591	20	X23417	Mouse MAP04-gamma
15	326.6	19.2	599	20	X24976	Mouse TRAIN-R (sho
16	326.6	19.2	623	20	X84623	Mouse TNFR superfa
17	326.6	19.2	636	21	X92408	cdna encoding murI
18	326.6	19.2	655	20	X87395	Mouse STRIFE2 (Tan
19	208.2	12.2	1133	20	X23416	Rat RAP04-alpha DN
20	154.8	9.1	932	21	X2411	cdna encoding huma
21	90.4	5.3	791	20	X24979	Clone G156 encodi
22	88.6	5.2	396	20	X23418	Mouse MAP04-beta D
23	87.4	5.1	181	19	V11423	Human secreted pro
24	87.4	5.1	201	20	X86655	EST clone AX92. H
25	81.2	4.8	546	21	X29410	cdna encoding huma
26	77.8	4.6	474	21	X29409	cdna encoding huma
27	44	2.6	10732	21	A10594	Gene encoding a su
28	37.4	2.2	1290	20	X23121	Human TANGO 129 (T
29	37.4	2.2	2570	20	X23120	Human TANGO 129 (T
30	37.4	2.2	2703	21	D00061	Human tumour necro
31	36.8	2.2	326	11	Q05546	Fragment 41-3 of t
32	36.4	2.1	1602	15	Q72217	Human adrenergic r
33	36.4	2.1	1978	15	Q72212	Truncated human al
34	36.4	2.1	1987	16	T11624	Human alpha-1C adr
35	36.4	2.1	1997	16	T11600	Human alpha-1C adr
36	36.4	2.1	1998	15	Q72213	Human alpha-1C adr
37	36.4	2.1	2004	16	T11599	Human alpha-1C adr
38	36.4	2.1	2005	15	Q72211	Human alpha-1C adr
39	36.2	2.1	330	21	A15982	Human protein clon
40	36.2	2.1	659	21	A15992	Human protein clon
41	36.2	2.1	2486	17	T09866	Human neurotransmi
42	36	2.1	2067	20	V99092	DNA methyltransfer
43	36	2.1	19440	20	V99129	DNA methyltransfer
44	35.6	2.1	1150	20	Z06928	Streptomyces hygro
45	35.2	2.1	1050	21	Z58975	Human cytoskeletal

ALIGNMENTS

RESULT 1
V33361
ID V33361 standard; cdna to mRNA; 1704 BP.
XX
AC V33361;
XX
DT 02-DEC-1998 (first entry)
XX
DE Nucleotide sequence of human alpha-OAF065.
XX
KW Human; alpha-OAF065; stroma cell; antibody; inflammatory;
KW cytokine-mediated disease; rheumatism; ulcerative colitis; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 45..1298
FT /*tag= a
FT /*product= "human alpha-OAF065 protein"
FT sig_peptide 45..119
FT mat_peptide /*tag= b
FT /*tag= c
FT /*transl_except= (pos:711..713, aa= Pro)
FT /*transl_except= (pos:714..716, aa= Arg)
XX
XX WO9838304-Al.
XX
XX 03-SEP-1998.
XX
XX 26-FEB-1998; 98WO-JP00799.
XX
XX 27-FEB-1997; 97JP-0043143.
XX
XX (ONCY) ONO PHARM CO LTD.

XX Fukushima D, Konishi M, Tada H;
XX WPI: 1998-481205/41.
DR P-PSDB; W70386.
XX Membrane polypeptide expressed by human stroma cells, and antibodies
PT recognising it - for treatment of inflammatory and other
PT cytokine-mediated diseases.
XX Claim 5; Pages 31-32; 54pp; Japanese.
XX This is the nucleotide sequence of the human alpha-OAF065, used in
CC the method of the invention. The process involves the use of peptides
CC expressed by stroma cells, and its antibodies are used for in the
CC prevention and treatment of inflammatory and other cytokine-mediated
CC diseases such as rheumatism, ulcerative colitis.
XX Sequence 1704 BP; 429 A; 426 C; 430 G; 419 T; 0 other;
SQ

Query Match 99.9%; Score 1702.4; DB 19; Length 1704;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1703; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 gggagcgtagaactctcccaacaataatacatattgataagaagaatggctttaaagtgc 60
DB 1 gggagcgtagaactctcccaacaataatacatattgataagaagaatggctttaaagtgc 60

QY 61 tactagaacaagaagaaacgtttttcactcttttagtattacttagctatttgcattga 120
DB 61 tactagaacaagaagaaacgtttttcactcttttagtattacttagctatttgcattga 120

QY 121 aagtgaacttgaaacaggagactgtagacagcaagaattcaggagatcgctggaact 180
DB 121 aagtgaacttgaaacaggagactgtagacagcaagaattcaggagatcgctggaact 180

QY 181 gtgttcctctcaaccagtgtggccaggcatggagtgtgtctaaggaaatggcttcggct 240
DB 181 gtgttcctctcaaccagtgtggccaggcatggagtgtgtctaaggaaatggcttcggct 240

QY 241 atggggaggatgcacagtgtgtgacgtgcggtgcacaggttcaaggaggactgggct 300
DB 241 atggggaggatgcacagtgtgtgacgtgcggtgcacaggttcaaggaggactgggct 300

QY 301 tccagaaatcaagccctgtctgagctgcagctgtgagatcggtgaaccgtttcagaaggcaatt 360
DB 301 tccagaaatcaagccctgtctgagctgcagctgtgagatcggtgaaccgtttcagaaggcaatt 360

QY 361 gttcagccaccagtgtatgccatctgvggagactgcttgcaggattttataggaaagcga 420
DB 361 gttcagccaccagtgtatgccatctgvggagactgcttgcaggattttataggaaagcga 420

QY 421 aacttgcgcttccaagacatggagtgtgtgctgtgagaccctctcctcttaag 480
DB 421 aacttgcgcttccaagacatggagtgtgtgctgtgagaccctctcctcttaag 480

QY 481 aacgcacatgtccagaaagtcaacctgtgaagatcggtccacggcctccagccac 540
DB 481 aacgcacatgtccagaaagtcaacctgtgaagatcggtccacggcctccagccac 540

QY 541 gggacacggcgctggctgaccttatctgcagcgctctgcgcaaccgtctgacctgc 600
DB 541 gggacacggcgctggctgaccttatctgcagcgctctgcgcaaccgtctgacctgc 600

QY 601 tcattctctgttcatctatttgaagagacagtttataggagaagaacccagctgtctc 660
DB 601 tcattctctgttcatctatttgaagagacagtttataggagaagaacccagctgtctc 660

QY 661 tgcgggtcacaggacattcagtaacaggctctgagctgtgctgttctttgacagccctcagc 720
DB 661 tgcgggtcacaggacattcagtaacaggctctgagctgtgctgttctttgacagccctcagc 720

RESULT 2

X24978

ID X24978 standard; cDNA; 2185 BP.

XX

QY 721 tccacgaatatgccacagagcctgtgccagtgcgcgcgtgactcagtgacagacctgcg 780
DB 721 tccacgaatatgccacagagcctgtgccagtgcgcgcgtgactcagtgacagacctgcg 780

QY 781 ggcgggtgcgcttgcctcccatccatgtctgtgagaggcctgcagcccaaccgcgcga 840
DB 781 ggcgggtgcgcttgcctcccatccatgtctgtgagaggcctgcagcccaaccgcgcga 840

QY 841 ctcttggttgggtgcattctgcagcagctcttcaggcaagaacagcggccagccgcg 900
DB 841 ctcttggttgggtgcattctgcagcagctcttcaggcaagaacagcggccagccgcg 900

QY 901 gggagatggcgactttcttcggatccctcacgcagtcacatctgtggcgagttttcag 960
DB 901 gggagatggcgactttcttcggatccctcacgcagtcacatctgtggcgagttttcag 960

QY 961 atgcttggcctctgatagcagaaatcccatgggtgggtgacaaatctcttttttgactctt 1020
DB 961 atgcttggcctctgatagcagaaatcccatgggtgggtgacaaatctcttttttgactctt 1020

QY 1021 atcctgaactcactggagaagacattcattctctcaatccagaactgaaagctcaacgt 1080
DB 1021 atcctgaactcactggagaagacattcattctctcaatccagaactgaaagctcaacgt 1080

QY 1081 ctttgattcaaatagcagtcgaagatttgggtggggtgttccagtcagctctcatt 1140
DB 1081 ctttgattcaaatagcagtcgaagatttgggtggggtgttccagtcagctctcatt 1140

QY 1141 ctgaaactttacagcagctactgtatttactagataataacacacactggtgagaatcag 1200
DB 1141 ctgaaactttacagcagctactgtatttactagataataacacacactggtgagaatcag 1200

QY 1201 catcaactcaggatgcactaaactatgagaagccagctagatcaggagagtggtgcctatca 1260
DB 1201 catcaactcaggatgcactaaactatgagaagccagctagatcaggagagtggtgcctatca 1260

QY 1261 tcaccacagcactcagcagctccctccaggaagctttaaagaacctgtcttcttctcagt 1320
DB 1261 tcaccacagcactcagcagctccctccaggaagctttaaagaacctgtcttcttctcagt 1320

QY 1321 agaagcgtgtgcttggaaacccaaagagtactccttctttagggttatggactggagcgtct 1380
DB 1321 agaagcgtgtgcttggaaacccaaagagtactccttctttagggttatggactggagcgtct 1380

QY 1381 ggaacctgcatgcttctgggcaaaaaataatctgaacccaaactgacggcatttgaagc 1440
DB 1381 ggaacctgcatgcttctgggcaaaaaataatctgaacccaaactgacggcatttgaagc 1440

QY 1441 ctttcagccagttgcttctgagccagacagcgtgaagctgaacctcaatgaatacaaa 1500
DB 1441 ctttcagccagttgcttctgagccagacagcgtgaagctgaacctcaatgaatacaaa 1500

QY 1501 gaaaagactccagcagctcatgatactctgcatcttctcatatgagaagcttctctg 1560
DB 1501 gaaaagactccagcagctcatgatactctgcatcttctcatatgagaagcttctctg 1560

QY 1561 ccacaaaagtgcattcaaaagcagatgggttgcagctggcagcctatgagacttgcacat 1620
DB 1561 ccacaaaagtgcattcaaaagcagatgggttgcagctggcagcctatgagacttgcacat 1620

QY 1621 atacaagaacacgaagtgcctcactgtcttatttctcatgtgtgtgtgttttacagac 1680
DB 1621 atacaagaacacgaagtgcctcactgtcttatttctcatgtgtgtgtgttttacagac 1680

QY 1681 tgaagacccagagataacttttcc 1704
DB 1681 tgaagacccagagataacttttcc 1704


```

Db 1281 accttcagcagctactgattttatctagataatacaacacactggtagaaatcagcatcaa 1340
QY 1207 ctcatgagtcactaactatgagaagccagctagatcagagagatgagcgtctatcatccacc 1266
Db 1341 ctcatgagtcactaactatgagaagccagctagatcagagagatgagcgtctatcatccacc 1400
QY 1267 cagccactcagacgtcctccaggaagcttaagaagcctgctctctctcagtagaagc 1326
Db 1401 cagccactcagacgtcctccaggaagcttaagaagcctgctctctcagtagaagc 1460
QY 1327 gctgctggaacccaagaagatctctcttctgtaggctttaggcttaggactgagcagctggaacct 1386
Db 1461 gctgctggaacccaagaagatctctcttctgtaggctttaggcttaggactgagcagctggaacct 1520
QY 1387 tgcattgctctggggcaaaaaataactgaacaaactgacggcatttgaagccctttca 1446
Db 1521 tgcattgctctggggcaaaaaataactgaacaaactgacggcatttgaagccctttca 1580
QY 1447 gccattgctctgagccagacagctgtaagctgaaacctcaatgaataacaagaagaag 1506
Db 1581 gccattgctctgagccagacagctgtaagctgaaacctcaatgaataacaagaagaag 1640
QY 1507 actccaggccagctatgatactctgcatcttctcatatgagaagcttctctgccacaa 1566
Db 1641 actccaggccagctatgatactctgcatcttctcatatgagaagcttctctgccacaa 1700
QY 1567 aagtgacttcaagagcagtgattgaagctgagcagcctatgagatgtggaacataaca 1626
Db 1701 aagtgacttcaagagcagtgattgaagctgagcagcctatgagatgtggaacataaca 1760
QY 1627 agaacagaaatgccctcagctattttctgtaggctgattggtggttttacaagactgaaga 1686
Db 1761 agaacagaaatgccctcagctattttctgtaggctgattggtggttttacaagactgaaga 1820
QY 1687 ccagagatatacttttc 1704
Db 1821 ccagagatatacttttc 1838

```

RESULT 3

```

V33362
ID V33362 standard; cDNA to mRNA; 1496 BP.
XX
AC V33362;
XX
DT 02-DEC-1998 (first entry)
XX
DE Nucleotide sequence of human beta-OAF065.
XX
KW Human; beta-OAF065; stroma cell; antibody; inflammatory;
KW cytokine-mediated disease; rheumatism; ulcerative colitis; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 45..1316
FT FT /*tag= a
FT FT /product= "human beta-OAF065 protein"
FT sig_peptide 45..119
FT FT /*tag= b
FT mat_peptide 120..1313
FT FT /*tag= c
FT FT /transl_except= (pos:711..713, aa= Pro)
FT FT /transl_except= (pos:714..716, aa= Arg)
XX
PN W09838304-A1.
XX
PD 03-SEP-1998.
XX
PF 26-FEB-1998; 98WO-JP00799.
XX
PR 27-FEB-1997; 97JP-0043143.

```

```

XX
PA (ONOY ) ONO PHARM CO LTD.
XX
PI Fukushima D, Konishi M, Tada H;
XX
DR WPI; 1998-481205/41.
DR P-PSDB; W70387.
XX
PT Membrane polypeptide expressed by human stroma cells, and antibodies
PT recognising it - for treatment of inflammatory and other
PT cytokine-mediated diseases.
XX
PS Disclosure; Pages 40-41; 54pp; Japanese.
XX
CC This is the nucleotide sequence of the human beta-OAF065, used in
CC the method of the invention. The process involves the use of peptides
CC expressed by stroma cells, and its antibodies are used for in the
CC prevention and treatment of inflammatory and other cytokine-mediated
CC diseases such as rheumatism, ulcerative colitis.
XX
SQ Sequence 1496 BP; 388 A; 360 C; 372 G; 376 T; 0 other;

Query Match 75.7%; Score 1290.4; DB 19; Length 1496;
Best Local Similarity 99.9%; Pred. NO. 0;
Matches 1291; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 gggaacgtgagaactctcccaacaataatacatattgataagaagaatggcttttaaaagtgc 60
Db 1 gggaacgtgagaactctcccaacaataatacatattgataagaagaatggcttttaaaagtgc 60
QY 61 tactagaacaagaaacgcttttccactcttttagtattactagctatttgcattgta 120
Db 61 tactagaacaagaaacgcttttccactcttttagtattactagctatttgcattgta 120
QY 121 aagtgacttgtgaacagagactgtagacagcaagaattcagggtatcggtctcggaaact 180
Db 121 aagtgacttgtgaacagagactgtagacagcaagaattcagggtatcggtctcggaaact 180
QY 181 gtgttccctgcaaccagtggtggccaggaatggatgtgtcctaaggaaatgagcttcggct 240
Db 181 gtgttccctgcaaccagtggtggccaggaatggatgtgtcctaaggaaatgagcttcggct 240
QY 241 atggggagagatgcacagtggtgacgtgcggctgcacaggttcaaggagactggggct 300
Db 241 atggggagagatgcacagtggtgacgtgcggctgcacaggttcaaggagactggggct 300
QY 301 tccagaaatgcaagccctgtctggaactgcagtggtgaaaccgttttcagaaggcaaat 360
Db 301 tccagaaatgcaagccctgtctggaactgcagtggtgaaaccgttttcagaaggcaaat 360
QY 361 gttcagccaccagtgatgccatctgcgggactgctgccagatgtttataggaagacga 420
Db 361 gttcagccaccagtgatgccatctgcgggactgctgccagatgtttataggaagacga 420
QY 421 aactgtcggctttcaagacatgagtggtgtgccttgtgagaccctctcctcccttacg 480
Db 421 aactgtcggctttcaagacatgagtggtgtgccttgtgagaccctctcctcccttacg 480
QY 481 aaccgcaactgtgcagcaaggttcaactcgtgaagatgcgctccacggcctccagcccac 540
Db 481 aaccgcaactgtgcagcaaggttcaactcgtgaagatgcgctccacggcctccagcccac 540
QY 541 gggacacgagcgtggtgcgtttatctgcagcgtcttgcggccacgctcctgctgcccctgc 600
Db 541 gggacacgagcgtggtgcgtttatctgcagcgtcttgcggccacgctcctgctgcccctgc 600
QY 601 tcactcctctgtctcatctattgtaagagacagtttatggagaagaacccagctggcttc 660
Db 601 tcactcctctgtctcatctattgtaagagacagtttatggagaagaacccagctggcttc 660
QY 661 tgcgggtcaacagagcattcagtaacaacggctcctgagctgtcgtctcttgacagacctcagc 720
Db 661 tgcgggtcaacagagcattcagtaacaacggctcctgagctgtcgtctcttgacagacctcagc 720

```

Db	661	tgcsgctcagagacattcagtaacaagcgctctgagctgtgtctgacagacctcagc	720
Qy	721	tcacgaatatgccacagagcctgtccagtgccgcgtgtaactcagtgacacotgcyg	780
Db	721	tcacgaatatgccacagagcctgtccagtgccgcgtgtaactcagtgacacotgcyg	780
Qy	781	ggcsgtgcgctgtcccatccatctgtctgtgagagcgctgcagcccacaaccgcga	840
Db	781	ggcsgtgcgctgtcccatccatctgtctgtgagagcgctgcagcccacaaccgcga	840
Qy	841	ctcttggttggtgggtgcattctgcagccagctcttcaggccaagaaaacgcagccagccg	900
Db	841	ctcttggttggtgggtgcattctgcagccagctcttcaggccaagaaaacgcagccagccg	900
Qy	901	ggagatggtgcgacctctcttcggatccctccagccagtcctatctgtggcgagtttccag	960
Db	901	ggagatggtgcgacctctcttcggatccctccagccagtcctatctgtggcgagtttccag	960
Qy	961	atgcctggcctctgtgcagaatcccatgggtgtgacacaatctctttttgtgactctt	1020
Db	961	atgcctggcctctgtgcagaatcccatgggtgtgacacaatctctttttgtgactctt	1020
Qy	1021	atcctgaactcactggagaagacattcattctctcattccagaaacttgaaagctcaacgt	1080
Db	1021	atcctgaactcactggagaagacattcattctctcattccagaaacttgaaagctcaacgt	1080
Qy	1081	cttgattccaatagcagctcaagatttggtgtggtggcgctgtccagtcagctcatt	1140
Db	1081	cttgattccaatagcagctcaagatttggtgtggtggcgctgtccagtcagctcatt	1140
Qy	1141	ctgaaactttacagcagctactgatttatctagatatacaacacacactggtagaatcag	1200
Db	1141	ctgaaactttacagcagctactgatttatctagatatacaacacacactggtagaatcag	1200
Qy	1201	catcaactcaggatgcactaacatgagaagccagctagatcagagagtggcgctatca	1260
Db	1201	catcaactcaggatgcactaacatgagaagccagctagatcagagagtggcgctatca	1260
Qy	1261	tcaccacgcactcagcagctccctccaggaa	1292
Db	1261	tcaccacgcactcagcagctccctccaggta	1292
RESULT 4			
XX	X08689	ID	X08689 standard; cDNA; 1502 BP.
XX	XX	AC	X08689;
XX	XX	DT	27-SEP-1999 (first entry)
XX	XX	DE	Novel nucleotide sequence encoding new protein (Clone AX92_3).
XX	KW	KW	Polynucleotide; protein; nutrition; cytokine; cell proliferation;
XX	KW	KW	cell differentiation; immunostimulation; immunosuppression;
XX	KW	KW	hematopoiesis regulation; tissue growth; activin; inhibin;
XX	KW	KW	chemotaxis; chemokinesis; haemostasis; thrombolysis; receptor;
XX	KW	KW	ligand; anti-inflammatory; tumour suppression; gene therapy; ds.
OS	XX	XX	Homo sapiens.
XX	XX	XX	Key
XX	XX	XX	Location/Qualifiers
XX	XX	XX	51..1322
XX	XX	XX	/tag= a
XX	XX	XX	/product= "Novel protein"
XX	XX	XX	WO9920644-A1.
XX	XX	XX	29-APR-1999.
XX	XX	XX	16-OCT-1998; 98WO-US22034.
XX	XX	XX	18-OCT-1997; 97US-0955557.
XX	XX	XX	PR

(GEMY) GENETICS INST INC.

Agostino MJ, Bowman MR, Evans C, Jacobs K, Lavallie ER;
McCoy JM, Merberg D, Racie LA, Spaulding V, Treacy M;
WPI: 1999-288272/24.
P-PSDB: W85724.

New polynucleotides encoding secreted human proteins

Claim 32: Page 116; 136pp; English.

The new human secreted proteins are encoded by polynucleotides obtained from human placenta, adult testes, fetal kidney, fetal brain, adult brain, adult brain and adult blood cDNA libraries. The polynucleotides and proteins are predicted to have biological activities which would make them suitable for treating, preventing or ameliorating medical conditions in humans and animals. Suggested activities include nutritional activity, cytokine and cell proliferation/differentiation activity, immune stimulating (e.g. as vaccines) or suppressing activity, haematopoiesis regulating activity, tissue growth activity, activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, receptor/ligand activity, anti-inflammatory activity, cadherin/tumour invasion suppressor activity, and tumour inhibition activity. The polynucleotides are also stated to be useful for gene therapy. The sequences are identified by a secretory leader sequence motif in the polynucleotide and it is thought that the encoded proteins have biological activity by virtue of their secreted nature. This clone was designated AX92_3. A probe for this clone is described in X08704.

Sequence 1502 BP; 388 A; 362 C; 375 G; 377 T; 0 other;

Query Match 75.6%; Score 1288.8; DB 20; Length 1502;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1290; Conservative 0; Mismatches 2; Indels 0; Gaps

Qy 1 ggggaactgagaactctccaacaataatacatattgataagaaagatggtttaaagatgc 60
Db 7 ggggaactgagaactctccaacaataatacatattgataagaaagatggtttaaagatgc 66
Qy 61 tactagaacaagaaagaaacgtttttcactcttttagtattactaggctattgtcattgta 120
Db 67 tactagaacaagaaagaaacgtttttcactcttttagtattactaggctattgtcattgta 126
Qy 121 aagtgacttgtgaacaggagactgttagacagacaagaattcagggtatcggtctggaact 180
Db 127 aagtgacttgtgaacaggagactgttagacagacaagaattcagggtatcggtctggaact 186
Qy 181 gtgttcctctgaaccagtgtgggccaggagcattgagttgtctagggaattgtggtctcggt 240
Db 187 gtgttcctctgaaccagtgtgggccaggagcattgagttgtctagggaattgtggtctcggt 246
Qy 241 atggggaggatgcacagtgtgtgacgtgcgcggctgcacaggttcaaggagactggggct 300
Db 247 atggggaggatgcacagtgtgtgacgtgcgcggctgcacaggttcaaggagactggggct 306
Qy 301 tccagaatccaagccctgtctgagactgcagctggtgacacgctttcagaaggcaatt 360
Db 307 tccagaatccaagccctgtctgagactgcagctggtgacacgctttcagaaggcaatt 366
Qy 361 gttcagccaccagtgtatgcattctcgggagactgcttgcaggattttataggaaagcga 420
Db 367 gttcagccaccagtgtatgcattctcgggagactgcttgcaggattttataggaaagcga 426
Qy 421 aacttgtgggtttcagaacaatggagtggtgtgctgtgagagacctctcctctacg 480
Db 427 aacttgtgggtttcagaacaatggagtggtgtgctgtgagagacctctcctctacg 486
Qy 481 aaccgcactgtgcccagacaaggtcaacctctgaagatctgcgtccagcgtctcagcccac 500

Db 267 aggatgcagtgctggtgctggtgacaggttcaagaggactggggtctccaga 326
Qy 307 aatgcagaacctgtctgactgcagtggtgaaacgcttttcagaagcaaatgtttcag 366
Db 327 aatgcagaacctgtctgactgcagtcgagtcgggaaacgcttttcagaagcaaatgtttcag 386
Qy 367 ccacagtgatgccatctgcgggactgcttgccaggattttataggaagacgaaacttg 426
Db 387 ccacagtgatgccatctgcgggactgcttgccaggattttataggaagacgaaacttg 446
Qy 427 tcgggtttcaagacatgagtggtgcttcttggaacccctctctctcttcttaccgaaccgc 486
Db 447 tcgggtttcaagacatgagtggtgcttcttggaacccctctctctcttcttaccgaaccgc 506
Qy 487 actgtgcagaaagtcacacctgcagatgcgctccacgctccacgctccacgacgggaca 546
Db 507 actgtgcagaaagtcacacctgcagatgcgctccacgctccacgctccacgacgggaca 566
Qy 547 cggcgctggctgaccttctctgcagcgtctggtgccacgctcgtggtgccctgctcatcc 606
Db 567 cggcgctggctgaccttctctgcagcgtctggtgccacgctcgtggtgccctgctcatcc 626
Qy 607 tctgtcatctatgtgaagacagtttatggagaagaacccagctggtctctgcggt 666
Db 627 tctgtcatctatgtgaagacagtttatggagaagaacccagctggtctctgcggt 686
Qy 667 cacaggacattcagtacaaacgctctgactgtcgtctgtcttgacagacctcagctccacg 726
Db 687 cacaggacattcagtacaaacgactgactgtcgtctgtcttgacagacctcagctccacg 746
Qy 727 aatagccacagagcctgctgccagtgccgcgtgactcagtcagacctgcgggcccgg 786
Db 747 aatagccacagagcctgctgccagtgccgcgtgactcagtcagacctgcgggcccgg 806
Qy 787 tgcgttgcctccatccatgtgctgtgagggagcctgcagcccaacccggcgactcttg 846
Db 807 tgcgttgcctccatccatgtgctgtgagggagcctgcagcccaacccggcgactcttg 866
Qy 847 gttgtggggtgctattctcagccagcttctcaggcaagaacagcagccagccggggaga 906
Db 867 gttgtggggtgctattctcagccagcttctcaggcaagaacagcagccagccggggaga 926
Qy 907 tgggtccgactttcttcggatccctccacgagctcctatctgtgaggttttcagatgcct 966
Db 927 tgggtccgactttcttcggatccctccacgagctcctatctgtgaggttttcagatgcct 986
Qy 967 ggcctctgatgcagaatcccatgggtgtgacaaacatctcttttctgactcttactctg 1026
Db 987 ggcctctgatgcagaatcccatgggtgtgacaaacatctcttttctgactcttactctg 1046
Qy 1027 aactcactggagaagacattctctcaatccgaaccttgaaagctcaacgctcttctgg 1086
Db 1047 aactcactggagaagacattctctcaatccgaaccttgaaagctcaacgctcttctgg 1106
Qy 1087 attcaaatagcagtcgaagatttgggtgtggtggggtgttccagtcagctctcttctgaaa 1146
Db 1107 attcaaatagcagtcgaagatttgggtgtggtggggtgttccagtcagctctcttctgaaa 1166
Qy 1147 actttacagcagctactgatttatctagatataaacaacacatggtagaaatcagatcaa 1206
Db 1167 actttacagcagctactgatttatctagatataaacaacacatggtagaaatcagatcaa 1226
Qy 1207 ctccagatgcactaaactatgagaaccagctagatcaggagagtggtgcgtctatccacc 1266
Db 1227 ctccagatgcactaaactatgagaaccagctagatcaggagagtggtgcgtctatccacc 1286
Qy 1267 cagccactcagacgtccctccaggaa 1292
Db 1287 cagccactcagacgtccctccaggta 1312

RESULT 6

X59346
ID X59346 standard; cDNA; 987 BP.
XX
AC X59346;
XX
DT 20-SEP-1999 (first entry)
XX
DE Human NTR-5 cDNA.
XX
KW NTR-5; human; receptor; signal transduction; bone; muscle;
KW diagnosis; therapy; ss.
XX
OS Homo sapiens.
XX
PH Key Location/Qualifiers
FT sig_peptide 1..57
FT mat_peptide /*tag= a
FT /*tag= b
XX
XX WO9933967-A2.
XX
XX 08-JUL-1999.
XX
XX 28-DEC-1998; 98WO-US27688.
XX
XX 29-DEC-1997; 97US-0068925.
XX
XX (REGE-) REGENERON PHARM INC.
XX
XX Valenzuela DM;
XX
XX WPI: 1999-419102/35.
XX
XX P-PSDB; Y06400.
XX
XX New mammalian receptor NTR-5 polypeptides
XX
XX Claim 2a; Page 21-22; 27pp; English.
XX
XX This is the claimed coding region of human cDNA encoding a novel
XX receptor, designated NTR-5 (see Y06400), that shows homology to
XX osteoprotegerin and tumour necrosis factor receptor. The cDNA was
XX isolated from a heart cDNA library using mouse NTR-5 cDNA (see
XX X59345) as probe. Homology to osteoprotegerin suggests that NTR-5
XX is involved in the regulation of bone mass, and may be useful for
XX regulating development, proliferation and death of osteoblast or
XX osteoclast cells or for regulating muscle metabolism, and that it
XX may be implicated in muscle diseases or disorders. A host-vector
XX system for production of NTR-5 is claimed. NTR-5 polypeptides can
XX be used as immunogens and in screening assays to identify NTR-5
XX ligands, agonists and antagonists. The NTR-5 polynucleotide is
XX useful as a diagnostic tool, and as a source of probes and primers.
XX The invention also provides for diagnostic and therapeutic methods
XX based on the interaction of NTR-5 and agents that initiate signal
XX transduction through binding to NTR-5.
XX
XX Sequence 987 BP; 220 A; 251 C; 278 G; 238 T; 0 other;

Query Match 49.0%; Score 835.6; DB 20; Length 987;
Best Local Similarity 99.5%; Pred. No. 3.6e-251;
Matches 838; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 45 atggcgttttaaaagtctactagaacaagaaaacgcttttcttcttattacta 104
Db 1 atggcgttttaaaagtctactagaacaagaaaacgcttttcttcttattacta 60
Qy 105 ggctatttgtcatgtataaagtactgtgaaacagagactgtagacagaaatcagg 164
Db 61 ggctatttgtcatgtataaagtactgtgaaacagagactgtagacagaaatcagg 120
Qy 165 gatcggctcggaaactgtgttccctgcaccagtgctggccaggatgagtgctaaag 224

Db 121 gatcggtgtgaaactgtgttccctcgcaaccagtggtggccaggcatggaggtgtctaaag 180
QY 225 gaatgtggcttcgcttatggagagatgcacagtgtgtgacgtgcggtcgacaggttc 284
Db 181 gaatgtggcttcgcttatggagagatgcacagtgtgtgacgtgcggtcgacaggttc 240
QY 285 aaggaggactggggcttccagaaatgcaagccctgtcttgactgcgcagtggtgaaccgc 344
Db 241 aaggaggactggggcttccagaaatgcaagccctgtcttgactgcgcagtggtgaaccgc 300
QY 345 ttccagaaggcaaatgttccagccaccagtgatgccatctgcgggactgcttgccaggga 404
Db 301 ttccagaaggcaaatgttccagccaccagtgatgccatctgcgggactgcttgccaggga 360
QY 405 ttctatagggaagcgaactgtcgcccttccagagacatgagtggtgccccttctgagac 464
Db 361 ttctatagggaagcgaactgtcgcccttccagagacatgagtggtgccccttctgagac 420
QY 465 cctcctcctcttaccgaaccgcactgtgccagcaaggtcaacctcgtgaagatcgcgtcc 524
Db 421 cctcctcctcttaccgaaccgcactgtgccagcaaggtcaacctcgtgaagatcgcgtcc 480
QY 525 acggctccagccacgggacacggcgctggctgcccgttatctgcagcgctctgcccacc 584
Db 481 acggctccagccacgggacacggcgctggctgcccgttatctgcagcgctctgcccacc 540
QY 585 gtccgtgcccctgcctcatcctctgtctatctatctattgtaagagacagtttatggagaag 644
Db 541 gtccgtgcccctgcctcatcctctgtctatctatctattgtaagagacagtttatggagaag 600
QY 645 aaaccagctggtctctgcggtcacaggacattcagtcacacggctcgtgagctgctggt 704
Db 601 aaaccagctggtctctgcggtcgaggacattcagtcacacggctcgtgagctgctggt 660
QY 705 ctgtgagacactcagctccacgaatatgccacagagcctgctgcagtgcccctgtgac 764
Db 661 ttgtgagacactcagctccacgaatatgccacagagcctgctgcagtgcccctgtgac 720
QY 765 tcagtgacagcctgcggcgctgctgtctccatccatgctgctgagggagcctgc 824
Db 721 tcagtgacagcctgcggcgctgctgtctccatccatgctgctgagggagcctgc 780
QY 825 agccccaaacccggcagctctgtgtgtgggggtgcatctctgcagccagctcttcagggaaga 884
Db 781 agccccaaacccggcagctctgtgtgtgggggtgcatctctgcagccagctcttcagggaagg 840
QY 885 aa 886
Db 841 aa 842

RESULT 7
X23413
ID X23413 standard; DNA; 1678 BP.
XX
AC X23413;
XX
DT 18-JUN-1999 (first entry)
XX
DE Mouse mAPO4-alpha (long) DNA.
XX
KW Tumour necrosis factor receptor; signal transducer molecule; TNF; APO4;
developmental abnormality; gestational abnormality; prostate cancer;
APO6; APO8; APO9; TNRL-1; TNRL-3; diagnosis; treatment; therapy; disease;
cytoplasmic domain; immunogen; antibody preparation; breast carcinoma;
apoptosis; mouse; mAPO4-alpha; ss.
XX
OS Mus sp.
XX
FH Key
FT CDS 72..1322
FT /*tag= a
FT /product= "mAPO4-alpha"

XX WO9911791-A2.
PN 11-MAR-1999.
PD
XX
PF 04-SEP-1998; 98WO-US18393.
XX
PR 05-SEP-1997; 97US-0924634.
XX
PA (UNIW) UNIV WASHINGTON.
XX
PI Chaudhary PM;
XX
DR WPI; 1999-205191/17.
XX
PT P-PSDB; W93579.
XX
PT New Tumor Necrosis Factor family receptor polypeptides and ligands -
developmental or gestational abnormalities
XX
PS Example IV; Fig 7A; 156pp; English.
XX
CC This invention describes isolated Tumor Necrosis Factor (TNF) family
receptor polypeptides: APO4, APO6, APO8 and APO9 or their active
fragments, and isolated TNF related ligands 1 and 3 (TNRL1 and TNRL3) or
their active fragments. APO4 is useful for diagnosing prostate cancer
by determining levels of APO4 in an individual. Prostate cancer can also
be treated using APO4 selective binding agents linked to a therapeutic
moiety. APO4 polypeptides are also useful for identifying selective
binding agents, useful in diagnosis/treatment of disease by binding of
agents to the polypeptide/active fragment which is extracellular, or
expressed on the cell surface. The binding is preferably performed in
vivo. APO4 polypeptides/ active fragments are also useful for screening
for agonists and antagonists by binding and observing the changer in APO4
activity. Effective pharmacological agents useful in diagnosis or
treatment of disease are also identified using APO4 polypeptides/active
fragments and APO4 signal transducer molecules that specifically interact
with a cytoplasmic domain of APO4 and detecting a change in level of APO4
activity. The method is performed in vivo or in vitro. APO polypeptides
are all useful as immunogens for preparing antibodies. APO4 is also
useful for diagnosis/treatment of developmental or gestational
abnormalities. APO8 was transfected to human breast carcinoma cell line
MCF-7, and induced apoptosis.
XX
SQ Sequence 1678 BP; 371 A; 467 C; 466 G; 374 T; 0 other;

Query Match 48.3%; Score 823; DB 20; Length 1678;
Best Local Similarity 71.6%; Pred. NO. 4.5e-247;
Matches 1191; Conservative 0; Mismatches 435; Indels 37; Gaps 7;

QY 22 aataaatacatttgataagaagaatggctttaaaagtctactagacaagaagaaacgt 81
Db 49 aataaacaagtttggtagagccatggcactcaaggctcctcctcacacagagcgtgc 108
QY 82 ttttctactcttttagtattactaggctatttgcattgaagtgcattgtgaacacggag 141
Db 109 tcttcgctgccattctcttctactccacctggcagtgataaaggagtgctgcaaacggag 168
QY 142 actgtagacagcaagaattcagggtgcgttctggaactgtgttccctgcacaccagtg 201
Db 169 attgcaggcagcaggattcaggatcgatctggaactgtgtcctctgcaaacagtcg 228
QY 202 ggcacagcagtgagtgcttaaggaatggtcctcgccatggggagagcagcagtg 261
Db 229 gacctggcatggagtgctccaaggaatggtcctcgccatggggagagtgatgcacagtg 288
QY 262 tgacgtgcggcgtgcacaggttcaaggagcagctggggtctccagaaatgcagccctgtc 321
Db 289 tgccctgcaggcgcaccggttcaaggagactggggtttccagaagtgaagccatgtg 348
QY 322 tggactgcgcagtggtgaaccgctttcagaaggcgaattgttcagccaccagtgatgcca 381

Db 349 cggactgtgcgtgtgaaccctttcagaggccaaactgtctcacacaccagtgatgctg 408
Qy 382 tctgcgggagactgctgcagagattttataggaagacagaaactgtgcgctttcaagaca 441
Db 409 tctgcgggagactgctgcagagattttaccggaagacacaaactgtgttttcaagaca 468
Qy 442 tggagtgctgctgtgagagaccctctccctctagaaacgcgactgtgcagcaagg 501
Db 469 tggagtgctgctgtgcggagaccacactccctccctagaaacacactgtaccagcaagg 528
Qy 502 tcaacctgtgaagatcgctgcagcgcctccagccacgcgagacgcgctggtgcgcg 561
Db 529 tgaacctgtgaagatcctccacgctctccagcctccgagcagcgctggtgcgcg 588
Qy 562 ttaactgcagcgtctggccacgcctcctgctgctgcctgcctcctcctgtgctcatt 621
Db 589 tcaactgcagcgtctggccacgcggtgctgctgcctgcctcctcctgtgctcatt 648
Qy 622 gtaagagacagttttgagagaagaacccagctgtctctgcgttcacagagacattcagt 681
Db 649 gcaagaggcagttcatgagagaagaacccagctgtctctgcgttcacagagacattcagt 708
Qy 682 acaacgctctgagctgctgtctgttgcagacacctcagctccacgaataatgccacagag 741
Db 709 acaatggctctgagctgtcatgctgttgcacagcctcgcgcgcagctgtgccatagag 768
Qy 742 cctgctgcagtcgcccgcgctgactcagtgacagacctgcgcccgcgctgtgcctccat 801
Db 769 catgctgcagtatcacgggactcagcccacatgtatggcctgttcaactgattccgt 828
Qy 802 ccatgctgtgagagagcctgcagccccacccgcgactctgtgtgtgggtgcatt 861
Db 829 cctgtgtgtgagagagccgcgactgtgctgcgcgagctgtgctgtgtgggtgcgtt 888
Qy 862 ctgcagcagtttccaggaagaacagcagccgcgagcgggagatgtgcgcgactttct 921
Db 889 ccccaactaccctccaggaagaacccgcgctctgtgggaacacgagtgcagcctct 948
Qy 922 tcggatccctcagcagtcctcctgtgctgagtttccagatcctgcctgctgagcaga 981
Db 949 tgggtctgttcccgcttccatctgcgcggagttttctgagtccttgccttgcgtgagcaga 1008
Qy 982 atccatgggtgtgacacatctcttttgcactcttctgcactcactcactgcagag 1041
Db 1009 atcctctggcggtg---acagctctctgtgactcttctgcactcactcactgcagag 1065
Qy 1042 acattcattctcaatcagacactgaaagctcaacgctcttgcatttgcataatagcagtc 1101
Db 1066 ataccaattccctcaatcccgaaaacgaaagcacagcactctctgattccagtgcgcc 1125
Qy 1102 aagatttggtgtgggtgttcagctccagctcctcctcctgaaactttacagcagcta 1161
Db 1126 aggatctggctggagcagctgcttagagtcttcttgggaattttcagaatctactgact 1185
Qy 1162 ctgatttactagatataacacacactggtgaatcagcatcaactcaggatgactaa 1221
Db 1186 cacctagacatggtgacactggtacagctggtgagcagcgtagctcaggatgctcaaa 1245
Qy 1222 cctagagaagcagctagatcagagagtgcgctatctccaccagcagcactcagact 1281
Db 1246 ggaactcagcgaagggctgggagacagagggaaacccctgaatctagccatgccacag 1305
Qy 1282 cctccaggaagcttaagaacactgcttcttctcagtagaagcgtgtgctggaaacca 1341
Db 1306 ccttcagagatcctgaag---gccatctctcagctgaggtgtggtctggacac- 1360
Qy 1342 aagagtactccttctgttagcttattgagctagcagctgtggacccttgcactgtcttgg 1401
Db 1361 -----gctgtgtaggctacagactgagcagctgtt-----gtgctcggaa 1404
Qy 1402 gcaaaaaataactgaacaaactgacggcatttgaagcctttcagcagctgtccttga 1461
Db 1405 gcaaaaaataactgaacaaactgacaaacttccatcttccagcactgactga 1464

Qy 1462 gccagaccagctgaagctgaacctcaatgaatacaagaagaaagactcca----ggccg 1517
Db 1465 gccagaccagctgaagctgaacctcaatgaatacaagaagaaagacttgactgtagcgcg 1524
Qy 1518 actcatgatactctgactcttcttctacatgagaagcttcttgcacacaaagtgacttca 1577
Db 1525 gctctgggacatgtcttcttctccaaagcgaacacacttagctggggcca-----atttga 1579
Qy 1578 aagacggatgggtgagctggcagcctatgagatttggacataatacaagaagaaagacagaa 1637
Db 1580 aggacccatgggtgaatgtgctgctgtgaacttggggcagca-----ggacccagc 1635
Qy 1638 tgccctcatgcttatttctcatgtgtgtgtgtgttttacaagac 1680
Db 1636 ctggctccttcttattgtccacggtgaatgtgtgtgttttacaagac 1678

RESULT 8
X23414
ID X23414 standard; DNA; 886 BP.
XX
AC X23414;
XX
DT 18-JUN-1999 (first entry)
XX
DE Mouse mAPO4-alpha (short) DNA.
XX
KW Tumour necrosis factor receptor; signal transducer molecule; TNF; APO4;
developmental abnormality; gestational abnormality; prostate cancer;
APO6; APO8; TNRL-1; TNRL-3; diagnosis; treatment; therapy; disease;
cytoplasmic domain; immunogen; antibody preparation; breast carcinoma;
apoptosis; mouse; mAPO4-alpha; ss.
OS Mus sp.
XX
FH Key Location/Qualifiers
CDS 72..716
FT /*tag= a
FT /product= "mAPO4-alpha short"
XX
PN WO9911791-A2.
XX
PD 11-MAR-1999.
XX
PF 04-SEP-1998; 98WO-US18393.
XX
PR 05-SEP-1997; 97US-0924634.
XX
PA (UNIW) UNIV WASHINGTON.
XX
PI Chaudhary PM;
XX
DR WPI; 1999-205191/17.
DR P-PSDB; W93580.
XX
PT New Tumour Necrosis Factor family receptor polypeptides and ligands -
useful for diagnosis and treatment of prostate cancer and
developmental or gestational abnormalities
XX
PS Example IV; Fig 7B; 156pp; English.
XX
CC This invention describes isolated Tumour Necrosis Factor (TNF) family
receptor polypeptides: APO4, APO6, APO8 and APO9 or their active
fragments, and isolated TNF related ligands 1 and 3 (TNRL1 and TNRL3) or
their active fragments. APO4 is useful for diagnosing prostate cancer
by determining levels of APO4 in an individual. Prostate cancer can also
be treated using APO4 selective binding agents linked to a therapeutic
moiety. APO4 polypeptides are also useful for identifying selective
binding agents, useful in diagnosis/treatment of disease by binding of
agents to the polypeptide/active fragment which is extracellular, or
expressed on the cell surface. The binding is preferably performed in
vivo. APO4 polypeptides/ active fragments are also useful for screening

CC for agonists and antagonists by binding and observing the changer in APO4
CC activity. Effective pharmacological agents useful in diagnosis or
CC treatment of disease are also identified using APO4 polypeptides/active
CC fragments and APO4 signal transducer molecules that specifically interact
CC with a cytoplasmic domain of APO4 and detecting a change in level of APO4
CC activity. The method is performed in vivo or in vitro. APO polypeptides
CC are all useful as immunogens for preparing antibodies. APO4 is also
CC useful for diagnosis/treatment of developmental or gestational
CC abnormalities. APO8 was transfected to human breast carcinoma cell line
CC MCF-7, and induced apoptosis.

XX SQ Sequence 886 BP; 204 A; 245 C; 247 G; 190 T; 0 other;

Query Match 27.0%; Score 460.8; DB 20; Length 886;
Best Local Similarity 81.9%; Pred. NO. 6.4e-134;
Matches 531; Conservative 0; Mismatches 117; Indels 0; Gaps 0;

QY 22 aataatacatttgataagaagaatggcttttaaaagtgtactagaacaagagaaacgt 81
DB 49 aataaacacgtttggtgagagccatggcactcaaggtctctacacaggaagcgtgc 108

QY 82 ttctacactcttagtattactaggctatttgcataagtgacttgcgaacaggag 141
DB 109 tcttcgtgcattctctctactccacctggcattgaaagtgaagtgagtggaacggag 168

QY 142 actgtagacagcaagaattcaggatgcgtctgaaactgttccctgcaacagtggtg 201
DB 169 attgcaggccgaggaattcaagatgcgtctgaaactgttccctgcaacagtggtg 228

QY 202 ggcaggcatggagttgtctaaagaaatgtgcttcggctatgggagatgcacagtggtg 261
DB 229 gaactggcagtggtgtccaaagaaatgtgcttcggctatgggagatgcacagtggtg 288

QY 262 tgactgcccggctgcacaggttcaaggaggaactggggcttccagaaatgcgaacccctgtc 321
DB 289 tgccctgcaggccgcacgggttcaagaaagactggggtttccagaaagtgaagccatgtg 348

QY 322 tgactgcgcagtggtgaacgcgttttcagaaaggcacaattgttcagccacagtgatgcca 381
DB 349 cggactgtgcgtgtgaaacggttttcagaaaggcacaactgttcacacacagtgatgctg 408

QY 382 tctgcggggactgcttgcaggatgtttataggaaagacgaactgtgctgcttccagaca 441
DB 409 tctgcggggactgcttgcaggatgtttaccgcgaagacaaactggtggttttccagaca 468

QY 442 tggagtgtgcttggagaccctctctctctacgaacgcgactgtgcccaggaagg 501
DB 469 tggagtgtgcttggagaccctctctctctacgaacgcgactgttaccagcaagg 528

QY 502 tcaacctgtgaagatcgctccacggcctccagccacgggacacggcgtggtgccc 561
DB 529 tgaacctgtgaagatcgctccacggcctccagccacggcgtggtgccc 588

QY 562 ttatctgcagcgtctgcccacgcgtctctggtgcccctgctcattctctgtgtcatctatt 621
DB 589 tcatctgcagcgtctgcccacgcgtctggtgcccctgctcattctctgtgtcatctact 648

QY 622 gtaagagacagatttatggagaagaacccacagctggctctctgctggtgtaac 669
DB 649 gcaagagcagttcatggagaagaacccacagctgtaagctcccatccc 696

RESULT 9

X24977

ID X24977 standard; cDNA; 942 BP.

XX AC X24977;

XX AC X24977;

DT 05-JUL-1999 (first entry)

XX Mouse TRAIN-R (long form) cDNA.

DE

XX

TRAIN-R; receptor; mouse; tumour necrosis factor receptor;
agonist; antagonist; cancer; immunological disease; therapy;
cytostatic; ss.

OS Mus musculus.

FH Key Location/Qualifiers

FT CDS 101..745

FT /*tag= a

XX W09913078-A1.

XX 18-MAR-1999.

XX 11-SEP-1998; 98WO-US19030.

XX 06-MAY-1998; 98US-0084422.

PR 12-SEP-1997; 97US-0058631.

XX (BIOJ) BIOGEN INC.

XX Hession C, Tschopp J;

XX WPI; 1999-229238/19.

DR P-PSDB; W98145.

XX New cysteine-rich tumor necrosis factor receptor

XX Claim 1; Page 26-27; 30pp; English.

CC The present sequence encodes a novel murine cysteine-rich tumour
CC necrosis factor receptor family member termed TRAIN-R (long form)
CC (see W98145). Murine TRAIN-R is expressed at high levels in brain
CC and lung, and at lower levels in liver, skeletal muscle and kidney.
CC Cell death can be induced by administering an agent capable of
CC inhibiting the binding of TRAIN-R to its ligand. A claimed method
CC of treating, or reducing, the advancement, severity or effects of
CC an immunological disease in a mammal comprises administering a
CC pharmaceutical composition which comprises a TRAIN-R blocking agent,
CC e.g. soluble TRAIN-R (see also W98144). TRAIN-R can be fused to an
CC immunoglobulin molecule to produce a fusion protein which may be
CC targeted to various sites. It can be used in binding assays, and
CC to identify antagonists and agonists. Anti-TRAIN-R receptor
CC antibodies can be used to reduce the severity of an immune response
CC or to treat cancer. TRAIN-R blocking agents can be used to reduce
CC the severity or effects of an immunological disease (all claimed).

XX SQ Sequence 942 BP; 219 A; 264 C; 258 G; 200 T; 1 other;

Query Match 27.0%; Score 460.8; DB 20; Length 942;

Best Local Similarity 81.9%; Pred. NO. 6.7e-134;

Matches 531; Conservative 0; Mismatches 117; Indels 0; Gaps 0;

QY 22 aataatacatttgataagaagaatggcttttaaaagtgtactagaacaagagaaacgt 81

DB 78 aataaacacgtttggtgagagccatggcactcaaggtctctacacaggaagcgtgc 137

QY 82 ttctcactcttttagtattactaggctatttgcataagtgacttgcgaacaggag 141

DB 138 tcttcgtgcattctctctactccacctggcattgaaagtgaagtgagtggaacggag 197

QY 142 actgtagacagcaagaattcaggatgcgtctgaaactgttccctgcaacagtggtg 201

DB 198 attgcaggccaggaattcaagatgcgtctgaaactgttccctgcaacagtggtg 257

QY 202 ggcaggcatggagttgtctaaagaaatgtgcttcggctatgggaggatgcacagtggtg 261

DB 258 gacctggcatggagttgtcccaagaaatgtgcttcggctatgggaggatgcacagtggtg 317

QY 262 tgactgtccggctgcacagattcaaggaggactggggcttccagaaatgcgaacccctgtc 321

DB 318 tgccctgcaggccgaccggttcaagaaagactggggtttccagaaagtgaagccatgtg 377

```
Qy 322 tggactgcagtggtgaaccgcttttcagaaggaacaaattgttcagccaccagtgatgcca 381
      ||||| || ||||| ||||| ||||| || || || || || || |||||
Db 378 cggactgctgctggtgaaccgcttttcagaaggccaactgctcacacacagtgatgctg 437
Qy 382 tctcgagggaactgctgcagagattttataggaagacgaaactgtgcgtttcaagaca 441
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 438 tctcgagggaactgctgcagagattttaccggaagacaaactgtgtgtttcaagaca 497
Qy 442 tggagtgtgcctgtgagacccctcctcctccttccttcagaaacgacactgtgccagaag 501
      ||||| ||||| || ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 498 tggagtgtgcctgtgcagacccactcctccttcagaaacacactgtaccagaag 557
Qy 502 tcaactgtgaagatcgctgcagcgcctccagcccgacacgacgctgctgctgcgcg 561
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 558 tgaacctgtgaagatcctccaccgctctccagccctcggaacgacgctgctgcgcg 617
Qy 562 ttatctgagcgtctgcccacgcctcctgctggtgcctgctcctcctcctcctccttatt 621
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 618 tcatctgcaagtctggtgccacggtgctgctgcgcctgctcctcctcctcctcctcctact 677
Qy 622 gtaagagacagttatgagaagaacacacagctggtcctcgtcgtcac 669
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 678 gcaagaggcagttatgagaagaacacacagctgtaagctccctccc 725

RESULT 10
X87394
ID X87394 standard; cDNA; 981 BP.
XX
AC X87394;
XX
DT 08-OCT-1999 (first entry)
XX
DE Mouse STRIFE1 (Tango 127a) cDNA.
XX
KW STRIFE1; Tango 127a; mouse; tumour necrosis factor receptor;
KW sepsis; circulatory collapse; toxic shock; infection;
KW immune disease; autoimmune disease; alcohol-induced hepatitis;
KW inflammation; graft versus host pathology; cancer; tumour;
KW cerebral malaria; multiple sclerosis; diagnosis; therapy; ss.
XX
OS Mus musculus.
XX
FH Key Location/Qualifiers
FT 5'UTR 1..106
FT /*tag= a
FT /note= "an isolated nucleic acid molecule
FT comprising this region of the sequence is
FT specifically claimed in Claim 3"
FT CDS 107..751
FT /*tag= b
FT /product= STRIFE1
FT /note= "an isolated nucleic acid molecule
FT comprising the coding region is
FT specifically claimed in Claim 2"
FT sig_peptide 107..193
FT /*tag= c
FT mat_peptide 194..748
FT /*tag= d
FT /note= "an isolated nucleic acid molecule
FT comprising the mature protein coding region
FT is specifically claimed in Claim 14"
FT 3'UTR 752..981
FT /*tag= e
FT /note= "an isolated nucleic acid molecule
FT comprising this region of the sequence is
FT specifically claimed in Claim 4"
XX
PN W09937818-AL.
XX
PD 29-JUL-1999.
XX
```

```
PF 27-JAN-1999; 99WO-US01679.
XX
PR 27-JAN-1998; 98US-0014195.
XX
PA (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
XX
PI Busfield SJ;
XX
DR WPI: 1999-458707/38.
XX
P-PSDB: Y06522.
XX
PT New STRIFE1 and STRIFEII polypeptides, proteins and nucleic acid
XX molecules useful for modulating TNFR associated disorders
XX
PS Claim 3; Fig 1A-B; 119pp; English.
XX
CC This is the nucleotide sequence of mouse STRIFE1 (also called
CC Tango 127a or T127a) cDNA. It encodes a protein (see Y05422) that
CC belongs to the tumour necrosis factor receptor (TNFR) superfamily.
CC 2 Splice forms of murine STRIFE have been identified, one that is
CC predicted to be membrane-bound (STRIFE1) and one that is secreted
CC (STRIFE2, see Y06523). STRIFE was identified as a TNFR homologue
CC by a computer-based search of public EST databases. The invention
CC provides STRIFE1 and STRIFE2 polynucleotides and polypeptides, as
CC well as fusion proteins, antigenic peptides and antibodies. It
CC also provides expression vectors, host cells and transgenic
CC animals, as well as diagnostic, screening and therapeutic methods.
CC STRIFE I and STRIFE II may play a role in mediating inflammatory,
CC immune and host defense functions and may play a role in various
CC neoplastic disease states. They may be useful as targets for
CC developing novel diagnostic and therapeutic agents for TNF- and
CC TNFR-associated disorders. Examples include sepsis syndrome,
CC circulatory collapse and shock resulting from bacterial infection,
CC acute and chronic parasitic or infectious processes, acute and
CC chronic immune and autoimmune pathologies, alcohol-induced
CC hepatitis, chronic inflammatory pathologies, vascular inflammatory
CC pathologies, graft-versus-host pathology, malignant pathologies
CC involving TNF-secreting tumors, cerebral malaria and multiple
CC sclerosis.
XX
SQ Sequence 981 BP; 247 A; 270 C; 264 G; 200 T; 0 other;

Query Match 27.0%; Score 460.8; DB 20; Length 981;
Best Local Similarity 81.9%; Pred. No. 6.8e-134;
Matches 531; Conservative 0; Mismatches 117; Indels 0; Gaps 0;

Qy 22 aataaatacattgataagaagaatggcttttaaaagtgtctactagaacaagaacagcgt 81
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 84 aataaacacgtttgtgagagccatggcactcaaggtcctactctacacagcaggtgc 143
Qy 82 ttttcactcttttagtattactaggctattgtcatgataaagtgtgaaacaggag 141
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 144 tcttcgctgccattctctctcctcctccctggcagtgataaagtgtgcgaaccggag 203
Qy 142 actgtagacagcaagaattcagggaatcgctcgtggaactgtgttccctgcaaccagtggtg 201
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 204 attgcaggcagcaggaattcaaggatcgatctcggaactgtgtcctctgcaaacagtgctg 263
Qy 202 ggcacaggcatggagtgtgtaaggaaatgtgcttcggtatggggagagatgcacagtggtg 261
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 264 gacctggcatggagttgtccaaggaaatgtggttcgctatggggagatgcacagtggtg 323
Qy 262 tgacgtgcgcgtgcacaggttcaaggagactggggttccagaaatgcagaccctgtc 321
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 324 tgcctgcagcgccgcaccgggttcaaggagactggggttccaggaagtgtacagcatgtg 383
Qy 322 tggactgcgcagtggtgaaccgctttcagaagcgaataattgttcagccaccagtgatgcca 381
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 384 cggactgtgctgtgaaccgctttcagagggccaactgtctcacacacagtgatgctg 443
Qy 382 tctgcggggaactgcttgccaggattttataggaagaacgaaactgtcgttccaagaca 441
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
```

Db 444 tctgcgggagctcctgcaggattttaccggaagaccacaaactggtgttttcaagaca 503
 QY 442 tggagtgctgtgtgagaccctctctctcttaccgaacgcactgtgccagaag 501
 Db 504 tggagtgctgtgtgagaccacccctctctcttaccgaacgcactgtgccagaag 503
 QY 502 tcaacctgtgaagatcgtgcctccacggcctccagccacgggacacggcgctgctgcg 501
 Db 564 tgaacctgtgaagatcctctccacgctctccagccctccggaacggcgctgctgcg 623
 QY 562 ttatctgcagcgtctgagccacgctcctgctgagccctctctctctctctctctatt 621
 Db 624 tcatctgcagctgtgagccacgctgctgctgagccctctctctctctctctctatt 683
 QY 622 gtaagagacatttatggagaagaaacccagctgctctgcggtcac 669
 Db 684 gcaagggcagttcatggagaagaaacccagctgtaagctcccatccc 731
 RESULT 11
 X84622
 ID X84622 standard; DNA; 893 BP.
 XX
 AC X84622;
 XX
 DT 16-SEP-1999 (first entry)
 XX
 DE Human TNFR superfamily soluble receptor coding sequence.
 XX
 KW TNFL1; human; TNFR superfamily; tumour necrosis factor ligand; TNF;
 KW tumour necrosis factor receptor; TNFR superfamily; cell proliferation;
 KW cell differentiation; cytokine production; immunoglobulin; hyperplasia;
 KW apoptosis inducer; activated T cell; autoimmune disease; inhibitor;
 KW myasthenia gravis; insulin-dependent diabetes mellitus; endotoxin shock;
 KW rheumatoid arthritis; multiple sclerosis; systemic lupus erythematosus;
 KW tumour; proliferative disorder; neoplasia; dysplasia; immunocompetence;
 KW lymphoid organogenesis; bacterial resistance; contact hypersensitivity;
 KW delayed type sensitivity; therapy; ss.
 XX
 OS Homo sapiens.
 XX
 PN W09933980-A2.
 XX
 PD 08-JUL-1999.
 XX
 PF 22-DEC-1998; 98MO-US27474.
 XX
 PR 16-DEC-1998; 98US-0212270.
 PR 30-DEC-1997; 97US-0068959.
 XX
 PA (CHIR) CHIRON CORP.
 XX
 PI Kassam A, Lamson G, Pot D, Tribouley C;
 XX
 DR WPI; 1999-405508/34.
 DR P-PSDB; Y22223.
 XX
 PT New tumour necrosis factor ligands, useful for induction of cell
 PT death and/or proliferation of cells
 XX
 PS Claim 15; Page 65-66; 69pp; English.
 XX
 CC This sequence encodes a tumour necrosis factor receptor (TNFR)
 CC superfamily soluble protein of the invention. The invention also relates
 CC to tumour necrosis factor (TNF) ligand (TNFL) family proteins. The TNFL
 CC proteins play regulatory roles in cell proliferation and/or
 CC differentiation, e.g. they can induce production of cytokines,
 CC immunoglobulins, etc. A variety of diseases can be treated by modulating
 CC the activity of TNFL proteins, e.g. they can induce apoptosis of
 CC activated T cells but rescue resting T cell from apoptosis. TNFL
 CC polypeptides can therefore be used to treat autoimmune diseases, such as
 CC myasthenia gravis, insulin-dependent diabetes mellitus, rheumatoid
 CC arthritis, multiple sclerosis, and systemic lupus erythematosus. TNFL

CC proteins also have tumour stimulating properties, so tumours can be
 CC treated by inhibiting the expression or activity of TNFL. Other
 CC proliferative disorders, such as neoplasias, dysplasias, and hyperplasia
 CC can also be treated using TNFL inhibitors. The TNFL polypeptides and
 CC polynucleotides can also be used to enhance or decrease TNF activity,
 CC thus providing therapeutic benefits such as induction of cell death,
 CC lymphoid organogenesis, or host bacterial resistance, and inhibition of
 CC endotoxin shock, contact hypersensitivity, delayed type sensitivity or
 CC immunocompetence of a transplant recipient. TNF and its receptors play a
 CC major role in host defence and immunosurveillance. As such, there is a
 CC need to identify new members of TNFR families. This invention provides
 CC this need.
 XX
 SQ Sequence 893 BP; 211 A; 240 C; 247 G; 195 T; 0 other;
 Query Match 26.2%; Score 447.2; DB 20; Length 893;
 Best Local Similarity 81.6%; Pred. No. 1.2e-129;
 Matches 529; Conservative 0; Mismatches 118; Indels 1; Gaps 1;
 QY 22 aataaacatttgataaagaagatgcttttaaaagctctactagaacaagagaacact 81
 Db 32 aataaacacgttggtagagccatggcactcaagctcactctctacacaggaaggtgc 91
 QY 82 tttcactcttttagtattactaggtctattgtcatgtaaaagtgaactgtgaaacagag 141
 Db 92 tctcgtgccattctcttactcactccactggcagtgtaaaagtgaactgtgaaacagag 151
 QY 142 actgtagacagcaagaattcaggatcgctgtggaactgtgtccctcgaacacagtgctg 201
 Db 152 attgcaggcagcaggaattcaaggatcgatctggaactgtgtccctcgaacacagtgctg 211
 QY 202 ggcagcagcagtgctgtcgaaggaatgtgctcgtgctcgtgagggaggtgcacagtgctg 261
 Db 212 gacctggctgaggtgtgtcgaaggaatgtgctcgtgctcgtgagggaggtgcacagtgctg 271
 QY 262 tgactgtcggcgtgcacaggttcaaggagactggggcgtccagaaatgcagagccctgtc 321
 Db 272 tgccctgcaggcgcacccggttcaaggagactgggggtttccagaagtgtgaagccatgtg 331
 QY 322 tggactgcgcagtggtgaaacccgcttcaagaagcaaatgttcagccacagtgatgcca 381
 Db 332 cggactgtgcgtgtgaaacccgcttcaaggaggtccactgctcacacacagtgatgctg 391
 QY 382 tctgcgggactcgtgtccaggaattttatagaaagcgaactgtcgcgtttcaagaca 441
 Db 392 tctgcgggactcgtgtccaggaattttatagaaagcgaactgtgtgttttcaagaca 451
 QY 442 tggagtgctgctgtgtgagacccctctctctctctcctcctacgaacgcactgtgccagaag 501
 Db 452 tggagtgctgctgtgtgagacccctctctctctcctcctcctacgaacgcactgtgccagaag 511
 QY 502 tcaacctgtgaagatcgtgctccacggcctccagccacgggacacggcgctgctgcg 561
 Db 512 tgaacctgtgaagatcctctccacgctctccagccctccagccacggcgctgctgcg 571
 QY 562 ttatctgcagcgtctgagccacgctcctcgtgctcctcgtcctctctctctctctatt 621
 Db 572 tcatctgcagctgctgagccacggtgctgctcgtcgtcgtcgtcgtgctgctattact 630
 QY 622 gtaagagacagtttatggagaagaaacccagctggtctctgcggtcac 669
 Db 631 gcaagggcagttcatggagaagaaacccagctgtaagctcccatccc 678
 RESULT 12
 X59345
 ID X59345 standard; cDNA; 538 BP.
 XX
 AC X59345;
 XX
 DT 20-SEP-1999 (first entry)
 XX

DE Mouse NTR-5 cDNA.
KW NTR-5; mouse; receptor; signal transduction; bone; muscle;
KW diagnosis; therapy; ss.
KW Mus musculus.

Key Location/Qualifiers
FT CDS 3..485
FT /*tag= a

PN W09933967-A2.

XX 08-JUL-1999.

XX 28-DEC-1998; 98WO-US27688.

XX 29-DEC-1997; 97US-0068925.

XX (REGE-) REGENERON PHARM INC.

XX Valenzuela DM;

DR WPI: 1999-419102/35.

DR P-PSDB; Y06399.

XX New mammalian receptor NTR-5 polypeptides

XX Example 1; Page 19; 27pp; English.

XX This is the nucleotide sequence of murine cDNA coding for a novel
CC receptor, designated NTR-5 (see Y06399), that shows homology to
CC osteoprotegerin and tumour necrosis factor (TNF) receptor. 2 cDNA
CC clones containing the present sequence were isolated following an
CC EST database search using human and mouse TNF family members as
CC query sequences. The murine NTR-5 cDNA was used as a probe in
CC the isolation of human NTR-5 cDNA (see X59346). Homology to
CC osteoprotegerin suggests that NTR-5 is involved in the regulation
CC of bone mass, and may be useful for regulating development,
CC proliferation and death of osteoblast or osteoclast cells or for
CC regulating muscle metabolism, and that it may be implicated in
CC muscle diseases or disorders. A host-vector system for production
CC of NTR-5 is claimed. NTR-5 polypeptides can be used as immunogens
CC and in screening assays to identify NTR-5 ligands, agonists and
CC antagonists. The NTR-5 polynucleotide is useful as a diagnostic
CC tool, and as a source of probes and primers. The invention also
CC provides for diagnostic and therapeutic methods based on the
CC interaction of NTR-5 and agents that initiate signal transduction
CC through binding to NTR-5.

XX Sequence 538 BP; 111 A; 153 C; 152 G; 122 T; 0 other;

Query Match 21.3%; Score 362.6; DB 20; Length 538;
Best Local Similarity 86.2%; Pred. No. 2.5e-103;
Matches 401; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

QY 205 caggcatgagttgttcaagaagtgtgcttcggtcatggtggagagatgcacagtgtgtga 264

DB 1 ctggcatgagttgtccaaggaaatgtggttcggtcatggtggagagatgcacagtgtgtgc 60

QY 265 cgtgcgggtgcacaggttcaaggagagactggggttcctcagaataatgcaagccctgtgtgg 324

DB 61 cctgcagccgcacccggttcaaggaaactggggttcctcagaagtgttaagccatgtgcgg 120

QY 325 actgcagagttgtgaaccgttttcagaaggcaaatgttcaagccacagtgatgcacatc 384

DB 121 actgtgcgtgtgaaccgcttttcagaggggccaactgtctcacacacagtgatgtgtct 180

QY 385 gcggggagctgttcgagatattataggaagacgaaactgtcggctttcaagacatgg 444

DB 181 gcggggagctgttcgagatattataccgggaagacccaactggtgtgtttcaagacatgg 240

QY 445 agtgtgtgctgttgagacccctctctcttcaacacccgactgtgcacgaagtga 504
DB 241 agtgtgtgctgttgagacccctctctcttcaacacccgactgtgcacgaagtga 300
QY 505 acctcgtgaagatcgcgtccacggcctccagccacggacacggcgtggctgcgtga 564
DB 301 accttgtgaagattctctccacgtctccagccctcggacacggcgtggctgcgtga 360
QY 565 tctgcagcgtctgcccaccgtccctcgtgctccctcgtcctcctctgtcctcattgtga 624
DB 361 tctgcagcgtctgcccaccgtgctgctgctgctccctcgtcctcgtgctcctactgtga 420
QY 625 agagacagtttatggagaagaacccacgctggtctctcgtcgtgcac 669
DB 421 agaggcagttcatggagaagaacccacgctgtaagctccatccc 465

RESULT 13

V11422

ID V11422 standard; cDNA; 371 BP.

XX V11422;

XX 23-JUL-1998 (first entry)

DE Human secreted protein clone AX92_3 cDNA 5'-end.

KW Secreted protein; prevention; treatment; gene therapy; ds.

XX Homo sapiens.

XX W09801554-A2.

PD 15-JAN-1998.

XX 07-JUL-1997; 97WO-US11876.

XX 09-JUL-1996; 96US-0677231.

PA (GENY) GENETICS INST INC.

PI Bowman M, Evans C, Jacobs K, LaVallie ER, McCoy JM;

PI Merberg D, Racie LA, Spaulding V, Treacy M;

DR WPI: 1998-110230/10.

DR P-PSDB; W58844.

PT Secreted proteins and polynucleotides encoding them - useful to
PT prevent, treat and ameliorate medical conditions

XX Claim 15; Page 57; 93pp; English.

CC V11422-V11424 encode fragments of a novel secreted protein derived from
CC clone AX92.3 which was isolated from a human adult testes cDNA library.
CC The protein can be used to prevent, treat or ameliorate a medical
CC condition, while the polynucleotides can be used for gene therapy.

XX Sequence 371 BP; 83 A; 96 C; 107 G; 82 T; 3 other;

Query Match 21.2%; Score 361.6; DB 19; Length 371;
Best Local Similarity 98.1%; Pred. No. 4e-103;
Matches 364; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 172 ctggaaactgttctcctcaaccagtggtggccaggcatggagttgtctaaagaatgtg 231

DB 1 ctggaaactgttctcctcaaccagtggtggccaggcatggagttgtctaaagaatgtg 60

QY 232 gcttcggctatggggagagatgcacagtgtgtgacgtgcccggcgtgcacagttcaaggagg 291

DB 61 gcttcggctatggggagagatgcacagtgtgtgacgtgcccggcgtgcacagttcaaggagg 120

QY 292 actggggcttccagaataatgcaagccctgtctggaactgcagtggtgaaccgctttcaga 351

FH	Key	Location/Qualifiers
ET	CDS	104..556
ET		/*tag= a

PN WO9913078-A1.

18-MAR-1999.

AA
PF 11-SEP-1998; 98WO-US19030.

XX	06-MAY-1998:	98US-0084422.
PR		

PR 12-SEP-1997; 97US-0058631.

PA (BIOJ) BIOGEN INC.

PI Hession C, Tschopp J;

WPI: 1999-229238/19.

DR P-PSDB; W98144.

PT New cysteine-rich tumor necrosis factor receptor

PS Claim 1: Page 26: 30pp: English.

The present sequence encodes a novel murine cysteine-rich tumour necrosis factor receptor family member termed TRAIN-R (short form) (see W98144). This putative natural soluble form of murine TRAIN-R may inhibit signalling by the full-length TRAIN-R (see W98145). Murine TRAIN-R is expressed at high levels in brain and lung, and at lower levels in liver, skeletal muscle and kidney. Cell death can be induced by administering an agent capable of inhibiting the binding of TRAIN-R to its ligand. A claimed method of treating, or reducing, the advancement, severity or effects of an immunological disease in a mammal comprises administering a pharmaceutical composition which comprises a TRAIN-R blocking agent, e.g. soluble TRAIN-R. TRAIN-R can be fused to an immunoglobulin molecule to produce a fusion protein which may be targeted to various sites. It can be used in binding assays, and to identify antagonists and agonists. Anti-TRAIN receptor antibodies can be used to reduce the severity of an immune response or to treat cancer. TRAIN-R blocking agents can be used to reduce the severity or effects of an immunological disease (all claimed).

Sequence 599 BP; 149 A; 147 C; 180 G; 123 T; 0 other;

Query Match	19.2%	Score	326.6;	DB	20;	Length	599;
Best Local Similarity	78.2%;	Pred. No.	4.9e-92;				
Matches	392;	Conservative	0;	Mismatches	109;	Indels	0;
						Gaps	0;

Qy 18 caacaataacatttqataaqaqaatqcccttataaaqtqctactagaacaagaaaa 77

Db 77 caqqaataaacacqtttqqqtgaqagccatgqccactcaaaqgtcctacctctacacaggacg 136

Qy 78 acgtttttcactctttttagtatttactagcctattttgtcatgtaaagtgaacttgtgaaaca 137

Db 137 gtgctcttcgctgccaattctcttcctactccacctggcatgtaaaagtgaatttcgaaacc 196

Ov 138 ggagactgtagacagcaagaattcagggaatcgaatctggaaactgtatctccctgcaaccag 197

Db 197 ggagattgcaggcagcagggaattcaaggatcgatctggaaactgtatcctctgcaaacg 256

0y 198 tttggccagacatggaatttctcctaaggaaatcttggttcggctatgggagcatcacacg 357

257
pb

0y 258 ttttttaccgtacctgggctccacaggttcaggaggaactgggactccagaatacacaacccc 317

317 ++++++
dp ++++++

[illegible]

100 90 80 70 60 50 40 30 20 10 0

THIS PAGE BLANK (USPTO)

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 2, 2001, 12:32:29 ; Search time 217.59 Seconds
(without alignments)
1262.085 Million cell updates/sec

Title: US-09-380-276A-2
Perfect score: 1704
Sequence: 1 gggaacgtagaactccaa.....gaccacagatattttc 1704

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 280836 seqs, 80580151 residues

Total number of hits satisfying chosen parameters: 561672

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_NA.*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq.*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq.*
3: /cgn2_6/ptodata/1/ina/6_COMB.seq.*
4: /cgn2_6/ptodata/1/ina/PCUTUS_COMB.seq.*
5: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	36.4	2.1	1601	1 US-08-722-001-7	Sequence 7, Appli
2	36.4	2.1	1987	1 US-08-722-001-26	Sequence 26, Appl
3	36.4	2.1	1997	1 US-08-722-001-27	Sequence 27, Appl
4	36.4	2.1	2004	1 US-08-722-001-11	Sequence 11, Appl
5	36.2	2.1	2485	1 US-08-424-424B-1	Sequence 1, Appli
6	36.2	2.1	2486	4 PCT-US94-05363A-1	Sequence 1, Appli
7	35.4	2.1	7218	1 US-08-232-463-14	Sequence 14, Appl
8	34.8	2.0	1639	1 US-08-334-698-5	Sequence 5, Appli
9	34.8	2.0	1639	1 US-08-228-932-5	Sequence 5, Appli
10	34.8	2.0	1639	1 US-08-468-939-5	Sequence 5, Appli
11	34.8	2.0	1639	2 US-08-406-855A-5	Sequence 5, Appli
12	34.8	2.0	1639	3 US-08-722-190-5	Sequence 5, Appli
13	34.8	2.0	1639	3 US-08-244-354-5	Sequence 5, Appli
14	34.8	2.0	1639	3 US-09-206-899-5	Sequence 5, Appli
15	34.8	2.0	1639	4 PCT-US95-04203-5	Sequence 5, Appli
16	34.6	2.0	5962	5 5386025-5	Patent No. 5386025
17	33.6	2.0	800	2 US-08-416-603-11	Sequence 11, Appl
18	33.4	2.0	4360	1 US-08-470-350B-1	Sequence 1, Appli
19	33	1.9	9472	1 US-08-325-547-9	Sequence 9, Appli
20	32.8	1.9	2230	1 US-08-200-512-1	Sequence 2, Appli
21	32.6	1.9	1593	2 US-08-524-828-2	Sequence 2, Appli
22	32.6	1.9	1593	2 US-08-975-114A-2	Sequence 2, Appli
23	32.6	1.9	1593	3 US-08-849-281A-2	Sequence 2, Appli
24	32.6	1.9	2247	2 US-08-524-828-1	Sequence 1, Appli
25	32.6	1.9	2247	2 US-08-975-114A-1	Sequence 1, Appli
26	32.6	1.9	3891	1 US-08-480-604A-27	Sequence 27, Appl
27	32.6	1.9	3891	1 US-08-405-496A-27	Sequence 27, Appl
28	32.4	1.9	1167	1 US-07-960-985-1	Sequence 1, Appli

Sequence 1, Appli
Sequence 3, Appli
Sequence 36, Appli
Sequence 36, Appli
Sequence 36, Appli
Sequence 36, Appli
Sequence 36, Appli
Sequence 36, Appli
Sequence 36, Appli
Sequence 36, Appli
Sequence 36, Appli
Sequence 11, Appli
Sequence 11, Appli
Sequence 6, Appli
Sequence 1, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-08-722-001-7
; Sequence 7, Application US/08722001
; Patent No. 5760054
; GENERAL INFORMATION:
; APPLICANT: Thompson, Wayne J.
; APPLICANT: Huff, Joel R.
; APPLICANT: Nerenberg, Jennie B.
; APPLICANT: Lee, Hee-Yoon
; APPLICANT: Bell, Ian M.
; TITLE OF INVENTION: ALPHAIIC ADRENERGIC RECEPTOR ANTAGONISTS
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: 126 Lincoln Avenue
; CITY: Rahway
; STATE: New Jersey
; COUNTRY: United States of America
; ZIP: 07065

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/722,001

FILING DATE:
CLASSIFICATION: 514

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/229,276

FILING DATE: 14-APR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Appollina, Mary A.

REGISTRATION NUMBER: 34,087
REFERENCE/DOCKET NUMBER: 19169Y

TELECOMMUNICATION INFORMATION:
TELEPHONE: (908)594-3462

TELEFAX: (908)594-4720
TELEX: 138825

INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:

LENGTH: 1601 base pairs
TYPE: nucleic acid

STRANDEDNESS: both
TOPOLOGY: both

MOLECULE TYPE: cDNA
HYPOTHETICAL: NO

ANTI-SENSE: NO
US-08-722-001-7

Db	1112	CGAGGACGAGACCATTCGCAGATCAACGAGAGCGGGCTACGTCCTTCTCGCGTCT	1171
Qy	578	ggccaccgtctcgtgccctcgtcatctctgttcctcatctatgttaagagacagatttat	637
Db	1172	GGCTCCTTCTACCTCGCTCTGCCCATCATCTCGTGCATGTACTGCCGCGTCTACGTGGT	1231
Qy	638	ggagaagaacccagctgtctctcgggtc	667
Db	1232	GGCCACGAGGGAGAGCGGGGGCTCAAGTC	1261

RESULT 3
 US-08-722-001-27
 ; Sequence 27, Application US/08722001
 ; Patent No. 5760054
 ; GENERAL INFORMATION:
 ; APPLICANT: Thompson, Wayne J.
 ; APPLICANT: Huff, Joel R.
 ; APPLICANT: Nerenberg, Jennie B.
 ; APPLICANT: Lee, Hee-yoon
 ; APPLICANT: Bell, Ian M.
 ; TITLE OF INVENTION: ALPHALC ADRENERGIC RECEPTOR ANTAGONISTS
 ; NUMBER OF SEQUENCES: 35
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Merck & Co., Inc.
 ; STREET: 126 Lincoln Avenue
 ; CITY: Rahway
 ; STATE: New Jersey
 ; COUNTRY: United States of America
 ; ZIP: 07065
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/722,001
 ; FILING DATE:
 ; CLASSIFICATION: 514
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/229,276
 ; FILING DATE: 14-APR-1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Appollina, Mary A.
 ; REGISTRATION NUMBER: 34,087
 ; REFERENCE/DOCKET NUMBER: 19169Y
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (908)594-3462
 ; TELEFAX: (908)594-4720
 ; TELEX: 138825
 ; INFORMATION FOR SEQ ID NO: 27:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1997 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: both
 ; TOPOLOGY: both
 ; MOLECULE TYPE: CDNA
 ; HYPOTHETICAL: NO
 ; ANTI-SENSE: NO
 US-08-722-001-27

Qy	518	cggtccacggctccagcccagggacacggcgtgctgcgttatctcagcgcctc	577
Db	1106	CGAGGACGAGACCATCTGCCAGATCAACGAGGAGCGGSGCTACGTGCTCTTCTCGGCTCT	1165
Qy	578	ggccacgctcgtcgccctgcctacccctcgtgtcctatttgaaagacagatttat	637

APPLICANT: LI, ET AL.
TITLE OF INVENTION: Neurotransmitter Transporter
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN.


```

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,939
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 41337-1B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0526
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1639 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: N
ANTI-SENSE: N
FEATURE:
NAME/KEY: CDS
LOCATION: 126..1523
OTHER INFORMATION:
US-08-468-939-5

Query Match      2.0%; Score 34.8; DB 1; Length 1639;
Best Local Similarity 52.0%; Pred. No. 0.99;
Matches 78; Conservative 0; Mismatches 72; Indels 0; Gaps 0;

QY 518 cgcgtccacggcctccagccacgggacgacgctggtcgctgtatctgcagcgctct 577
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 635 CGAGGACGAGACCATCTGCCAGATCAACGAGAGCGCGGTACTGCTCTTCTCAGCGCT 694

QY 578 ggcacgcgtctgctggtccctgtctctctgtctgtctatctgttaagagacagttat 637
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 695 GGGCTCTTCTTACTGCTCTGCGCATCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 754

QY 638 ggagagaaacccagctgtctctgcggtc 667
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 755 GGCCAAAGAGGAGAGCGGGGCGCTCAAGTC 784

RESULT 11
US-08-406-855A-5
Sequence 5, Application US/08406855A
Patent No. 5861309
GENERAL INFORMATION:
APPLICANT: Jonathan A. Bard et al.
TITLE OF INVENTION: DNA Encoding Human Alpha 1 Adrenergic
TITLE OF INVENTION: Receptors and Uses Thereof
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/406,855A
FILING DATE: 21-AUG-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 41337-A-PCT-US/JPW/KDB

```

```

TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0526
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1639 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: N
ANTI-SENSE: N
FEATURE:
NAME/KEY: CDS
LOCATION: 126..1523
OTHER INFORMATION:
US-08-406-855A-5

Query Match      2.0%; Score 34.8; DB 2; Length 1639;
Best Local Similarity 52.0%; Pred. No. 0.99;
Matches 78; Conservative 0; Mismatches 72; Indels 0; Gaps 0;

QY 518 cgcgtccacggcctccagccacgggacgacgctggtcgctgtatctgcagcgctct 577
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 635 CGAGGACGAGACCATCTGCCAGATCAACGAGAGCGCGGTACTGCTCTTCTCAGCGCT 694

QY 578 ggcacgcgtctgctggtccctgtctctctgtctgtctatctgttaagagacagttat 637
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 695 GGGCTCTTCTTACTGCTCTGCGCATCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 754

QY 638 ggagagaaacccagctgtctctgcggtc 667
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 755 GGCCAAAGAGGAGAGCGGGGCGCTCAAGTC 784

RESULT 12
US-08-722-190-5
Sequence 5, Application US/08722190
Patent No. 5990128
GENERAL INFORMATION:
APPLICANT: Charles Gluchowski, Carlos C. Forray, George
APPLICANT: Chiu, Theresa A. Brancheck, John M. Wetzel and Paul R. Hartig
TITLE OF INVENTION: USE OF ALPHA-1C SPECIFIC COMPOUNDS TO
TITLE OF INVENTION: TREAT BENIGN PROSTATIC HYPERPLASIA
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/722,190
FILING DATE: 4-APR-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 41878-D-PCT/JPW/AGL
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
TELEX:
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1639 base pairs

```


GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 2, 2001, 03:50:01 ; Search time 8955.7 Seconds
(without alignments)
1942.344 Million cell updates/sec

Title: US-09-380-276A-1
 Perfect score: 1269
 Sequence: 1 atgggttttaaagtgtact.....ggcagcgactgggttcctg 1269

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1118133 seqs, 6853842396 residues
Total number of hits satisfying chosen parameters: 2236266

```
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
```

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

```

Database :
GenEmbl.*
1: gb_ba1.*
2: gb_ba2.*
3: gb_om.*
4: gb_ov.*
5: gb_ph.*
6: gb_pl1.*
7: gb_pl2.*
8: gb_pr1.*
9: gb_pr2.*
10: gb_pr3.*
11: gb_ro.*
12: gb_sy.*
13: gb_un.*
14: en_fun.*
15: en_hum1.*
16: en_hum2.*
17: en_in.*
18: en_om.*
19: en_or.*
20: en_ov.*
21: en_pat.*
22: en_ph.*
23: en_pl.*
24: en_ro.*
25: en_sts.*
26: en_sy.*
27: en_un.*
28: en_vi.*
29: gb_htg1.*
30: gb_htg2.*
31: gb_in1.*
32: gb_in2.*
33: en_ba1.*
34: en_ba2.*
35: en_hum3.*
36: en_hum4.*
37: gb_pr4.*
38: gb_htg3.*
39: gb_htg4.*
40: gb_htg5.*
41: gb_htg6.*
42: gb_htg7.*
43: en_htg1.*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES									
Result No.	Score	Query %		Length	DB	ID	Description		
		Match	Length						
1	1264.2	99.6	1364	8	A8040434	AB040434	Homo sapi		
2	1256.2	99.0	1489	37	AF167555	AF167555	Homo sapi		
3	732.4	57.7	3964	11	AB040432	AB040432	Mus muscu		
4	729.2	57.5	1678	11	AF167552	AF167552	Mus muscu		
5	680.8	53.6	1075	11	AF173166	AF173166	Mus muscu		
6	449	35.4	744	11	AB040433	AB040433	Mus muscu		
7	449	35.4	886	11	AF167553	AF167553	Mus muscu		
8	428.8	33.8	143608	67	AL161422	AL161422	Homo sapi		
9	428.8	33.8	178256	66	AL139080	AL139080	Homo sapi		
10	314	24.7	591	11	AF167554	AF167554	Mus muscu		
11	73	5.8	188351	67	AL353136	AL353136	Homo sapi		
12	73	5.8	205736	51	AC023560	AC023560	Homo sapi		
13	65.4	5.2	205736	51	AC023560	AC023560	Homo sapi		
14	43.6	3.4	160214	54	AC034198	AC034198	Homo sapi		
15	43.6	3.4	180511	42	AC018836	AC018836	Homo sapi		
16	43.6	3.4	209876	10	AC011599	AC011599	Homo sapi		
17	42	3.3	207166	42	AC018843	AC018843	Homo sapi		
18	38.8	3.1	200948	38	AC010331	AC010331	Homo sapi		
19	38.8	3.1	204573	41	AC016589	AC016589	Homo sapi		
20	38.4	3.0	145934	67	AL353611	AL353611	Homo sapi		
21	38.4	3.0	148018	67	AL159992	AL159992	Homo sapi		

```

c 22 38.4 3.0 171491 50 AC022606 AC022606 Homo sapi
23 37.8 3.0 108774 70 AF001862 AP001862 Homo sapi
24 37.8 3.0 177014 8 AC004063 AC004063 Homo sapi
25 37.8 3.0 189239 53 AC026557 AC026557 Homo sapi
26 37.6 3.0 38532 73 SCE94 AL049828 Streptomy
27 37.6 3.0 186797 49 AC021965 AC021965 Homo sapi
28 37.6 3.0 188351 67 AL353136 AL353136 Homo sapi
29 37.4 2.9 32354 73 SCD84 AL353816 Streptomy
30 37.4 2.9 73868 55 AC055762 AC055762 Homo sapi
31 37 2.9 154378 7 AP001383 AP001383 Oryza sat
32 37 2.9 159099 69 AL359749 AL359749 Homo sapi
33 37 2.9 171031 51 AC024503 AC024503 Homo sapi
34 36.8 2.9 680 4 CHRC1A201 J00821 Chicken alp
35 36.8 2.9 162025 9 AC005730 AC005730 Homo sapi
36 36.6 2.9 15355 1 AE005026 AE005026 Halobacte
37 36.6 2.9 166712 39 AC012213 AC012213 Homo sapi
38 36.4 2.9 2890 10 AF030177 AF030177 Homo sapi
39 36.4 2.9 2921 8 AB003723 AB003723 Homo sapi
40 36.4 2.9 32723 32 CEM88 Z34802 Caenorhabdi
41 36.4 2.9 41906 73 SC5C7 AL031515 Streptomy
42 36.2 2.9 3154 56 LMCCR2 X69521 L.migratori
43 36.2 2.9 31261 32 CELF33G12 U41278 Caenorhabdi
44 36.2 2.9 71412 54 AC040891 AC040891 Homo sapi
45 36.2 2.9 159397 53 AC027040 AC027040 Homo sapi

```

ALIGNMENTS

```

RESULT 1
AB040434 1364 bp mRNA PRI 22-JUL-2000
LOCUS Homo sapiens mRNA for hTROY, complete cds.
ACCESSION AB040434
VERSION AB040434.1 GI:9392329
KEYWORDS hTROY.
SOURCE Homo sapiens cDNA to mRNA.
ORGANISM Homo sapiens
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (sites)
Kojima,T., Morikawa,Y., Copeland,N.G., Gilbert,D.J., Jenkins,N.A.,
Senba,E. and Kitamura,T.
TROY, a newly identified member of the tumor necrosis factor
receptor superfamily, exhibits a homology with Edar and is
expressed in embryonic skin and hair follicles
J. Biol. Chem. 275 (27), 20742-20747 (2000)
2037167
2 (bases 1 to 1364)
Kojima,T. and Kitamura,T.
Direct Submission
Submitted (23-MAR-2000) to the DDBJ/EMBL/GenBank databases. Tetsuo
Kojima, Chugai Research Institute for Molecular Medicine, Inc.,
Cytochrome Research Program, 153-2 Nagai, Nihari, Ibaraki 300-4101,
Japan (E-mail:kojima@ciimmed.com, Tel:81-298-306211,
Fax:81-298-306270)
Sequence updated (06-Apr-2000).
FEATURES
Source
1..1364
/organism="Homo sapiens"
/db_xref="taxon:9606"
37..1308
/gene="hTroy"
37..1308
/gene="hTroy"
/codon_start=1
/product="hTROY"
/protein_id="BAB03269.1"
/db_xref="GI:9392330"
/translaton="WALKVLEQKEFTFTLLVLLGLYLSCKVTCESGDRQROEFRDRSG
NCVPCNCGPGMELSKGFGYDAQCVCRLHFRKEDWGFKCKPCIDCAVNRFO
KANCSTDAIGDCLPGFYRTKLVGFQDMCEVPCGPPPPPEPHCAKSNLVKIAS
TASSPRDIALAAGVLSALATVLLALLILCVYCKRQFMKRPKRSWLSRSDIOYNGSEL

```

```

BASE COUNT 325 a 351 c 358 g 330 t
ORIGIN
Query Match 99.6%; Score 1264.2; DB 8; Length 1364;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1266; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 atggctttaaagtgctactagaacaagagaaacgttttctactcttttagtattacta 60
Db ATGGCTTTAAAGTGTCTACTAGAACAGAGAAACGCTTTTCTACTCTTTTAGTATTACTA 96
QY 61 ggcattttgtcatgtaaaagtacttgaaacaggagagatgtagacagacaagaattcagg 120
Db GGCATTTTGTCTATGTAAGTGAATTCAGGAGAGATGTAGACAGCAAGAAATTCAGG 156
QY 121 gatcgatctggaaactgtgttccctcaaccagtgctggccagggcatggagttgctaaag 180
Db GATCGGTCTGGAAACACTGTGTTCCCTGCCAACACAGTGTGGCCAGGCATGGAGTTGCTAAG 216
QY 181 gaatgtggcttcgggctatggggaggatgcacagtgctgacgtgcccggctgcacaggttc 240
Db GAATGTGGCTTCGGCTATGGGGAGGATGCACAGTGTGTGACGTGCCGCTGCACAGGTTT 276
QY 241 aaggaggactggggcttcagaaaatcaaggccctgtctggagctgcagtggtgaaccgc 300
Db AAGGAGGACTGGGGCTTCCAGAAATGCAAGCCCTGTCTGACTTGGCAGTGGTGAACCCG 336
QY 301 ttccagaagcaaaattgttcagccaccagtgatgccatctgcgggactgcttgccagaa 360
Db TTTCAGAAAGCAAAATTTGTTACGCCACCACCATGATGCCATCTCGCGGGACTGCTTGCCAGGA 396
QY 361 ttctataggaagacgaacactgtcggtctttcaagacatggagtgctgcttgtagagac 420
Db TTTTATAGGAAGACGAACAACTTGTGCGCTTTCAAGACATGGAGTGTGCTTGTGGAGAC 456
QY 421 cctctcctctcttaagaaacgaactgtgcagcaaggctcaaacctctgaagatcggcttc 480
Db CCTCTCTCTCTTACGAACCGCACTGTGCCAGCAAGGTCAACCTCGTAGAATTCGCGTCC 516
QY 481 aaggctccagccacggagacacggcgctggctggcttatctgcagcctctggccacc 540
Db ACGGCTCCACCCACCGGACACGGCGCTGGCTGCCGCTTATCTGCAGCGCTCTGGCCACC 576
QY 541 gtctgtggcctgtctatcctctgttctatctatgttaagagacagtttatggagaag 600
Db GTCTGTGGCTGTCTATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 636
QY 601 aaaccagctgtctctcggttcacaggacattcagacagcgtctcagctgtcgtgt 660
Db AAACCCAGCTGGTCTCTGGGGTCCACAGGACATTCAGTACAAACGGCTCTGAGCTGTCTGT 696
QY 661 cttgcagacacctcagctccacgaatatgccacagagctgctgcagtgcccgctgtac 720
Db TTGACAGACCTCAGCTCCACGAAATATGCCACAGAGACCTGCTGCCAGTGCCTGCTGAC 756
QY 721 tcagtgacacctgcggcggtgctgcttccctccatccatgctgctgtagaggagcctgc 780
Db TCAGTGCAGACCTTCGCGGGCGGTGCGCTGCTCCCATCCATGCTGCTGCTGCTGCTGCTG 816
QY 781 agccccaacccggcgactcttggttggtgggtgctcttctgcagcagctcttcaggagaag 840
Db AGCCCCAACCCGGCGACTCTTGGTGTGGGGTGCATTTCTGCAGCCAGTCTTTCAGGCAAGA 876
QY 841 aacgcaggccacggcggtgagatgggtgcgaccttcttcggaacctccctcagcagctccatc 900
Db AAGCAGGCCACCGCCGGGAGATGGTGGCGACTTTCTTCCGATCCCTCAGCAGTCCATC 936
QY 901 tgtggcgagtttttcagatgccttgccctctgtatgcagaaatcccatgggtgtgacaacatc 960

```

```

|||||
Db 937 TGTGCGAGTTTTCAGATGCGCTCTGATGCGAATCCATGGGTGGTGCAACATC 996
|||||
Qy 961 tctttttgactcttctgaactcaactcagagagaacattctctcaatccagaa 1020
|||||
Db 997 TCTTTTGTGACTCTTATPCTTGAATCTACTCGGAGAGACATTCATCTCAATCCAGAA 1056
|||||
Qy 1021 ctgaaagctcaagctctttgattcaaatagcagctcaagatttggttgggtgggtctgtt 1080
|||||
Db 1057 CTGGAAGCTCAAGCTCTTTGGATTCAATAGCAGCTCAAGATTGGTGGTGGGCTGTT 1116
|||||
Qy 1081 ccagtcagctctattctgaaactttacagcagctactgattttatctagatatacaaac 1140
|||||
Db 1117 CCAGTCCAGTCTCATCTGAAACTTTACAGCAGCTACTGATTTATCTAGATATAACAAC 1176
|||||
Qy 1141 acactgtagaatcagatcaactcagatcagatcactaatactatgagaagccagctagatcag 1200
|||||
Db 1177 ACATGGTAGAATCAGCATCAACTCAGGATGCATTAAGTATGAGAAGCCAGCTAGATCAG 1236
|||||
Qy 1201 gagagtgccgtctatcatccaccagccactcagacgtccctccaggttaagcagcagctg 1260
|||||
Db 1237 GAGAGTGGCGTGTATCATCCAGCCACTCAGAGTCCCTCCAGGTAAAGCAGGACTG 1296
|||||
Qy 1261 ggttccctg 1269
|||||
Db 1297 GGTTCCTCG 1305

RESULT 2
AF167555 AF167555 1489 bp mRNA PRI 25-MAY-2000
LOCUS Homo sapiens TAJ-alpha mRNA, complete cds.
DEFINITION AF167555
ACCESSION AF167555
VERSION AF167555.1 GI:8071643
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1489)
AUTHORS Eby,M.T., Jasmin,A., Kumar,A., Sharma,K. and Chaudhary,P.M.
TITLE TAJ, a Novel Member of the Tumor Necrosis Factor Receptor Family,
Activates the c-Jun N-terminal Kinase Pathway and Mediates
Caspase-Independent Cell Death
J. Biol. Chem. 275 (20), 15336-15342 (2000)
10809768
JOURNAL PUBMED
REFERENCE 2 (bases 1 to 1489)
AUTHORS Chaudhary,P.M.
TITLE Direct Submission
JOURNAL Submitted (12-JUL-1999) Internal Medicine, UT Southwestern Medical
Center, 5323 Harry Hines Blvd., Dallas, TX 75235-8593, USA
FEATURES
Source 1..1489
/organism="Homo sapiens"
/db_xref="taxon:9606"
65..1336
/codon_start=1
/product="TAJ-alpha"
/protein_id="AAF71828.1"
/db_xref="GI:8071644"
/translation="MALKVLLEQEKFTTLLVLGLYSCKVTCSGDCRQEQFDRDSG
NCVPCNCGPMELSKCEGFGYGEDAQCVARLHRFRKEDWGFQKPCLDCAVYNRFQ
KANGSATSDAICGCLPGFYRKTLGVQDMCEVPCGDPDPPEPHKASKVNLVKIAS
TASSPRDTALAAVICSLATVLLALLILCVYCKRFMEKKPWSLSRQDIQYNETEL
SCFPRPOLHEVAHRACQCRDVSQTCGPVRLPSCMCEEACSPNPATLGGGVHSAS
LOARNAGPAGENVPTFFGSLTQSCIGFSDANWPLMQNPMGDNISFDCSPFELGEDI
HSLAPELSFSLDSNSQDLGGAVPVQSHSENFATATDLSRYNNLTLPESASTQDAL
TMRSQLQESGAVTHPATQYRQRLGSL"
BASE COUNT 361 a 366 c 380 g 382 t
ORIGIN

```

Query Match 99.0%; Score 1256.2; DB 37; Length 1489;

```

Best Local Similarity 99.4%; Pred. No. 0;
Matches 1261; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 1 atgctcttaaaagtgtactactagaacaagagaaaaacgctttttcaactcttttagtattacta 60
Db 65 ATGCGCTTTAAAGTGTCTACTAGAAACAGAGAAAAACGTTTTTCACTCTTTTATGATTACTA 124
Qy 61 ggctatttgcattgaagtactgtgaaacagagagacttagacagcaagaatcaagg 120
Db 125 GGCTATTTGTTCATGTAAAGTCACTTTGTAATCAGGAGACTGTAGACAGCAGAATTTCAGG 184
Qy 121 gatcggctctgaaactgtgttccctgcaaccagttgtggccaggcgaatggagttgtctaag 180
Db 185 GATCGGCTGTGAAACTGTGTTCCCTGCAACAGTGTGGCCAGGCATGAGTGTGTCTAAG 244
Qy 181 gaatgtggcttcggctatgggagagatgacacagtgtgtgacgtgcccgtgcacaggttc 240
Db 245 GAATGTGGCTTCGGCTATGGGAGAGATGCACAGTGTGTGGCGTGCCTGCTGCACAGGTTTC 304
Qy 241 aagagagactgggcttcacagaaatgcaagccctgtctggactgcgcagtggtgaaccgc 300
Db 305 AAGGAGGACTGGGCTTCCAGAAATGCAAGCCCTGTCTGGACTGGCAGTGGTGAACCGC 364
Qy 301 ttccagaaggcaaatgtttcagccaccagtgatgccatctcgggggactgtttgccaggga 360
Db 365 TTTCAGAAAGGCAAAATTTGTTACGCCACCAGTGTATGCCATCTCGGGGACTGTCTTGCACGGA 424
Qy 361 tttatagaagaacgaaacttgtcggctttcaagacataggagtggtccttggagagac 420
Db 425 TTTTATAGAAAGACGAAACTTTGTGGCTTTCAAGACATGGAGTGTGTGCCCTGTGGAGAC 484
Qy 421 cctcctcctctacgaaccgcactgtgccagcaaggtcaacctctgtgaagatcgctcc 480
Db 485 CCTCTCTCTCTTAGAAACCGCCTGTGCCAGCAAGGTCAACCTGCTGAAGATCGCGTCC 544
Qy 481 acggctccagcccaacgggacacggcgctggtctgttatctgcagcgctctgtggccacc 540
Db 545 ACGGCTCCAGCCACGGGACACGGCGCTGGCTGCGGTATCTGCAGCGCTCTTGGCCACC 604
Qy 541 gtcctgtggccctgtctcactcctctgtctatctattgtaagacagatttatgagaag 600
Db 605 GTCTGTCTGGGCGCTGCTCATCTCTGTGTCACTATTATTAAAGAGACAGTTTATGGAAGA 664
Qy 601 aaaccagctggtctctcgtcggtccacagacattcagtaacacggctctgagctgtcgtgt 660
Db 665 AAACCCAGCTGGTCTCTCGGGTTCACAGACATTCAGTACACGAGACTGAGCTGTCTGT 724
Qy 661 ctgacagacctcagctccacgaatatgccacagagcgtgctgcagtcgcccgtgac 720
Db 725 TTTGACAGACCTCAGCTCAGCAATATGCCACAGAGCGTGTGTGCAGTGGCGCGGTGAC 784
Qy 721 tcagtgacagacctgcccggcggtgctgttccatccatcattgtgtgagagagccctgc 780
Db 785 TCAGTGCAGACCTTGGGCGCGGTGCGCTGTCTCCCATCATGTGTGTGAGAGGCGCTGC 844
Qy 781 agccccaacccggcgactctgtgtgtgggtggatctctgcagccagctcttcaggaaga 840
Db 845 AGCCCCAACCCGGCGACTCTTTGGTGTGGGTGCACTTTCGACGCGCAGTCTTTCAGGCAAGA 904
Qy 841 aacgcaggccacgcggggagatggtgcgactcttctcgtatccctcacgcagtcacatc 900
Db 905 AACGCAGGCCACCGCGGGAGATGTCGCCACTTTCTTCGGATCCTCACGCAAGTCCATC 964
Qy 901 tctgctgagtttctcagatgcctcgtctgtatgcaagaatccccatgggtggtgacaacatc 960
Db 965 TGTGCGAGATTTTTCAGATGCCCTGGCCCTCTGTATGCAGAAATCCCATGGGTGGTGCAACATC 1024
Qy 961 tctttttgactcttctgaactcactggaagcactggaagacattctctctcaatccagaa 1020
Db 1025 TCTTTTGTGACTCTTATCTGAACCTACTGGGAGAGACATTTCATTTCTCAATCCAGAA 1084
Qy 1021 cttgaaagctcaacgtctttgagattcaaatagcagctcaagatttggttgggtgggtctgt 1080
|||||

```

Db 1085 CTTGAAAGCTCAACGCTTTTGGATTCAAAATAGCAGTCAAGATTGGTTGGTGGGCTGTT 1144
 QY 1081 ccagtcagctctattctgaaactttacagcagctactgatttattctagataaacaac 1140
 Db 1145 CCAGTCCAGTCTCATCTGAAACTTTACAGCAGCTACTGATTTACTAGATTATACAAC 1204
 QY 1141 acatggtagaatcagcatcaactcaggatgcactaactatgagaagccagctagatcag 1200
 Db 1205 ACTAGGTAGAAATCAGCATCAACTCAGGATGCACCTAACTATGAGAAGCCAGCTAGATCAG 1264
 QY 1201 gagatggcgtctatccaccagccactcagcagctccctccagtaagcgagcagctg 1260
 Db 1265 GAGAGTGGCGCTGTCACTCCACCAGCCACTCAGACGCTCCCTCCAGGTAAAGCAGCTG 1324
 QY 1261 ggtccctg 1269
 Db 1325 GGTTCCTG 1333

 RESULT 3
 AB040432 3964 bp mRNA ROD 22-JUL-2000
 LOCUS Mus musculus mRNA for TROY, complete cds.
 DEFINITION AB040432
 ACCESSION AB040432.1 GI:9392325
 VERSION
 KEYWORDS TROY.
 SOURCE Mus musculus cDNA to mRNA.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 Senba, E. and Kitamura, T.
 Kojima, T., Morikawa, Y., Copeland, N.G., Gilbert, D. J., Jenkins, N.A.,
 1 (sites)
 TROY, a newly identified member of the tumor necrosis factor
 receptor superfamily, exhibits a homology with Edar and is
 expressed in embryonic skin and hair follicles
 J. Biol. Chem. 275 (27), 20742-20747 (2000)
 20347167
 2 (bases 1 to 3964)
 Kojima, T.
 Direct Submission
 Submitted (23-MAR-2000) to the DDBJ/EMBL/GenBank databases. Tetsuo
 Kojima, Chugai Research Institute for Molecular Medicine, Inc.,
 Cytokine Research Program; 153-2 Nagai, Nihari, Ibaraki 300-4101,
 Japan (E-mail: kojima@climmed.com, Tel:81-298-306211,
 Fax:81-298-306270)
 FEATURES
 Location/Qualifiers
 1..3964
 /organism="Mus musculus"
 /db_xref="taxon:10090"
 127..1377
 /gene="Troy"
 127..1377
 /gene="Troy"
 /note="a member of TNFR superfamily exhibits a homology
 with Edar"
 /codon_start=1
 /product="TROY"
 /protein_id="BAB03267.1"
 /db_xref="GI:9392326"
 /translation="MAKVLPLHRTVLFALILLLHACKVSCETGDCRQBFKDRSG
 NVLCCKOCGMELSKCEGFGYEDACQVPCRPKREKDWGFKKPCACDCAVLNRFQ
 RANCSHTSDAVCGDCLPGFYRKTKLVGFODMECPKGDPPPEPHCTSKVNLVKISS
 TVSSPRDTALAIVICSAATVLLALILVICKRPFMEKPSWSLRSDIOYNGSEL
 SCFDQPLRHCAHRCQYHRDSAPMIGPVHLIPSLCCBEARSSARAVJUGLSRPTN
 LQERNPASVGMDFPFGVSRSICAEFSDAMPQMPLGDSLSDSCLDSYPELTGDTN
 SLNPENESAASLDSSGQDLAGTAALLESSGNVSESDSPRHGDTGTWQTLAQDAQR
 TPSQGWEDRENLIAMP"AFQDA"
 BASE COUNT 984 a 958 c 980 g 1041 t 1 others
 ORIGIN
 Query Match 57.7%; Score 732.4; DB 11; Length 3964;

Best Local Similarity 74.8%; Pred. No. 3.5e-187;
 Matches 932; Conservative 0; Mismatches 311; Indels 3; Gaps 1;
 QY 1 atggttttaaaagtgtactagaaagaagaaaaacgttttttcaactcttttagtattacta 60
 Db 127 ATGGCACTCAAGGTCTTACCTTACACAGGACGGTCTCTTCGCTGCCATCTCTTCCCTA 186
 QY 61 ggtattttgcatgtaagtgtctgtgaaacagagagactgtagacagcaagaattcagg 120
 Db 187 CTCACCTGGCATGTAAAGTGAGTTGGGAAACCGGAGATTGCAGGACGAGGAATTCAG 246
 QY 121 gatcgttctggaaactgtttcccttcaaccagctgtgggcccagggcatggagttgtctaa 180
 Db 247 GATCGATCTGAAACTGTGTCTCTGCAACACAGTGGCGACCTGCCATGGAGTTGTCCAAG 306
 QY 181 gaatgtggttcggtcgtatggggagagatgacagctgtgtgacgtgcccgtgcagaggttc 240
 Db 307 GAATGTGGCTTCGGCTATGGGGAGGATGCACAGTGTGCCCCGACAGCGCCGCTTC 366
 QY 241 aaggagactggggtctccagaaaatgcaagccctgtctggaactgcagctgtgtgaaccgc 300
 Db 367 AAGGAAGACTGGGGTTCAGAAAGTGTAAAGCATGTCCGAGACTGTGGCTGGTGAACCCG 426
 QY 301 ttccagaaggcaaatgttccagccaccagtgatgccatctgcgggactgttgcaggga 360
 Db 427 TTTTACAGAGGGCAACTGCTCACACACAGTGTCTGTGGGGGACTGCTCTGCCAGGA 486
 QY 361 ttattatagaagcgaactgttcggtcttcaagacatggagtggtgcttctgtgagac 420
 Db 487 TTTTACCGGGAAGCAACACTGGTTGGTTTTCAGACATGGAGTGTGTGCCCTCGGAGAC 546
 QY 421 cctcctcctcttaccgaacccgactgtgccagcaaggtcaacctcgtgaagatcgcgtcc 480
 Db 547 CCAGCTCTCTCCCTACGAACCCACTGTACCGAAGGTTGAACCTTGTGAAGATCTCCTCC 606
 QY 481 acggcttccagcccaaggacacggcgctgtgctgcccgttatctgcagcgctctggccacc 540
 Db 607 ACCGTCTCCAGCCTCGGGACACGGCGCTGGCTGCCGTCTCTGCTGCTGCTGGCCACG 666
 QY 541 gtctgctggcgctgtcctctctctgtgtgtatattgttaagagacagtttatggagaag 600
 Db 667 GTCTGTCTGCCCTGTCTATCTCTGTGTCTACTTGCAGAGAGGAGGAGTTCATGGAGAG 726
 QY 601 aaaccagctggtctctgcggtcacaggacattcagtaacacggctctgcagctgtcgtgt 660
 Db 727 AAACCCAGCTGTCTCTGCGGTACAGGACATTCAGTACAAATGGCTCTGASCTGTCTATGC 786
 QY 661 cttagacagactcagctccacgaatatgccacacagcgtgctgcccagtgcccgcgtgac 720
 Db 787 TTTGACCAAGCCTCGGCTCCGCCACTGTGCCCATAGAGACTGCTGTAGTATCATCCGGGAC 846
 QY 721 tcagtcgagacctgcgggcccgtgtgcgtgtgtctcccatccatgtgtgtgagggagcctgc 780
 Db 847 TCAGCCCCAATGTATGGGCTGTGTACCTGATTCGCTGTGTGTGTGTGAAGAGGCCCGC 906
 QY 781 agcccaaacccgcgactctgtgtgtgggtgcatcttcagccagctcttcaggaaga 840
 Db 907 AGTCTGCCCGAGCTGTGTGTGGCTGTGGGCTGGGTTCTCCCACTACCTTCCAGGAGAGA 966
 QY 841 aacgcaggcccccagccggggagatggtgtgccactttcttcggatccctcacgagtcctc 900
 Db 967 AACCCGGCTTCTGTGGGGACAGATGCCACGCTCTCTTCGGGTCTGTTCCTCCGCTTCCATC 1026
 QY 901 tgtggcgagtttcaagatgcctggcctctgtagcagaatccccatgggtgtgacacatc 960
 Db 1027 TGGGCTGAATTTTCTGATGTGCTGCCCTCTGATGAGAATCTCTGGGTGTG---ACAGC 1083
 QY 961 tcttttgtactcttctcgaactcactgcagagacattctctcaatccagaa 1020
 Db 1084 TCCTCTGTGACCTTATCTCTGACTCAGTGGAGAGATACCAATTCCTTCAATCCGAA 1143
 QY 1021 cttgaaagctcaacgtcttcttggtattcaaaatagcagctcaagatttgggtggggtcgtt 1080

Db	1144	AACGAAGCCGACGATCTCTGGATTCACGATGCGGCGCAGGATCTGGCTGGACAGCTGCT	1203
Qy	1081	ccagtcctcagtcctcattctgaaactttcacagcagctactgattattatagataataacaac	1140
Db	1204	CTAGAGTCTTCGGGAATGTTTCAGAACTTACTGACTCACCTAGACATGTTGACATGGT	1263
Qy	1141	acactgtagaatcagcatcaactcagatcagatgcactaactatgagaagccagctagatcag	1200
Db	1264	ACAGTCTGGGAGCAGACGCTAGCTCAGGATGCTCAAGGACTCCAAGCCCAAGGAGGCTGG	1323
Qy	1201	gagagtgcgctatcatccaccagcagcaactcagacgctccctccagg	1246
Db	1324	GAAGACAGGGAACCTGGAATCTAGCCATGCCACACGCTTCCAGG	1369
RESULT 4			
AF167552	AF167552	1678 bp	25-MAY-2000
LOCUS	Mus musculus TAJ-alpha long mRNA, complete cds.	ROD	
DEFINITION	AF167552		
VERSION	AF167552.1	GI:8071637	
KEYWORDS	house mouse.		
SOURCE	Mus musculus		
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
REFERENCE	1 (bases 1 to 1678)		
AUTHORS	Eby, M.T., Jasmin, A., Kumar, A., Sharma, K. and Chaudhary, P.M.		
TITLE	TAJ, a Novel Member of the Tumor Necrosis Factor Receptor Family, Activates the c-Jun N-terminal Kinase Pathway and Mediates Caspase-Independent Cell Death		
JOURNAL	J. Biol. Chem. 275 (20), 15336-15342 (2000)		
PUBMED	10809768		
REFERENCE	2 (bases 1 to 1678)		
AUTHORS	Chaudhary, P.M.		
TITLE	Direct Submission		
JOURNAL	Submitted (12-JUL-1999) Internal Medicine, UT Southwestern Medical Center, 5323 Harry Hines Blvd., Dallas, TX 75235-8593, USA		
FEATURES	Location/Qualifiers		
source	1..1678		
	/organism="Mus musculus"		
	/db_xref="taxon:10090"		
CDS	72..1322		
	/codon_start=1		
	/product="TAJ-alpha long"		
	/protein_id="AAE71825.1"		
	/db_xref="GI:8071638"		
	/translation="MALKVLPLHRTVLFAILFLHLACKVSCETGDCRQEPKDRSG NCVLKQCGMELSEKCGFYGEDAQVPCPRHREFKDMGFKQKPCADALVNRFG RANCSHTSDAVCGDCLPGFYRKTLVGFQDMECVPGDPPPYEPHCTSKVNLVKIS TVSSPRDIAAVGICSAALAVYLLALLILCYICKROFMKKPKSWRSODIOYNGSEL SCFDQPLRHCARACCOVHRDSPAPWGPVHLIPSLCCPEARSSARAVLGCGLRSPPT LQSPNRSVGNTHPAGGSVRSICAEFSDAWPLMONPLIGDSSLDSDSPELTGDTN SLAPNESTASLDSQGVSLRACAEFSSNGVSESDSPRHGDTGTWQETLQAQDAQR TPSSQGWEDRENILAMPTAFQDA"		
BASE COUNT	371 a 467 c 466 g 374 t		
ORIGIN			
Query Match 57.58; Score 729.2; DB 11; Length 1678;			
Best Local Similarity 74.6%; Pred. No. 2.5e-186;			
Matches 930; Conservative 0; Mismatches 313; Indels 3; Gaps 1;			
Qy	1	atgcttttaaagtcctactagaacaagaaaaagcttttccactcttttagtattacta	60
Db	72	ATGGCATCAAGGTCTTACCTCTACACAGGAGCGTGTCTTCGCTGCCATCTCTTCTTA	131
Qy	61	ggctatttgcctgataagtgactgtgaaacagagagactgtagacagcaagaattcagg	120
Db	132	CTCCACCTGGCATGTAAAGTCAGTTGGCAACCGAGATTCGACGACGACGAGATTCAAG	191
Qy	121	gatcggcttgaaactgtgttccctgcaaacagtgatggcgccaggtgagtgcttaag	180

Db	192	GATCGATCTGGAACACTGTGTCTCTGCAAAACAGTGCAGACCTGGCATGAGAGTTGTCCAAG	251
Qy	181	gaatgtggtctcggtctatgggagagatcacagtgtagcgtgcggctgcacaggttc	240
Db	252	GAATGTGGCTTTCGGCTATGGGAGGATGCACTGTGTGCCCTGCAGGCCGACCGGTTCC	311
Qy	241	aagagagactggggcttcacagaaatgcagaaacctctggactgcagtggtgaaccgc	300
Db	312	AAGGAAGACTGGGTTTCCAGAAGTGAAGCCATGTGCGGACTGTGCGCTGGTCAACCGC	371
Qy	301	tttcagaaggcaaatgttcaagccaccagtgatgcattctgcggggactgcttccaggaa	360
Db	372	TTTCAGAGGCCAACTGCTCACACACCACTGATGTCTGCGGGACTGCTCTGCCAAGAA	431
Qy	361	ttttatggaagcagaaactgttcggcttcaagacatggagtgtagcttggagac	420
Db	432	TTTTTACCGGAAGCAAACTGGTTGGTTTTCAAGACATGGAGTGTGTGCCCTGCGGAGAC	491
Qy	421	cctctcctcttcacgaacgcgactgtgccagcaaggtcaacctctggaagatcgcttc	480
Db	492	CCACCTCTCCCTACGAACCCACACTGTACCAGCAAGTGAACCTTGTGAAGATCTCTCTCC	551
Qy	481	acggctctcaagcccaacggagacagcgctgtgctgcggttatctgcagcgctctggccacc	540
Db	552	ACCGTCTCCAGCCCTCGGGACACGGCGCTGGCTGGCGCTCATCTGCAAGTGTCTGGCCACG	611
Qy	541	gtcctgctggcctgctcatcctctgtgcatctattgtaagagacagtttatggagaag	600
Db	612	GTGCTGTCTCCCTCTCATCTCTGTGTGTATCTACTGCAAGAGCCAGTTTCATGGAGAAG	671
Qy	601	aaacccagctggtctctgcgggtcacaggacattcagtaacacggctctgagctgctggt	660
Db	672	AAACCCAGCTGGTCTCGGGTTCACAGGACATTCACTACAATGGCTCTGAGCTGTGTCATGC	731
Qy	661	cttgacaagactcagctccacgaaatagcccaacagcctgctgcagtgccgcgcgtgac	720
Db	732	TTTTCACACAGCTCGGGTCCGCCACTGTGCCCATAGAGCATGCTGTCACTATCACCGGGAC	791
Qy	721	tcagtgcagacctgcggccggtgcctgtgccatccatgctgtgagagagcctgc	780
Db	792	TCACGCCAATGATGGGCTGTTCACTGATTCCTGCTCTGTGTGTGTGAAGAGCCCGC	851
Qy	781	agccccaacccggcgactcttggtgtgggtgtgattctgcagccagctcttcaggcaaga	840
Db	852	AGCTCTCCCCGAGCTGTGCTTGGCTGTGGCTGCGTCTCTCCACATACCTCCAGGAGAGA	911
Qy	841	aacgcagcccgccggggagatgtgcgcgaactttctggataccctcacgcagtcacatc	900
Db	912	AACCCGGCTTCTGTGGGGAAACAGATGCCAGGCTTCTTTGGGTCTGTTTCCCGTTCCTATC	971
Qy	901	tgtggcagttttcagatgcttgccctctgatgcagaatccccatgggtggtgacaaatc	960
Db	972	TGCGCGGAGTTTCTGATGCTGGCCCTCTGATGTGCAGAAATCTCTGCGGGCGGTG---ACAGC	1028
Qy	961	tcttttgtactcttatccctgaactcaactgcaggaagacattctctcctaaccagaa	1020
Db	1029	TCTCTCTGTGACTTATTATCTGAACCTACTGGAGAAGATACCAATTTCCCTCAATCCCCGAA	1088
Qy	1021	cttgaaagctcaacgctttttgagattcaaatagcagtcagaatttggttggtggggcgtgtt	1080
Db	1089	AACGAAAGCACAGCATCTCTGGATTCACGTGGCGCCAGGATCTGGCTGGGACAGACTGCT	1148
Qy	1081	ccagtccagtcctcatctgaaaaactttacagcagctactgatttatctagataataaac	1140
Db	1149	CTAGAGTCTTCTGGGAATGTTTTCAGAAATCTACTGTACTCACTTAGACATGGTGACACTGGT	1208
Qy	1141	acactggttagaatcagcatcaactcaggatgcactaaactatgagaagccagcgtagatcag	1200
Db	1209	ACAGTCTGGGAGCAGCGCTAGCTCAGGATGCTCAAGGACTCCAAAGCAAGGAGGCTGG	1268
Qy	1201	gagagtggtgctatcatccaccagccactcagacgtccctccagg	1246
Db	1269	GAAGACAGGAAACCTGTAATCTTAGCCATGCCACAGCCCTCCAGG	131

Japan (E-mail:kojimat@immed.com, Tel:81-298-306211,
Fax:81-298-306270)

```
FEATURES
Source      1..744
             Location/Qualifiers
             1..744
             /organism="Mus musculus"
             /db_xref="taxon:10090"
             /chromosome="14"
             67..711
             /gene="dtroy"
             67..711
             /gene="dtroy"
             /note="a member of TNFR superfamily exhibits a homology
             with Edar"
             /codon_start=1
             /product="dtroy"
             /protein_id="BAB03268.1"
             /db_xref="GI:9392328"
             /translation="MALKVLPLHRTVLFAAILFLLHLACKVSCETGDCROEKFDRSG
             NCVLKQCGPMELSKCEGFGYEDACVPCPHRFKEDMGFKCKPCADCALVNRQ
             RANGSHTSDAVGDCPLGFKYKTKLVGFQDMECVPCGDPPIPPYEPHCTSKVNLVKISS
             TVSSPRDTALAAVTCASALATVLLALLILCVYCKRQFMKKPSKCLPSLCTVK"

BASE COUNT  162 a 208 c 211 g 163 t
ORIGIN
Query Match      35.4%; Score 449; DB 11; Length 744;
Best Local Similarity 82.4%; Pred. No. 1.5e-110;
Matches 515; Conservative 0; Mismatches 110; Indels 0; Gaps 0;

Qy 1 atgggtttaaagtctactagaacagagaaacgcttttctactcttttagtattacta 60
   ||||| || || || || || || || || || || || || || || || || || || ||
Db 67 ATGGGCACTCAAGGTCTACCTCTACACAGGAGCGGTCTCTTCGCTGCCATCTCTTCCTA 126

Qy 61 ggcatttgcatgataaagtactgtgaaacagagagactgtagacacagaattcagg 120
   || || || || || || || || || || || || || || || || || || || || ||
Db 127 CTCACCTGGCATGTAAAGTGAAGTGGCAACCGAGAGATGCGAGCAGCAGGAATTCAG 186

Qy 121 gatcggtctggaactgttctccctgcaaccagtggtggccaggcatggagtgtcttaag 180
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 187 GATCGATCTGGAACTGTGTCTCTGCAACACAGTCGCGGACCTGGCATGGAGTGTGCCAAG 246

Qy 181 gaatggtctgggtatggggagagatgcacagtggtgacgtgcccgtgcacagggttc 240
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 247 GAATGTGCTTCGGGTATGGGAGAGATGCACAGTGTGTGCCCTGCGGCGGACCGCGGTTC 306

Qy 241 aaggaggactgggcttcagaaatgcagccctgtctggactgcgcagtggtgacaccgc 300
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 307 AAGGAAGACTGGGGTTCAGAAAGTGTAAAGCATGTGCGGAGTGTGCGTGTGTGAACCGC 366

Qy 301 ttccagaaggcaaatgtttccagccaccagtgatgccatctgctggggagctgcttgcaggga 360
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 367 TTTCAGAGGGCCAACTGTCTACACACACAGTGTGTGTCTGCGGGGACTGCGCTGCCAGGA 426

Qy 361 ttttataagaagacaaaactgtcgttttaagaacatggagtggtgcttggtagagac 420
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 427 TTTTACCGGAAGACCAAACTGGTGGTGTTCAGACATGGAGTGTGTGCCCTGCGGAGAC 486

Qy 421 cctctctctcttacgaaccgcacgtgtgcccagcaaggttcaacctgtgaaagatcgcttc 480
   || || || || || || || || || || || || || || || || || || || || ||
Db 487 CCACCTCTCTCTACGAACCACTGTACCAACAGAGGTGAACCTGTGAAGATCTCTCTCC 546

Qy 481 acggctccagccccagggacacgcgcgtggtgcgttatctgacgcgtcttgccacc 540
   || || || || || || || || || || || || || || || || || || || || ||
Db 547 ACCGCTCTCCAGCCCTCGGACACCGGCGTGGCTGCGCGTCTATCTGCAGTGTCTTGCCACG 606

Qy 541 gtctgtgtggcctgtctatctctgtgtcatctattgttaagagacagatttatggagaag 600
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 607 GTGCTGCTGCGCTGTCTACTCTGTGTCTATCTACTGCAAGAGCGCATCTATGTGAGAAG 666

Qy 601 aaacccagctgtctctgctgggtcac 625
   ||||| ||||| || || || || || || || || || || || || || || || || ||
Db 667 AAACCCAGCTGTAAAGTCTCCATCCC 691
```

RESULT 7

```
AF167553      886 bp      mRNA      ROD      25-MAY-2000
LOCUS      Mus musculus TAU-alpha short mRNA, complete cds.
DEFINITION      AF167553
ACCESSION      AF167553
VERSION      AF167553.1 GI:8071639
KEYWORDS
SOURCE      house mouse.
ORGANISM      Mus musculus
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE      1 (bases 1 to 886)
AUTHORS      Eby,M.T., Jasmin,A., Kumar,A., Sharma,K. and Chaudhary,P.M.
TITLE      TAJ, a Novel Member of the Tumor Necrosis Factor Receptor Family,
              Activates the c-Jun N-terminal Kinase Pathway and Mediates
              Caspase-Independent Cell Death
JOURNAL      J. Biol. Chem. 275 (20), 15336-15342 (2000)
PUBMED      10809768
REFERENCE      2 (bases 1 to 886)
AUTHORS      Chaudhary,P.M.
TITLE      Direct Submission
JOURNAL      Submitted (12-JUL-1999) Internal Medicine, UT Southwestern Medical
              Center, 5323 Harry Hines Blvd., Dallas, TX 75235-8593, USA
FEATURES
source      1..886
              /organism="Mus musculus"
              /db_xref="taxon:10090"
              /clone_lib="Soares p3NMF19.5"
              72..716
              /note="decoy receptor"
              /codon_start=1
              /product="TAJ-alpha short"
              /protein_id="AAF71826.1"
              /db_xref="GI:8071640"
              /translation="MALKVLPLHRTVLFAAILFLLHLACKVSCETGDCROEKFDRSG
              NCVLKQCGPMELSKCEGFGYEDACVPCPHRFKEDMGFKCKPCADCALVNRQ
              RANGSHTSDAVGDCPLGFKYKTKLVGFQDMECVPCGDPPIPPYEPHCTSKVNLVKISS
              TVSSPRDTALAAVTCASALATVLLALLILCVYCKRQFMKKPSKCLPSLCTVK"

BASE COUNT  204 a 245 c 247 g 190 t
ORIGIN
Query Match      35.4%; Score 449; DB 11; Length 886;
Best Local Similarity 82.4%; Pred. No. 1.5e-110;
Matches 515; Conservative 0; Mismatches 110; Indels 0; Gaps 0;

Qy 1 atgggtttaaagtctactagaacagagaaacgcttttctactcttttagtattacta 60
   ||||| || || || || || || || || || || || || || || || || || || ||
Db 72 ATGGCACTCAAGGTCTACCTCTACACAGGAGCGGTCTCTTCGCTGCCATCTCTTCCTA 131

Qy 61 ggcatttgcatgataaagtactgtgaaacagagagactgtagacacagaattcagg 120
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 132 CTCACCTGGCATGTAAAGTGAAGTGGCAACCGAGAGATGCGAGCAGCAGGAATTCAG 191

Qy 121 gatcggtctgaaactgttctccctgcaaccagtggtggccaggcatggagtgtcttaag 180
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 192 GATCGATCTGGAACTGTGTCTCTGCAACACAGTCGCGGACCTGGCATGGAGTGTGCCAAG 251

Qy 181 gaatggtctgggtatggggagagatgcacagtggtgacgtgcccgtgcacagggttc 240
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 252 GAAATGTGCTTCGGGTATGGGAGAGATGCACAGTGTGTGCCCTGCGGCGGACCGCGGTTC 311

Qy 241 aaggaggactgggcttcagaaatgcagccctgtctggactgcgcagtggtgacaccgc 300
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 312 AAGGAAGACTGGGGTTCAGAAAGTGTAAAGCATGTGCGGAGTGTGCGCTGTGTGAACCGC 371

Qy 301 ttccagaaggcaaatgtttccagccaccagtgatgccatctgctggggagctgcttgcaggga 360
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 372 TTTCAGAGGGCCAACTGTCTACACACAGCAGTGTGTGTCTGCGGGGACTGCGCTGCCAGGA 431

Qy 361 ttttataagaagacaaaactgtcgttttaagaacatggagtggtgcttggtagagac 420
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
```

Db 432 TTTTACGGGAAGCAAACTGTTGGTTTTTCAAGACATGAGTGTGTGCCCTCGGAGAC 491
QY 421 cctccctctcttaccagcactgtgcccagagtaacctctgaagatcgcgtcc 480
Db 492 CCACCTCTCTCCCTACGAACCACTGTACCAAGGAGTGAACCTGTGAAGATCTCCTCC 551
QY 481 acgctctcagccagcgggacagcgctggtgctgctgtatctgcagcgcctctggccacc 540
Db 552 ACCGTCTCCAGCCCTCGGGACACGGCGTGGCTGCGCTCATCTGCAGTGTCTGGCCACG 611
QY 541 gtctgtcgtgcccgtctatcctctctgtgctatctgttaagagacagtttatggagaag 600
Db 612 GTCTGCTGCCCCCTGTCTATCTGTGTCTATCTACTGCAAGAGGCGATTTCATGGAGAAG 671
QY 601 aaaccagctggtctctggtgctac 625
Db 672 AAACCCAGCTGTAAAGTCCCATCCC 696

RESULT 8
AL161422
LOCUS AL161422 143608 bp DNA HTG 20-SEP-2000
DEFINITION Homo sapiens chromosome 13 clone RP11-168G12, *** SEQUENCING IN
PROGRESS ***, 3 unordered pieces.
ACCESSION AL161422
VERSION AL161422
KEYWORDS HTG: HTGS_PHASE1; HTGS_DRAFT.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 143608)
Pearce.A.
Direct Submission
Submitted (19-SEP-2000) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
requests: clonerequest@sanger.ac.uk
On Sep 22, 2000 this sequence version replaced gi:10190601.
----- Genome Center
Center: Sanger Centre
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
----- Project Information
Center project name: BA168G12
----- Summary Statistics
Assembly program: XGAP4; version 4.5
Sequencing vector: pLasmid; L08752; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 143007 bases at least Q40
Consensus quality: 143260 bases at least Q30
Consensus quality: 143347 bases at least Q20
Insert size: 143408; sum-of-ctnigs
Insert size: 145175; 5.9% error; agarose-fp
Quality coverage: 8.55x in Q20 bases; sum-of-ctnigs Quality
coverage: 8.58x in Q20 bases; agarose-fp

* NOTE: This is a 'working draft' sequence. It currently
* consists of 3 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 2992: contig of 2992 bp in length
* 2993 3092: gap of 100 bp
* 3093 129375: contig of 126283 bp in length
* 129376 129475: gap of 100 bp
* 129476 143608: contig of 14133 bp in length.
* Location/Qualifiers
1 .143608
/organism="Homo sapiens".

FEATURES
source

/db_xref="taxon:9606"
/chromosome="13"
/clone="RP11-168G12"
/clone_lib="RPC1-11.1"
1..2992
/note="assembly_fragment:01799
fragment_chain:1"
3093..129375
/note="assembly_fragment:02957
fragment_chain:1
clone_end:T7
vector_side:left"
129476..143608
/note="assembly_fragment:00106"
BASE COUNT 41121 a 29506 c 30419 g 42362 t 200 others
ORIGIN

Query Match 33.8%; Score 428.8; DB 67; Length 143608;
Best Local Similarity 99.5%; Pred. No. 4.9e-105;
Matches 430; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 838 agaaacgcagggccagccggggagatgggtccgagactttcttgcgagtcctccacgcagtc 897
Db 84813 AGAAACGCAGGCCCCAGCGGGAGATGGTGGCCACTTCTTCGGATCCCTCAGCAGTCC 84872

QY 898 atctgtgagagttttcagatgcctggcctctgagatcagaatcccatgggtgagcaac 957
Db 84873 ATCTGTGGCGAGTGTTCAGATGCTGGCCTCTGTATCGAAGTCCCATGGTGGTGACAAC 84932

QY 958 atctcttttggagactcttctcctgaactcaactggagagacattctctcctcaatcca 1017
Db 84933 ATCTCTTTTGTGACTTATCTCTGAACCTCAGTGGAGAGACATTCTCTCAATCCA 84992

QY 1018 gaactggaagctcaacgtcttttggattcaaatagcagtcgaagattgttgggtgggct 1077
Db 84993 GAACCTTGAAGCTCAACAGCTTTTGGATTCAAAATAGCAGTCAAGATTGTGGTGGGCT 85052

QY 1078 gtccagtcagctctattctgaaaactttacagcagctactgattctatctagataac 1137
Db 85053 GTTCCAGTCCAGTCTCTTCTGAAAACCTTTACAGCAGTACTGATTTTCTAGATATAAC 85112

QY 1138 aacacactgtagaatcagcatcaactcaactcaggatgcactaatatgagaagcagctagat 1197
Db 85113 AACACACTGGTAGAATCAGCATCACTCAGGATGCCTAACTATGAGAGCCAGCTAGAT 85172

QY 1198 caggagagtggtgctatcatccaccagccactcagacgtccctccaggtaaggcgagcga 1257
Db 85173 CAGGAGAGTGGTGTCTGTCTATCCACCCAGCCACTCAGACGCTCCCTCCAGGTAAGCGCGA 85232

QY 1258 ctgggttccctg 1269
Db 85233 CTGGGTTCCTCG 85244

RESULT 9
AL139080
LOCUS AL139080 178256 bp DNA HTG 29-SEP-2000
DEFINITION Homo sapiens chromosome 13 clone RP11-173N17 map q12.11-12.3, ***
SEQUENCING IN PROGRESS ***, 15 unordered pieces.
ACCESSION AL139080
VERSION AL139080.8 GI:10443032
KEYWORDS HTG: HTGS_PHASE1; HTGS_DRAFT.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 178256)
Burton.J.
Direct Submission
Submitted (28-SEP-2000) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
requests: clonerequest@sanger.ac.uk

COMMENT

On Oct 1, 2000 this sequence version replaced gi:10129398.
 ----- Genome Center
 Center: Sanger Centre
 Center code: SC
 Web site: <http://www.sanger.ac.uk>
 Contact: humquery@sanger.ac.uk
 ----- Project Information
 Center project name: bal173N17
 ----- Summary Statistics
 Assembly program: XGAP4; version 4.5
 Sequencing vector: plasmid; 108752; 100% of reads
 Chemistry: Dye-terminator Big Dye; 100% of reads
 Consensus quality: 168976 bases at least Q40
 Consensus quality: 172107 bases at least Q30
 Consensus quality: 173780 bases at least Q20
 Insert size: 176856; sum-of-contigs
 Insert size: 163577; 8.6% error; agarose-fp
 Quality coverage: 3.73x in Q20 bases; sum-of-contigs Quality
 coverage: 4.07x in Q20 bases; agarose-fp

* NOTE: This is a 'working draft' sequence. It currently
 * consists of 15 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

1 8223: contig of 8223 bp in length
 * 8224 8323: gap of 100 bp
 * 8324 25426: contig of 17103 bp in length
 * 25427 25526: gap of 100 bp
 * 25527 28263: contig of 2737 bp in length
 * 28264 28363: gap of 100 bp
 * 28364 34273: contig of 5910 bp in length
 * 34274 34373: gap of 100 bp
 * 34374 42235: contig of 7862 bp in length
 * 42236 42335: gap of 100 bp
 * 42336 53917: contig of 11582 bp in length
 * 53918 54017: gap of 100 bp
 * 54018 71972: contig of 17955 bp in length
 * 71973 72072: gap of 100 bp
 * 72073 81711: contig of 9639 bp in length
 * 81712 81811: gap of 100 bp
 * 81812 88644: contig of 6833 bp in length
 * 88645 88744: gap of 100 bp
 * 88745 95048: contig of 6304 bp in length
 * 95049 95148: gap of 100 bp
 * 95149 107455: contig of 12307 bp in length
 * 107456 107555: gap of 100 bp
 * 107556 125465: contig of 17910 bp in length
 * 125466 125565: gap of 100 bp
 * 140009 140108: contig of 1443 bp in length
 * 140109 144761: gap of 100 bp
 * 144762 144861: contig of 4653 bp in length
 * 144862 178256: contig of 3395 bp in length.
 Location/Qualifiers
 1..178256
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /chromosome="13"
 /map="q12.11-12.3"
 /clone="RP11-173N17"
 /clone_lib="RPC1-11.1"
 1..8223
 /note="assembly_fragment:01724
 fragment_chain:1"
 8324..25426
 /note="assembly_fragment:00074
 fragment_chain:1"
 25527..28263
 /note="assembly_fragment:01884

FEATURES
source

misc_feature

misc_feature

misc_feature

misc_feature
 fragment_chain:1"
 28364..34273
 /note="assembly_fragment:00979
 fragment_chain:1"
 34374..42235
 /note="assembly_fragment:00126
 fragment_chain:2"
 42336..53917
 /note="assembly_fragment:00364
 fragment_chain:2"
 54018..71972
 /note="assembly_fragment:01769
 fragment_chain:2"
 72073..81711
 /note="assembly_fragment:00399
 fragment_chain:3"
 81812..88644
 /note="assembly_fragment:01132
 fragment_chain:3"
 88745..95048
 /note="assembly_fragment:01416
 fragment_chain:3"
 95149..107455
 /note="assembly_fragment:00061
 fragment_chain:4"
 107556..125465
 /note="assembly_fragment:00302
 fragment_chain:4"
 125566..140008
 /note="assembly_fragment:01438
 fragment_chain:5"
 140109..144761
 /note="assembly_fragment:01533
 fragment_chain:5"
 144862..178256
 /note="assembly_fragment:01008"
 BASE COUNT 52999 a 37393 c 36460 g 49998 t 1406 others
 ORIGIN
 Query Match 33.8%; Score 428.8; DB 66; Length 178256;
 Best Local Similarity 99.5%; Pred. No. 4.9e-105;
 Matches 430; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 838 agaaacgcagcccgaggagatggtgcgcgactttcttcggtacccctcacgcagtc 897
 Db 46631 AGAAAGCAGGCCAGCCGCGGAGATGTCGCGACTTTCTTCGGATCCCTCACGCAGTCC 46690
 QY 898 atctgtgcgagatttcagatgcctgcctctgatgcagaatcccatgggtggtgacaac 957
 Db 46691 ATCTGTGCGAGATTTTCAGATGCCCTGGCCTCTGTGATCGAGATCCCATGGGTGACAAC 46750
 QY 958 atctcttttgcactcttctgaactcactgcagagacattcattctctcaatcca 1017
 Db 46751 ATCTCTTTTGTGACTCTTATCTCTGAACCTGCTGAGAAGACATTCATTCCTCAATCCA 46810
 QY 1018 gaacttgaagctcaacgtcttttgattcaaatagcagtcgaagatttggtggtgggct 1077
 Db 46811 GAACCTGAAGCTCAACGCTTTTGATTCAAATACAGTCAGATTTGGTGTGGGCT 46870
 QY 1078 gtccagtcagctctcatcttgaataacttacagcagctactgattctctagataaac 1137
 Db 46871 GTTCAGTCCAGCTCTCATCTCTGAAACCTTACAGCAGCTACTGATTTATCTAGATATAAC 46930
 QY 1138 aacacactggtagatcagcatcaactcagatgcactcaactatagagccagctagat 1197
 Db 46931 AACACACTGGTAGAATCAGATCAACTCAGGATGCACCACTATGAGAAGCCAGCTAGAT 46990
 QY 1198 caggagagtggcgctatcatccaccaccgacctcagagctccctcaggttaaggcagcga 1257
 Db 46991 CAGGAGAGTGGTGTGTCTATCCACCCAGCCACTCAGAGCTCCCTCCAGTAAGGACGCGA 47050
 QY 1258 ctgggttccctg 1269

Db 47051 CTGGGTTCCCTG 47062

RESULT 10
AF167554 591 bp mRNA 25-MAY-2000
LOCUS Mus musculus TAJ-beta1 mRNA, complete cds.
DEFINITION AF167554
ACCESSION AF167554
VERSION AF167554.1 GI:8071641
KEYWORDS house mouse.
SOURCE Mus musculus
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 591)
AUTHORS Eby,M.T., Jasmin,A., Kumar,A., Sharma,K. and Chaudhary,P.M.
TITLE TAJ, a Novel Member of the Tumor Necrosis Factor Receptor Family,
Activates the c-Jun N-terminal Kinase Pathway and Mediates
Caspase-independent Cell Death
J. Biol. Chem. 275 (20), 15336-15342 (2000)
PUBMED 10809768
REFERENCE 2 (bases 1 to 591)
AUTHORS Chaudhary,P.M.
TITLE Direct Submission
JOURNAL Submitted (12-JUL-1999) Internal Medicine, UT Southwestern Medical
Center, 5323 Harry Hines Blvd., Dallas, TX 75235-8593, USA
FEATURES
source Location/Qualifiers
1..591
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone_lib="Soares p3NMF19.5"
95..547
/note="soluble receptor"
/codon_start=1
/product="TAJ-beta1"
/protein_id="AAF71827.1"
/db_xref="GI:8071642"
/translation="NALKVLPLHRTVLFPAAILLLHACKVSCETGDCRQEFKDRSG
NCVLKQCPGHELSKECGFGYGEDAQCPVCPHFKEDWQKPKPCADCALVRFQ
RANCSHTSDAVGCDLPGFYRKLKLVGFDMECVPGDPPPPYEPHCE"
BASE COUNT 148 a 145 c 175 g 123 t
ORIGIN

Query Match 24.7%; Score 314; DB 11; Length 591;
Best Local Similarity 78.9%; Pred. NO. 4.8e-74;
Matches 374; Conservative 0; Mismatches 100; Indels 0; Gaps 0;
Qy 1 atggctttaagtgctactagacaagaaacgctttttcactcttttagtattacta 60
Db 95 ATGGCACTCAAGTCTACTCTACAGAGACGGTGCTCTCGCTGCCATTCTTCCTA 154
Qy 61 ggctattgtcattgaagtgacttggaaacaggagactgtatagacagcaagaattcagg 120
Db 155 CTCACCTGGCATGTAAGTGAGTTGCGAAACCGGAGATTGCGAGGACGAGGAATTCAAG 214
Qy 121 gatcggtctgaaactgtgttcctctcaaccagtggtggccaggcagtgagttgtctaag 180
Db 215 GATCGATCTGGAACATGTGCTCTGCAAAACAGTGGCGGACCTGGCATGGATGGTCCAAG 274
Qy 181 gaatgtggtctcgctatggggaggatgcacagtggtgtgacgtgctgcggtgcacaggttc 240
Db 275 GAATGTGGCTTCGCTATGGGAGGATGCACAGTGTGTGCCCTGCGAGCGCACCGGTTT 334
Qy 241 aaggagactggggcttccagaataatgcaagccctgtctgtgactgcgcagtggtgaaccgc 300
Db 335 AAGGAAGACTGGGGTTTCCAGAAAGTGTAAAGCCATGTGCGGACTGTGCGTGGTGAACCG 394
Qy 301 ttcaagaagcgaattgtttcagccaccagtgatgccatctgcggggaactgttgcaggga 360
Db 395 TTTCAGAGGGCCCAACTGCTCACACACACAGTGTGCTGTCTGCGGGGACTGCCCTGCCAGGA 454

Qy 361 ttttataggaaagcaaacctgtcgcttttcaagacatggagtgtgtccttggagac 420
Db 455 TTTTACCGGAAGACCAACTGGTTGTTTTCAGACATGGAGTGTGCGCTCCGAGAC 514
Qy 421 cctctcctcttctacgaacgcactgtgccagcaaggtcaaacctcgtgaagatc 474
Db 515 CCACCTCCTCCTTACGAACACACACTGTGAGTGATGTGCCAAGTGGCAGCAGAC 568
RESULT 11
AL353136/c
LOCUS Homo sapiens chromosome X clone RP11-133K18, *** SEQUENCING IN
DEFINITION PROGRESS ***, 16 unordered pieces.
ACCESSION AL353136
VERSION AL353136.6 GI:9796991
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 18351)
AUTHORS Pavitt,R.
TITLE Direct Submission
JOURNAL Submitted (09-AUG-2000) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
requests: clonerequest@sanger.ac.uk
On Aug 12, 2000 this sequence version replaced gi:9368011.
COMMENT
----- Genome Center
Center: Sanger Centre
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
----- Project Information
Center project name: bA13K18
----- Summary Statistics
Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid; L08752; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 176827 bases at least Q40
Consensus quality: 181768 bases at least Q30
Consensus quality: 184650 bases at least Q20
Insert size: 186851; sum-of-contigs
Insert size: 162009; 18.4% error; agarose-fp
Quality coverage: 3.49x in Q20 bases; sum-of-contigs Quality
Coverage: 4.02x in Q20 bases; agarose-fp

* NOTE: This is a 'working draft' sequence. It currently
* consists of 16 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 25437: contig of 25437 bp in length
* 25438 25537: gap of 100 bp
* 25538 27653: contig of 2116 bp in length
* 27654 27753: gap of 100 bp
* 27754 45836: contig of 18083 bp in length
* 45837 45936: gap of 100 bp
* 45937 58298: contig of 12362 bp in length
* 58299 58398: gap of 100 bp
* 58399 63898: contig of 5500 bp in length
* 63899 63998: gap of 100 bp
* 63999 70792: contig of 6794 bp in length
* 70793 70892: gap of 100 bp
* 70893 83402: contig of 12510 bp in length
* 83403 83502: gap of 100 bp
* 83503 112513: contig of 29011 bp in length
* 112514 112613: gap of 100 bp
* 112614 120587: contig of 7974 bp in length
* 120588 120687: gap of 100 bp

* 120688 126817: contig of 6130 bp in length
 * 126818 126917: gap of 100 bp
 * 126918 135398: contig of 8481 bp in length
 * 135399 135498: gap of 100 bp
 * 135499 149082: contig of 13584 bp in length
 * 149083 149182: gap of 100 bp
 * 149183 157907: contig of 8725 bp in length
 * 157908 158007: gap of 100 bp
 * 158008 163704: contig of 5697 bp in length
 * 163705 163804: gap of 100 bp
 * 163805 175258: contig of 11454 bp in length
 * 175259 175358: gap of 100 bp
 * 175359 188351: contig of 12993 bp in length.

FEATURES

source
 1. 188351
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /chromosome="X"
 /clone="RP11-133K18"
 /clone_lib="RPC1-11.1"
 1. 25437
 /note="assembly_fragment:01650
 clone_end:SP6
 vector_side:left"
 25538. .27653
 /note="assembly_fragment:00293
 fragment_chain:1"
 27754. .45836
 /note="assembly_fragment:01209
 fragment_chain:1"
 45937. .58298
 /note="assembly_fragment:01684
 fragment_chain:1"
 58399. .63898
 /note="assembly_fragment:00037
 fragment_chain:1"
 63999. .70792
 /note="assembly_fragment:01432
 fragment_chain:2"
 70893. .83402
 /note="assembly_fragment:00471
 fragment_chain:2"
 83503. .112513
 /note="assembly_fragment:00822
 fragment_chain:2"
 112614. .120587
 /note="assembly_fragment:00509
 fragment_chain:3"
 120888. .126817
 /note="assembly_fragment:01092
 fragment_chain:3"
 126918. .135398
 /note="assembly_fragment:00273"
 135499. .149082
 /note="assembly_fragment:00291"
 149183. .157907
 /note="assembly_fragment:01278"
 158008. .163704
 /note="assembly_fragment:00964
 fragment_chain:4"
 163805. .175258
 /note="assembly_fragment:00415
 fragment_chain:4"
 175359. .188351
 /note="assembly_fragment:00856
 fragment_chain:4
 clone_end:17
 vector_side:right"
 57974 a 35482 c 35967 g 57418 t 1510 others

Query Match

5.8%; Score 73; DB 67; Length 188351;

Best Local Similarity 60.2%; Pred. No. 8.3e-09;
 Matches 121; Conservative 0; Mismatches 80; Indels 0; Gaps 0;
 QY 179 aggaatgtgcttgcgtatggaggagatgcacagtgtagcgtgacggtgcagcaggt 238
 ||||| ||||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 143334 AGGATTGTGTTATGGAGAGGGTGGAGATGCCTACTACACACCCCTCCTCGCAGGT 143275
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 239 tcaaggaggactgggcttccagaaatcaagccctgtctggactgcagcagtggtgaacc 298
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 143274 ACMAAGCAGCTGGGCCACACAGATGTCAGATTGTCATCACCTGCTGTCTCATCATC 143215
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 299 gcttccagaaggcaaatgttccagccaccagtcagtcattgctggggactgcctgccag 358
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 143214 GTGTTCAAGAGTCAACTGCACAGCTACCTCTAATGCTGTCTGTGGGACTGTTTGCCCA 143155
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 359 gatattatagaagacaaac 379
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 143154 GGTGAGCTTGCTTTATGAGAC 143134
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 12

AC023560/c
 LOCUS AC023560 205736 bp DNA HTG 12-MAR-2000
 DEFINITION Homo sapiens chromosome 17 clone RP11-85I20 map 17, WORKING DRAFT
 SEQUENCE, 34 unordered pieces.
 AC023560
 AC023560.2 GI:7229913
 VERSION
 HTG; HTGS_PHASE1; HTGS_DRAFT.
 KEYWORDS
 SOURCE
 human.

ORGANISM

Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE
 1 (bases 1 to 205736)
 AUTHORS
 Birren, B., Linton, L., Nusbaum, C. and Lander, E.
 TITLE
 Homo sapiens chromosome 17, clone RP11-85I20
 JOURNAL
 Unpublished
 REFERENCE
 2 (bases 1 to 205736)

AUTHORS

Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N.,
 Anderson, S., Baldwin, J., Barna, N., Bada, F., Boquslavsky, L.,
 Boukhalter, B., Brown, A., Burkett, G., Campopiano, A., Castle, A.,
 Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P.,
 Dearellano, K., Dewar, K., Dodge, S., Domino, M., Doyle, M.,
 Fenebor, J., Ferreira, P., FitzHugh, W., Forrest, C., Gage, D.,
 Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L.,
 Grand-Pierre, N., Grant, G., Hagos, B., Heaford, A., Horton, L.,
 Howland, J. C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A.,
 Klein, J., Landers, T., Larcocque, K., Lehoczy, J., Levine, R.,
 Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McCarthy, M.,
 McEwan, P., McGurk, A., McKernan, K., McPheeters, R., Meldrum, J.,
 Meneus, L., Mihova, T., Miranda, C., Mienga, V., Morrow, J., Naylor, J.,
 Norman, C. H., O'Connor, T., O'Donnell, P., O'Neill, D., Ollivar, T. M.,
 Peterson, K., Pierre, N., Pisan, C., Pollara, V., Raymond, C.,
 Riley, R., Rogov, P., Rothman, D., Roy, A., Santos, R., Schauer, S.,
 Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N.,
 Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A.,
 Travers, M., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B.,
 Wu, X., Wyman, D., Ye, W. J., Young, G., Zainoun, J., Zimmer, A. and
 Zody, M.

TITLE

Direct Submission
 Submitted (15-FEB-2000) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA
 On Mar 12, 2000 this sequence version replaced gi:6978256.
 COMMENT
 All repeats were identified using RepeatMasker;
 Smit, A.F.A. & Green, P. (1996-1997)
 http://ftp.genome.washington.edu/RM/RepeatMasker.html

Center: Whitehead Institute/ MIT Center for Genome Research
 Center code: WIBR
 Web site: <http://www-seq.wi.mit.edu>
 Contact: sequence.submissions@genome.wi.mit.edu
 ----- Project Information
 Center project name: L6741
 Center clone name: 85_I-20

----- Summary Statistics -----
 Sequencing vector: M13; M77815; 100% of reads
 Chemistry: Dye-terminator Big Dye; 100% of reads
 Assembly program: Phrap; version 0.960731
 Consensus quality: 178666 bases at least Q40
 Consensus quality: 190940 bases at least Q30
 Consensus quality: 197088 bases at least Q20
 Insert size: 194000; agarose-fp
 Insert size: 202436; sum-of-contigs
 Quality coverage: 4.2 in Q20 bases; agarose-fp
 Quality coverage: 4.0 in Q20 bases; sum-of-contigs

 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 34 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

```

1      1267: contig of 1267 bp in length
*      1268 1367: gap of 100 bp
*      1368 2402: contig of 1035 bp in length
*      2403 2502: gap of 100 bp
*      2503 3524: contig of 1022 bp in length
*      3525 3624: gap of 100 bp
*      3625 4913: contig of 1289 bp in length
*      4914 5013: gap of 100 bp
*      5014 6289: contig of 1276 bp in length
*      6290 6389: gap of 100 bp
*      6390 7655: contig of 1266 bp in length
*      7656 7755: gap of 100 bp
*      7756 9267: contig of 1512 bp in length
*      9268 9367: gap of 100 bp
*      9368 11138: contig of 1771 bp in length
*      11139 11238: gap of 100 bp
*      11239 13822: contig of 2584 bp in length
*      13823 13922: gap of 100 bp
*      13923 16968: contig of 3046 bp in length
*      16969 17068: gap of 100 bp
*      17069 20185: contig of 3117 bp in length
*      20186 20285: gap of 100 bp
*      20286 22634: contig of 2349 bp in length
*      22635 22734: gap of 100 bp
*      22735 27012: contig of 4278 bp in length
*      27013 27112: gap of 100 bp
*      27113 29342: contig of 2230 bp in length
*      29343 29442: gap of 100 bp
*      29443 33381: contig of 3939 bp in length
*      33382 33481: gap of 100 bp
*      33482 36562: contig of 3081 bp in length
*      36563 36662: gap of 100 bp
*      36663 40982: contig of 4320 bp in length
*      40983 41082: gap of 100 bp
*      41083 45520: contig of 4438 bp in length
*      45521 45620: gap of 100 bp
*      45621 50623: contig of 5003 bp in length
*      50624 50723: gap of 100 bp
*      50724 55610: contig of 4887 bp in length
*      55611 55710: gap of 100 bp
*      55711 61038: contig of 5328 bp in length
*      61039 61138: gap of 100 bp
*      61139 66159: contig of 5021 bp in length
*      66160 66259: gap of 100 bp
*      66260 73479: contig of 7220 bp in length
*      73480 73579: gap of 100 bp
*      73580 80554: contig of 6975 bp in length
*      80555 80654: gap of 100 bp
*      80655 89313: contig of 8659 bp in length
*      89314 89413: gap of 100 bp
*      89414 98132: contig of 8719 bp in length
*      98133 98232: gap of 100 bp
*      98233 107469: contig of 9237 bp in length

```

```

*      107470 107569: gap of 100 bp
*      107570 117873: contig of 10304 bp in length
*      117874 117973: gap of 100 bp
*      117974 130973: contig of 13000 bp in length
*      130974 131073: gap of 100 bp
*      131074 143236: contig of 12163 bp in length
*      143237 143336: gap of 100 bp
*      143337 154478: contig of 11142 bp in length
*      154479 154578: gap of 100 bp
*      154579 169967: contig of 15389 bp in length
*      169968 170067: gap of 100 bp
*      170068 187347: contig of 17280 bp in length
*      187348 187447: gap of 100 bp
*      187448 205736: contig of 18289 bp in length.

FEATURES
      Location/Qualifiers
      1..205736
        /organism="Homo sapiens"
        /db_xref="taxon:9606"
        /chromosome="17"
        /map="17"
        /clone="Rp11-85I20"
        /clone_lib="RPC1-11 Human Male BAC"
      1..1267
        misc_feature
      1368..2402
        misc_feature
      2503..3524
        misc_feature
      3625..4913
        misc_feature
      5014..6289
        misc_feature
      6390..7655
        misc_feature
      7756..9267
        misc_feature
      9368..11138
        misc_feature
      11239..13822
        misc_feature
      13923..16968
        misc_feature
      17069..20185
        misc_feature
      20286..22634
        misc_feature
      22735..27012
        misc_feature
      27113..29342
        misc_feature
      clone_end=T7
      vector_side:right
      29443..33381
        misc_feature
      33482..36562
        misc_feature
      36663..40982
        misc_feature
      41083..45520
        misc_feature
      45621..50623
        misc_feature
      50724..55610
        misc_feature
      55711..61038
        misc_feature
      61139..66159
        misc_feature
      66260..73479
        misc_feature
      73580..80554
        misc_feature
      80655..89313
        misc_feature

```



```
* 80655 89133: contig of 8659 bp in length
* 89314 89413: gap of 100 bp
* 89414 98132: contig of 8719 bp in length
* 98133 98232: gap of 100 bp
* 98233 107469: contig of 9237 bp in length
* 107470 107569: gap of 100 bp
* 107570 117873: contig of 10304 bp in length
* 117874 117973: gap of 100 bp
* 117974 130973: contig of 13000 bp in length
* 130974 131073: gap of 100 bp
* 131074 143236: contig of 12163 bp in length
* 143237 143336: gap of 100 bp
* 143337 154478: contig of 11142 bp in length
* 154479 154578: gap of 100 bp
* 154579 169967: contig of 15389 bp in length
* 169968 170067: gap of 100 bp
* 170068 187347: contig of 17280 bp in length
* 187348 187447: gap of 100 bp
* 187448 205736: contig of 18289 bp in length.
```

FEATURES

```
source
1..205736
    /organism="Homo sapiens"
    /db_xref="taxon:9606"
    /chromosome="17"
    /map="17"
    /clone="RP11-85120"
    /clone_lib="RPC1-11 Human Male BAC"
misc_feature
1..1267
    /note="assembly_fragment"
misc_feature
1368..2402
    /note="assembly_fragment"
misc_feature
2503..3524
    /note="assembly_fragment"
misc_feature
3625..4913
    /note="assembly_fragment"
misc_feature
5014..6289
    /note="assembly_fragment"
misc_feature
6390..7655
    /note="assembly_fragment"
misc_feature
7756..9267
    /note="assembly_fragment"
misc_feature
9368..11138
    /note="assembly_fragment"
misc_feature
11239..13822
    /note="assembly_fragment"
misc_feature
13923..16968
    /note="assembly_fragment"
misc_feature
17069..20185
    /note="assembly_fragment"
misc_feature
20286..22634
    /note="assembly_fragment"
misc_feature
22735..27012
    /note="assembly_fragment"
misc_feature
27113..29342
    /note="assembly_fragment"
    clone_end:77
    vector_side:right
misc_feature
29443..33381
    /note="assembly_fragment"
misc_feature
33482..35652
    /note="assembly_fragment"
misc_feature
36663..40982
    /note="assembly_fragment"
misc_feature
41083..45520
    /note="assembly_fragment"
misc_feature
45621..50623
    /note="assembly_fragment"
misc_feature
50724..55610
    /note="assembly_fragment"
misc_feature
55711..61038
    /note="assembly_fragment"
misc_feature
61139..66159
    /note="assembly_fragment"
```

```
misc_feature
66260..73479
    /note="assembly_fragment"
misc_feature
73580..80554
    /note="assembly_fragment"
misc_feature
80655..89313
    /note="assembly_fragment"
misc_feature
89414..98132
    /note="assembly_fragment"

Query Match
Best Local Similarity 5.2%; Score 65.4; DB 51; Length 205736;
Matches 114; Conservative 0; Mismatches 181; Indels 0; Gaps 0;

QY 179 aggaatgtgtcttcctgctatggaggatgcacagtggtgacgtgctccggtcacaggt 238
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 154301 AGGAGAGTGTGATGGAGAGGTGGAGATGCCTACTGTGCAGACTGTCTCTCAGGT 154360

QY 239 tcaaggagactgggggtctccagaaatgcaagccctgtctggactgcagtggtgaacc 298
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 154361 ACACAAGCAGCTGGGGCCACACACATGTCAGAGATGCATCACCTGTGCTCATCAATC 154420

QY 299 gcttcagaagcaaatgttccagccaccagtgatccatctctcggggactgttccag 358
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 154421 GCGTTCACAAGGTGAATGCGCACATACCTCTTAATGCTGTGTGGGACTGTGTGCCNN 154480

QY 359 gatttataggagacgaaactgtctggttcaagacatggagtggtgacctgtg99ag 418

Db 154481 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 154540

QY 419 acctctctctcttacgaaccgactgtgccagcaggctcaacctcgtgaagat 473
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 154541 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 154595
```

```
RESULT 14
AC034198/c
LOCUS
DEFINITION
AC034198 Homo sapiens chromosome 3 clone RP11-767C1 map 3p, WORKING DRAFT
SEQUENCE, 25 unordered pieces.
ACCESSION
AC034198
VERSION
AC034198.4 GI:10190766
KEYWORDS
HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 160214)
AUTHORS
Bao,J., Bao,Q., Bao,W., Bian,X., Cao,T., Chen,C., Chen,J., Ding,H.,
Dong,W., Fan,H., Feng,X., Guan,Q., Gu,X., Guo,D., He,L., Hu,S.,
Huang,F., Jin,Y., Kang,N., Li,C., Li,C., Li,G., Li,J., Li,L.,
Li,S., Li,T., Liu,Y., Liu,N., Liu,B., Liu,Y., Li,W., Li,W., Li,Y.,
Luo,J., Niu,Y., Qi,Q., Qi,X., Song,S., Sun,M., Sun,W., Sun,Y.,
Tao,R., Wang,H., Wang,J., Wang,J., Wang,L., Wang,L., Wang,R.,
Wang,X., Wang,X., Wang,Y., Wu,D., Wu,Q., Xie,F., Xuan,Z., Xue,Y.,
Yan,C., Yang,X., Yu,B., Zeng,Y., Zhang,G., Zhang,H., Zhang,H.,
Zhang,L., Zhang,M., Zhang,X., Zhang,X., Zhang,Y., Zhang,Y.,
Zhang,Z., Zhu,B., Yu,J. and Yang,H.
Unpublished
Chromosome 3p genomic sequence
TITLE
JOURNAL
REFERENCE
2 (bases 1 to 160214)
AUTHORS
Kang,N., Hu,S., Dong,W., Wang,J., Zhang,Y., Zhang,H., Liu,B.,
Bao,W., Sun,Y., Wu,Q., Wang,H., Yang,X., Cheng,C., Wang,Y., Niu,Y.,
Qi,X., Li,T., Zhang,H., Liu,N., Wu,D., Yu,B., Fan,H., Liu,Y.,
Li,G., Li,C., Bao,Q., Bao,J., Wang,X., Song,L., Zhang,L., Guo,D.,
Huang,F., Zhang,G., Li,J., Bian,X., Zhang,M., Li,L., Feng,X., Yu,J.
and Yang,H.
Direct Submission
Submitted (05-APR-2000) Human Genomic Center, Institute of
Genetics, Chinese Academy of Sciences, Datun Road, Beijing, Beijing
100101, P.R.China
COMMENT
On Sep 19, 2000 this sequence version replaced gi:8101278.
-----Genome Center
Center:Beijing Center
```


Query Match	3.4%	Score 43.6;	DB 54;	Length 160214;
Best Local Similarity	48.4%;	Pred. No. 0.74;		
Matches 121;	Conservative	0;	Mismatches 129;	Indels 0;
Gaps 0;				

Qy	637	tacaacggcctc	gagctgtcgtgtc	tttgacagac	ctcagctccac	gatatgccacaga	696

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 2, 2001, 03:55:46 ; Search time 553.05 Seconds

(without alignments)
861.976 Million cell updates/sec

Title: US-09-380-276a-1

Perfect score: 1269

Sequence: 1 atgctttaaagtact.....ggcagcgactgggttcctg 1269

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 480022 seqs, 187831343 residues

Total number of hits satisfying chosen parameters: 960044

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_36:*

- 1: /SID56/gcgdata/geneseq/geneseq/NA1980.DAT:*
- 2: /SID56/gcgdata/geneseq/geneseq/NA1981.DAT:*
- 3: /SID56/gcgdata/geneseq/geneseq/NA1982.DAT:*
- 4: /SID56/gcgdata/geneseq/geneseq/NA1983.DAT:*
- 5: /SID56/gcgdata/geneseq/geneseq/NA1984.DAT:*
- 6: /SID56/gcgdata/geneseq/geneseq/NA1985.DAT:*
- 7: /SID56/gcgdata/geneseq/geneseq/NA1986.DAT:*
- 8: /SID56/gcgdata/geneseq/geneseq/NA1987.DAT:*
- 9: /SID56/gcgdata/geneseq/geneseq/NA1988.DAT:*
- 10: /SID56/gcgdata/geneseq/geneseq/NA1989.DAT:*
- 11: /SID56/gcgdata/geneseq/geneseq/NA1990.DAT:*
- 12: /SID56/gcgdata/geneseq/geneseq/NA1991.DAT:*
- 13: /SID56/gcgdata/geneseq/geneseq/NA1992.DAT:*
- 14: /SID56/gcgdata/geneseq/geneseq/NA1993.DAT:*
- 15: /SID56/gcgdata/geneseq/geneseq/NA1994.DAT:*
- 16: /SID56/gcgdata/geneseq/geneseq/NA1995.DAT:*
- 17: /SID56/gcgdata/geneseq/geneseq/NA1996.DAT:*
- 18: /SID56/gcgdata/geneseq/geneseq/NA1997.DAT:*
- 19: /SID56/gcgdata/geneseq/geneseq/NA1998.DAT:*
- 20: /SID56/gcgdata/geneseq/geneseq/NA1999.DAT:*
- 21: /SID56/gcgdata/geneseq/geneseq/NA2000.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1269	100.0	1496	19	V33362 Nucleotide sequenc
2	1267.4	99.9	1502	20	X08689 Novel nucleotide s
3	1256.2	99.0	1489	20	X23415 Human hAPO4-alpha
4	1244.8	98.1	1704	19	V33361 Nucleotide sequenc
5	1240	97.7	2185	20	X24978 Human TRAIN-R cDNA
6	835.6	65.8	987	20	X59346 Human NTR-5 cDNA
7	729.2	57.5	1678	20	X23413 Mouse mAPO4-alpha
8	449	35.4	886	20	X23414 Mouse mAPO4-alpha
9	449	35.4	942	20	X24977 Mouse TRAIN-R (lon
10	449	35.4	981	20	X87394 Mouse STRIFE1 (Tan
11	435.4	34.3	893	20	X84622 Human TNFR superfa
12	362.6	28.6	538	20	X59345 Mouse NTR-5 cDNA.

13	361.6	28.5	371	19	V11422 Human secreted pro
14	314	24.7	591	20	X23417 Mouse mAPO4-gamma
15	314	24.7	599	20	X24976 Mouse TRAIN-R (sho
16	314	24.7	623	20	X84623 Mouse TNFR superfa
17	314	24.7	636	21	X29408 cDNA encoding murI
18	314	24.7	655	20	X87395 Mouse STRIFE2 (Tan
19	154.8	12.2	932	21	X24111 cDNA encoding huma
20	121.8	9.6	1133	20	X23416 Rat rAPO4-alpha DN
21	90.4	7.1	791	20	X24979 Clone GJ156 encodi
22	87.4	6.9	181	19	V11423 Human secreted pro
23	87.4	6.9	201	20	EST clone AX92. H
24	82	6.5	396	20	X23418 Mouse mAPO4-beta D
25	81.2	6.4	546	21	X29410 cDNA encoding huma
26	77.8	6.1	474	21	X29409 cDNA encoding huma
27	44	3.5	10732	21	A10594 Gene encoding a su
28	37.4	2.9	1290	20	X23121 Human TANGO 129 (T
29	37.4	2.9	2570	20	X23120 Human TANGO 129 (T
30	37.4	2.9	2703	21	D00061 Human tumour necro
31	36.4	2.9	1602	15	Q72217 Human adrenegic r
32	36.4	2.9	1978	15	Q72212 Truncated human al
33	36.4	2.9	1987	16	T11624 Human truncated al
34	36.4	2.9	1997	16	T11600 Human alpha-1C adr
35	36.4	2.9	1998	15	Q72213 Human alpha-1C adr
36	36.4	2.9	2004	16	T11599 Human alpha-1C adr
37	36.4	2.9	2005	15	Q72211 Human alpha-1C adr
38	36.2	2.9	330	21	A15982 Human protein clon
39	36.2	2.9	659	21	A15992 Human neurotransmi
40	36.2	2.9	2486	17	T09866 DNA methyltransfer
41	36	2.8	2067	20	V99092 DNA methyltransfer
42	36	2.8	19440	20	V99129 Streptomyces hygro
43	35.6	2.8	1150	20	Z06928 Human cytoskeletal
44	35.2	2.8	1050	21	Z58975 Fragment 41-3 of t
45	35	2.8	326	11	Q05546

ALIGNMENTS

RESULT 1	
V33362	
ID V33362 standard; cDNA to mRNA; 1496 BP.	
XX	
AC V33362;	
XX	
DT 02-DEC-1998 (first entry)	
XX	
DE Nucleotide sequence of human beta-OAF065.	
XX	
KW Human; beta-OAF065; stroma cell; antibody; inflammatory;	
KW cytokine-mediated disease; rheumatism; ulcerative colitis; ss.	
XX	
OS Homo sapiens.	
XX	
EH Key Location/Qualifiers	
FT CDS 45..1316	
FT	/*tag= a
FT	/product= "human beta-OAF065 protein"
FT	45..119
FT	/*tag= b
FT	mat_peptide 120..1313
FT	/*tag= c
FT	
FT	/transl_except= (pos:711..713, aa= Pro)
FT	/transl_except= (pos:714..716, aa= Arg)
XX	
PN W09838304-A1.	
XX	
PD 03-SEP-1998.	
XX	
PF 26-FEB-1998; 98WO-JP00799.	
XX	
PR 27-FEB-1997; 97JP-0043143.	
XX	
PA (ONOY) ONO PHARM CO LTD.	

XX Fukushima D, Konishi M, Tada H;
XX WPI: 1998-481205/41.
DR P-PSDB; W70387.
XX
PT Membrane polypeptide expressed by human stroma cells, and antibodies
PT recognising it - for treatment of inflammatory and other
PT cytokine-mediated diseases.
XX
PS Disclosure; Pages 40-41; 54pp; Japanese.
XX
CC This is the nucleotide sequence of the human beta-OAF065, used in
CC the method of the invention. The process involves the use of peptides
CC expressed by stroma cells, and its antibodies are used for in the
CC prevention and treatment of inflammatory and other cytokine-mediated
CC diseases such as rheumatism, ulcerative colitis.
XX
SQ Sequence 1496 BP; 388 A; 360 C; 372 G; 376 T; 0 other;

Query Match 100.0%; Score 1269; DB 19; Length 1496;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1269; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 atggctttaaaagtgtctactagacaagaagaaaacgtttttcactcttttagtattacta 60
DB 45 atggctttaaaagtgtctactagacaagaagaaaacgtttttcactcttttagtattacta 104
QY 61 ggcattttgtcattgaagtgtctgtgaaacaggagactgtgacagcaagaattcagg 120
DB 105 ggcattttgtcattgaagtgtctgtgaaacaggagactgtgacagcaagaattcagg 164
QY 121 gatcgtctgaaactgtgttcctgcacacagatgtggccagcagatgagttgtctaa 180
DB 165 gatcgtctgaaactgtgttcctgcacacagatgtggccagcagatgagttgtctaa 224
QY 181 gaatgtgcttcgctatgggaggtgacagtggtgacgtgcccgtgcagagttc 240
DB 225 gaatgtgcttcgctatgggaggtgacagtggtgacgtgcccgtgcagagttc 284
QY 241 aaggagagactggggtctccagaataatgaaacccctgtctggaactgcagtggaaccc 300
DB 285 aaggagagactggggtctccagaataatgaaacccctgtctggaactgcagtggaaccc 344
QY 301 ttccagaagcaaatgttcagccacagtgatgccatctgcgggaactgtgccagga 360
DB 345 ttccagaagcaaatgttcagccacagtgatgccatctgcgggaactgtgccagga 404
QY 361 ttctataggaagcgaataatgtcggctttcagaagacatggagtgtgtccttggagac 420
DB 405 ttctataggaagcgaataatgtcggctttcagaagacatggagtgtgtccttggagac 464
QY 421 cctcctcctcttcagaacgcgactgtgccagaagaatgcaacctcgtgaagatcgcttc 480
DB 465 cctcctcctcttcagaacgcgactgtgccagaagaatgcaacctcgtgaagatcgcttc 524
QY 481 acggctccagccagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 540
DB 525 acggctccagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 584
QY 541 gtctgtggtccctgtcctcctcctgtgtctatctattgttaagagacagtttatggaga 600
DB 585 gtctgtggtccctgtcctcctcctgtgtctatctattgttaagagacagtttatggaga 644
QY 601 aaacccagctgtgtctgtcgtggttcacaggacattcagtaaacagcgtctgtagctgtc 660
DB 645 aaacccagctgtgtctgtcgtggttcacaggacattcagtaaacagcgtctgtagctgt 704
QY 661 ctgtgacagacctcagctccacgaatgcccacagacagcagcagcagcagcagcagcag 720
DB 705 ctgtgacagacctcagctccacgaatgcccacagacagcagcagcagcagcagcagcag 764

QY 721 tcagtgcagacctgcggccggtgcgcttgcctccatgccttccttccttccttccttccttc 780
DB 765 tcagtgcagacctgcggccggtgcgcttgccttccttccttccttccttccttccttcct 824
QY 781 agcccaaaccccgagcactcttgggtgtgagtgatcttcgagccagcttccttcggaaga 840
DB 825 agcccaaaccccgagcactcttgggtgtgagtgatcttcgagccagcttccttcggaaga 884
QY 841 aacgcagggcccgagcgggagatggtgcgacatttcttcggatcccttcacgagctccatc 900
DB 885 aacgcagggcccgagcgggagatggtgcgacatttcttcggatcccttcacgagctccatc 944
QY 901 tggcgaggttttcagatgcctgcctcttcgattcacaatagcagtcagatttgggtggcgtgt 960
DB 945 tggcgaggttttcagatgcctgcctcttcgattcacaatagcagtcagatttgggtggcgtgt 1004
QY 961 tcttttggactcttcctgaactcactgcagtcagtcagtcagtcagtcagtcagtcagtcag 1020
DB 1005 tcttttggactcttcctgaactcactgcagtcagtcagtcagtcagtcagtcagtcagtcag 1064
QY 1021 ctggaagctcaacgtcttttggattcacaatagcagtcagatttgggtggcgtgt 1080
DB 1065 ctggaagctcaacgtcttttggattcacaatagcagtcagatttgggtggcgtgt 1124
QY 1081 ccagtcagctctctctctgaaactttacagcagctcactgatttctatagataaacaac 1140
DB 1125 ccagtcagctctctctgaaactttacagcagctcactgatttctatagataaacaac 1184
QY 1141 acactgtgagaaatcagcatcaactcaggatgcactaactatgagaagccagctagatcag 1200
DB 1185 acactgtgagaaatcagcatcaactcaggatgcactaactatgagaagccagctagatcag 1244
QY 1201 gagagtggtgctatccaccagcactcagcagcagcagcagcagcagcagcagcagcagcag 1260
DB 1245 gagagtggtgctatccaccagcactcagcagcagcagcagcagcagcagcagcagcagcag 1304
QY 1261 ggttcctctg 1269
DB 1305 ggttcctctg 1313

RESULT 2
X08689
ID X08689 standard; cDNA; 1502 BP.
XX
AC X08689;
XX
XX 27-SEP-1999 (first entry)
XX
DE Novel nucleotide sequence encoding new protein (Clone AX92_3).
XX
KW Polynucleotide; protein; nutrition; cytokine; cell proliferation;
KW cell differentiation; immunostimulation; immunosuppression;
KW haematopoiesis regulation; tissue growth; activin; inhibitor;
KW chemotaxis; chemokinesis; haemostasis; thrombolysis; receptor;
KW ligand; anti-inflammatory; tumour suppression; gene therapy; ds.
XX
OS Homo sapiens.
XX
XX
FH Key Location/Qualifiers
CDS 51..1322
FT /*tag= a
FT /product= "Novel protein"
XX
PN WO9920644-A1.
XX
XX 29-APR-1999.
XX
XX 16-OCT-1998; 98WO-US22034.
XX
XX 18-OCT-1997; 97US-0955557.
XX
XX (GEM) GENETICS INST INC.

XX Agostino MJ, Bowman MR, Evans C, Jacobs K, Lavallie ER;
 PI McCoy JM, Merberg D, Racie LA, Spaulding V, Treacy M;
 XX
 DR WPI: 1999-288272/24.
 XX P-PSDB: W85724.
 XX
 XX New polynucleotides encoding secreted human proteins
 PS Claim 32; Page 116; 136pp; English.
 XX
 CC The new human secreted proteins are encoded by polynucleotides
 CC obtained from human placenta, adult testes, fetal kidney, fetal
 CC brain, adult brain, adult brain and adult blood cDNA libraries.
 CC The polynucleotides and proteins are predicted to have biological
 CC activities which would make them suitable for treating, preventing or
 CC ameliorating medical conditions in humans and animals. Suggested
 CC activities include nutritional activity, cytokine and cell
 CC proliferation/differentiation activity, immune stimulating (e.g. as
 CC vaccines) or suppressing activity, haematopoiesis regulating
 CC activity, tissue growth activity, activin/inhibin activity,
 CC chemotactic/chemokinetic activity, haemostatic and thrombolytic
 CC activity, receptor/ligand activity, anti-inflammatory activity,
 CC adherin/tumour invasion suppressor activity, and tumour inhibition
 CC activity. The polynucleotides are also stated to be useful for gene
 CC therapy. The sequences are identified by a secretory leader
 CC sequence motif in the polynucleotide and it is thought that the
 CC encoded proteins have biological activity by virtue of their secreted
 CC nature. This clone was designated AX92.3. A probe for this clone is
 CC described in X08704.
 XX
 SQ Sequence 1502 BP; 388 A; 362 C; 375 G; 377 T; 0 other;

Query Match
 Best Local Similarity 99.9%; Score 1267.4; DB 20; Length 1502;
 Matches 1268; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 atgctttaaagtctactagaacagagaaaacgttttcaactcttttagtattacta 60
 Db
 Qy 61 ggctatttgcattgtaaaagtactgtgaacagagagactgtacacagcaagaattcagg 120
 Db
 Qy 111 ggcatttgcattgtaaaagtactgtgaacagagagactgtacacagcaagaattcagg 170
 Qy 121 gatcggtctgaaactgttctccctgcacacagtggtgcccaggtgagttgtcttaag 180
 Db 171 gatcggtctgaaactgttctccctgcacacagtggtgcccaggtgagttgtcttaag 230
 Qy 181 gaatggtctcggtctatgggagagatgcacagtggtgacgtgcggtgcacaggttc 240
 Db 231 gaatggtctcggtctatgggagagatgcacagtggtgacgtgcggtgcacaggttc 290
 Qy 241 aagagagactgggtcttcagaaaaatgaagccctgtctggactgcggtggtgaacgcg 300
 Db 291 aagagagactgggtcttcagaaaaatgaagccctgtctggactgcggtggtgaacgcg 350
 Qy 301 ttccagaaggcaaatgttccagccaccagtgatgcacatctcggtggagctgcttcaggga 360
 Db 351 ttccagaaggcaaatgttccagccaccagtgatgcacatctcggtggagctgcttcaggga 410
 Qy 361 tttatagaagacgaaactgtcgttttcaagacatggagtggtgcttctgtggagac 420
 Db 411 tttatagaagacgaaactgtcgttttcaagacatggagtggtgcttctgtggagac 470
 Qy 421 cctctcctccttaccagccgactgtgtccagcaaggtcaacctgtgtaagatcgctgcc 480
 Db 471 cctctcctccttaccagccgactgtgtccagcaaggtcaacctgtgtaagatcgctgcc 530
 Qy 481 acgggctccagccacgggacacgctgctgctgcgttatctgcagcgcctgtgcccacc 540
 Db 531 acgggctccagccacgggacacgctgctgctgcgttatctgcagcgcctgtgcccacc 590

Qy 541 gtccctgctggccctgtcctcatcctctgtctcatctattgttaagagacagatttatgagaag 600
 Db 591 gtccctgctggccctgtcctcatcctctgtctcatctattgttaagagacagatttatgagaag 650
 Qy 601 aaacccagctggtctctgctgggtcagcagacattcagtaacacggctctgagctgctgtg 660
 Db 651 aaacccagctggtctctgctgggtcagcagacattcagtaacacggctctgagctgctgtg 710
 Qy 661 cttgacagacctcagctccacgaatatgccacagagacctgtccagctgcgcgtgac 720
 Db 711 cttgacagacctcagctccacgaatatgccacagagacctgtccagctgcgcgtgac 770
 Qy 721 tcagtgcagacctgcggccggtgcgctgtgctccatccatgctgtgagagagcctgc 780
 Db 771 tcagtgcagacctgcggccggtgcgctgtgctccatccatgctgtgagagagcctgc 830
 Qy 781 agccccaacccggcgactcttgggtggtggtgcttctgcagcagctcttcaggcaaga 840
 Db 831 agccccaacccggcgactcttgggtggtggtgcttctgcagcagctcttcaggcaaga 890
 Qy 841 aacgcagcccgagcgggagatggtgccgacttcttcgactccctcacgagctccacc 900
 Db 891 aacgcagcccgagcgggagatggtgccgacttcttcgactccctcacgagctccacc 950
 Qy 901 tgtggcgagtttccagatgcctgctctgcagaaatcccatgggtggtgacaacatc 960
 Db 951 tgtggcgagtttccagatgcctgctctgcagaaatcccatgggtggtgacaacatc 1010
 Qy 961 tcttttgcgactcttctgaaactcactgcagagacatcattctctcaatccagaa 1020
 Db 1011 tcttttgcgactcttctgaaactcactgcagagacatcattctctcaatccagaa 1070
 Qy 1021 cttgaaactcaagctcttggattcaaatagcagctcaagatttgggtgggctctt 1080
 Db 1071 cttgaaactcaagctcttggattcaaatagcagctcaagatttgggtgggctctt 1130
 Qy 1081 ccagtcctcagctctctgaaactttacagcagctactgtattctatagataaacac 1140
 Db 1131 ccagtcctcagctctctgaaactttacagcagctactgtattctatagataaacac 1190
 Qy 1141 acactggtagaaatcagcactcactcagcagatgcactaactatgagaagcagctagatcag 1200
 Db 1191 acactggtagaaatcagcactcactcagcagatgcactaactatgagaagcagctagatcag 1250
 Qy 1201 gagagtggtcgtatcatccacccagcactcagacgttccctccaggttaaggcagcagctg 1260
 Db 1251 gagagtggtcgtatcatccacccagcactcagacgttccctccaggttaaggcagcagctg 1310
 Qy 1261 ggttccctg 1269
 Db 1311 ggttccctg 1319

RESULT 3
 X23415
 ID X23415 standard; DNA; 1489 BP.
 XX
 AC X23415;
 XX
 DT 18-JUN-1999 (first entry)
 XX
 DE Human HAP04-alpha DNA.
 XX
 KW Tumour necrosis factor receptor; signal transducer molecule; TNF; APO4;
 KW developmental abnormality; gestational abnormality; prostate cancer;
 KW APO6; APO8; APO9; TNRL-1; TNRL-3; diagnosis; treatment; therapy; disease;
 KW cytoplasmic domain; immunogen; antibody preparation; breast carcinoma;
 KW apoptosis; human; APO4-alpha; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers

FT	CDS	65..1336	
FT	FT	/tag= a	
FT	FT	/product= "hAPO4-alpha"	
XX	XX	WO9911791-A2.	
XX	XX	11-MAR-1999.	
PD	XX	04-SEP-1998; 98WO-US18393.	
PF	XX	05-SEP-1997; 97US-0924634.	
XX	XX	(UNIW) UNIV WASHINGTON.	
XX	XX	Chaudhary PM;	
XX	XX	WPI; 1999-205191/17.	
DR	DR	P-PSDB; W93581.	
XX	XX	New Tumor Necrosis Factor family receptor polypeptides and ligands -	
PT	PT	useful for diagnosis and treatment of prostate cancer and	
PT	PT	developmental or gestational abnormalities	
XX	XX	Example IV; Fig 7C; 156pp; English.	
PS	XX	This invention describes isolated Tumor Necrosis Factor (TNF) family	
XX	CC	receptor polypeptides; APO4, APO6, APO8 and APO9 or their active	
CC	CC	fragments, and isolated TNF related ligands 1 and 3 (TNRL1 and TNRL3) or	
CC	CC	their active fragments. APO4 is useful for diagnosing prostate cancer	
CC	CC	by determining levels of APO4 in an individual. Prostate cancer can also	
CC	CC	be treated using APO4 selective binding agents linked to a therapeutic	
CC	CC	moiety. APO4 polypeptides are also useful for identifying selective	
CC	CC	binding agents, useful in diagnosis/treatment of disease by binding of	
CC	CC	agents to the polypeptide/active fragment which is extracellular, or	
CC	CC	expressed on the cell surface. The binding is preferably performed in	
CC	CC	vivo. APO4 polypeptides/ active fragments are also useful for screening	
CC	CC	for agonists and antagonists by binding and observing the change in APO4	
CC	CC	activity. Effective pharmacological agents useful in diagnosis or	
CC	CC	treatment of disease are also identified using APO4 polypeptides/active	
CC	CC	fragments and APO4 signal transducer molecules that specifically interact	
CC	CC	with a cytoplasmic domain of APO4 and detecting a change in level of APO4	
CC	CC	activity. The method is performed in vivo or in vitro. APO polypeptides	
CC	CC	are all useful as immunogens for preparing antibodies. APO4 is also	
CC	CC	useful for diagnosis/treatment of developmental or gestational	
CC	CC	abnormalities. APO8 was transfected to human breast carcinoma cell line	
CC	CC	MCF-7, and induced apoptosis.	
XX	XX	Sequence 1489 BP; 361 A; 366 C; 380 G; 382 T; 0 other;	
SQ			
	Query Match	99.0%; Score 1256.2; DB 20; Length 1489;	
	Best Local Similarity	99.4%; Pred. No. 0;	
	Matches 1261; Conservative	0; Mismatches 8; Indels 0; Gaps 0;	
QY	1	atggcctttaaagtgtacttagaacaagagaaacgtttttcactcttttagtattacta 60	
DB	65	atggcctttaaagtgtacttagaacaagagaaacgtttttcactcttttagtattacta 124	
QY	61	ggctatttgcataaagtgaactgtgtaacacagagagactgtagacagcaagaattcagg 120	
DB	125	ggctatttgcataaagtgaactgtgtaacacagagagactgtagacagcaagaattcagg 184	
QY	121	gacggcttgaaactgtgtccctgcacacagctgtggccagcagtgaggtgtctaag 180	
DB	185	gacggcttgaaactgtgtccctgcacacagctgtggccagcagtgaggtgtctaag 244	
QY	181	gaatgtggcttcggctatggggaggatgcacagtggtgtgacgtgcccgtgcacaggttc 240	
DB	245	gaatgtggcttcggctatggggaggatgcacagtggtgtgacgtgcccgtgcacaggttc 304	
QY	241	aaggagagactggggctccagaataacagacccctgtctgagactgcagtggtgaaccgc 300	
DB	305	aaggagagactggggctccagaataacagacccctgtctgagactgcagtggtgaaccgc 364	

RESULT 4
V33361
ID V33361 standard; cDNA to mRNA; 1704 BP.

QY	301	tttcagaagggcaaatgtttcagccaccagtgtgcccattctgcggggagctgttgcacaga 360	
DB	365	tttcagaagggcaaatgtttcagccaccagtgtgcccattctgcggggagctgttgcacaga 424	
QY	361	ttttataggaagacgaacttgcggctttcagagacatggagtgtgtccttctgttgagac 420	
DB	425	ttttataggaagacgaacttgcggctttcagagacatggagtgtgtccttctgttgagac 484	
QY	421	ctctctctcttctttagaaccgcactgtgcacgaaggtcaaacctcgtgaagatcgcgtcc 480	
DB	485	ctctctctcttctttagaaccgcactgtgcacgaaggtcaaacctcgtgaagatcgcgtcc 544	
QY	481	acggcctccagccacgggacacgcgcgtggtggtccgtttatctgcagcgtctctggccacc 540	
DB	545	acggcctccagccacgggacacgcgcgtggtggtccgtttatctgcagcgtctctggccacc 604	
QY	541	gtcctgtgcccctgcctcatctctgtgtcatctatttgaagagacagtttatgggaag 600	
DB	605	gtcctgtgcccctgcctcatctctgtgtcatctatttgaagagacagtttatgggaag 664	
QY	601	aaacccagctgtctctgcgggtcaacagacattcagatacaacggctctcgtcgtcgt 660	
DB	665	aaacccagctgtctctgcgggtcaacagacattcagatacaacggctcgtcgtcgt 724	
QY	661	cttgacagacctcagctccacgaatatgccacagagcctgctgccagtgccgcctgac 720	
DB	725	tttgacagacctcagctccacgaatatgccacagagcctgctgccagtgccgcctgac 784	
QY	721	tcagtgcagacctgcggcggtgcgttgcctcccatccatgctgctgtgagagggcctgc 780	
DB	785	tcagtgcagacctgcggcggtgcgttgcctcccatccatgctgctgtgagagggcctgc 844	
QY	781	agcccaaccccgagcactttggtgtgggtgcatcttgcagcagcttccaggaaga 840	
DB	845	agcccaaccccgagcactttggtgtgggtgcatcttgcagcagcttccaggaaga 904	
QY	841	aacgcagggccacggcggtgagatggtgcgcgactttctcggaacctccacgcagtcac 900	
DB	905	aacgcagggccacggcggtgagatggtgcgcgactttctcggaacctccacgcagtcac 964	
QY	901	tgtggcgagttttcagatgcctggcctctctgacagaaatcccatgggtggtgacaaac 960	
DB	965	tgtggcgagttttcagatgcctggcctctctgacagaaatcccatgggtggtgacaaac 1024	
QY	961	cttttctgactcttctcgaactcactggagagacattcattctctcattccagaa 1020	
DB	1025	cttttctgactcttctcgaactcactggagagacattcattctctcattccagaa 1084	
QY	1021	cttgaagctcaacgtcttttgattcaaatagcagtcgaagatttggtggggcgtgtt 1080	
DB	1085	cttgaagctcaacgtcttttgattcaaatagcagtcgaagatttggtggggcgtgtt 1144	
QY	1081	ccagtcagctctcattctgaaactttacagcagctactgatttactatagataaacac 1140	
DB	1145	ccagtcagctctcattctgaaactttacagcagctactgatttactatagataaacac 1204	
QY	1141	acactgtgagaatcagcatcaactcaggatgcaactaatcagagccagctagatcag 1200	
DB	1205	acactgtgagaatcagcatcaactcaggatgcaactaatcagagccagctagatcag 1264	
QY	1201	gagagtggcgctatctccaccagcactcagacgtccctccaggaaggcagcagctg 1260	
DB	1265	gagagtggcgctatctccaccagcactcagacgtccctccaggaaggcagcagctg 1324	
QY	1261	ggttccctg 1269	
DB	1325	ggttccctg 1333	

```

XX AC V33361;
XX DT 02-DEC-1998 (first entry)
XX DE Nucleotide sequence of human alpha-OAF065.
XX KW Human; alpha-OAF065; stroma cell; antibody; inflammatory;
XX OS cytokine-mediated disease; rheumatism; ulcerative colitis; ss.
XX PH Homo sapiens.
XX FT Key Location/Qualifiers
XX FT CDS 45..1298
XX FT /*tag= a
XX FT /product= "human alpha-OAF065 protein"
XX FT sig_peptide 45..119
XX FT /*tag= b
XX FT mat_peptide 120..1295
XX FT /*tag= c
XX FT /transl_except= (pos:711..713, aa= Pro)
XX FT /transl_except= (pos:714..716, aa= Arg)
XX PN W09838304-A1.
XX PD 03-SEP-1998.
XX PF 26-FEB-1998; 98WO-JP00799.
XX PR 27-FEB-1997; 97JP-0043143.
XX PA (ONOI ) ONO PHARM CO LTD.
XX PI Fukushima D, Konishi M, Tada H;
XX DR WPI: 1998-481205/41.
XX DR P-FSDb; W70386.
XX PT Membrane polypeptide expressed by human stroma cells, and antibodies
XX PT recognising it - for treatment of inflammatory and other
XX PS cytokine-mediated diseases.
XX PS Claim 5; Pages 31-32; 54pp; Japanese.
XX CC This is the nucleotide sequence of the human alpha-OAF065, used in
XX CC the method of the invention. The process involves the use of peptides
XX CC expressed by stroma cells, and its antibodies are used for in the
XX CC prevention and treatment of inflammatory and other cytokine-mediated
XX CC diseases such as rheumatism, ulcerative colitis.
XX SO Sequence 1704 BP; 429 A; 426 C; 430 G; 419 T; 0 other;

Query Match 98.18; Score 1244.8; DB 19; Length 1704;
Best Local Similarity 99.88; Pred. No. 0;
Matches 1246; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 atggcttttaaagtgtactgaacagagaaacgtttttcaactcttttagtattacta 60
Db 45 atggcttttaaagtgtactgaacagagaaacgtttttcaactcttttagtattacta 104
Qy 61 ggcattttgtcatgtaaagtactgtgaaacaggagagacttagacagaaattcagg 120
Db 105 ggcattttgtcatgtaaagtactgtgaaacaggagagacttagacagaaattcagg 164
Qy 121 gatcggtctgaactgttccctgcaacacagatgtggccaggcatgtgtcttaag 180
Db 165 gatcggtctgaactgttccctgcaacacagatgtggccaggcatgtgtcttaag 224
Qy 181 gaattggtcttcgctatgggagagatgcacagtgtgtgacgtgcggtgcacaggttc 240
Db 225 gaattggtcttcgctatgggagagatgcacagtgtgtgacgtgcggtgcacaggttc 284

```

RESULT 5
X24978
ID X24978 standard; cDNA; 2185 BP.
XX

AC X24978;
 XX
 DT 05-JUL-1999 (first entry)
 XX
 DE Human TRAIN-R cDNA.
 XX
 KW TRAIN-R; receptor; human; tumour necrosis factor receptor;
 KW agonist; antagonist; cancer; immunological disease; therapy;
 KW cytostatic; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT 179..1432
 FT CDS /*tag= a
 FT sig_peptide 179..253
 FT /*tag= b
 FT mat_peptide 254..1429
 FT /*tag= c
 XX
 PN WO9913078-A1.
 XX
 PD 18-MAR-1999.
 XX
 PF 11-SEP-1998; 98WO-US19030.
 XX
 PR 06-MAY-1998; 98US-0084422.
 PR 12-SEP-1997; 97US-0058631.
 XX.
 PA (BIOJ) BIOGEN INC.
 XX
 PI Hession C, Tschoep J;
 XX
 XX WPI: 1999-229238/19.
 DR P-PSDB; W98146.
 XX
 PT New cysteine-rich tumor necrosis factor receptor
 XX
 PS Claim 1; Page 27; 30pp; English.
 XX
 CC The present sequence encodes a novel human cysteine-rich tumour
 CC necrosis factor receptor family member termed TRAIN-R (see W98146).
 CC It is a composite of 2 overlapping lambda gt10 clones (GJ159 and
 CC GJ158) from a Clontech human adult lung cDNA library. Human
 CC TRAIN-R was also cloned from a second sequence subclone of a
 CC lambda gt10 cDNA (GJ156, see X24979). Human TRAIN-R is expressed
 CC at low levels in every tissue and cell line tested thus far, with
 CC higher expression detected in heart, prostate, ovary, testis,
 CC peripheral blood lymphocytes, thymoid and adrenal gland.
 CC Cell death can be induced by administering an agent capable of
 CC inhibiting the binding of TRAIN-R to its ligand. A claimed method
 CC of treating, or reducing, the advancement, severity or effects of
 CC an immunological disease in a mammal comprises administering a
 CC pharmaceutical composition which comprises a TRAIN-R blocking agent,
 CC e.g. soluble TRAIN-R. TRAIN-R can be fused to an immunoglobulin to
 CC produce a fusion protein which may be targeted to various sites.
 CC It can be used in binding assays, and to identify antagonists and
 CC agonists. Anti-TRAIN-R antibodies can be used to reduce the
 CC severity of an immune response or to treat cancer. TRAIN-R
 CC blocking agents can also be used to reduce the severity or effects
 CC of an immunological disease (all claimed).
 XX
 SQ Sequence 2185 BP; 546 A; 551 C; 550 G; 538 T; 0 Other;

Query Match 97.7%; Score 1240; DB 20; Length 2185;
 Best Local Similarity 99.6%; Pred. No. 0;
 Matches 1243; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 1 atggctttaaagtgtactagacaagagaaaacgttttcaactcttttagtattacta 60
 DB 179 atggctttaaagtgtactagacaagagaaaacgttttcaactcttttagtattacta 238

QY 61 ggctattgtcatgtaaagtgtactgtgaaacagagagactgtagacagcaaatcagg 120
 DB 239 ggctattgtcatgtaaagtgtactgtgaaacagagagactgtagacagcaaatcagg 298
 QY 121 gatcggctggaactgtgttccctgcaaccagtggtggccagggaatgagttgtctaaag 180
 DB 299 gatcggctggaactgtgttccctgcaaccagtggtggccagggaatgagttgtctaaag 358
 QY 181 gaatgtggtctcggtatggtggagagatgcacagtgtgtacgtgcgcggtgcacaggttc 240
 DB 359 gaatgtggtctcggtatggtggagagatgcacagtgtgtacgtgcgcggtgcacaggttc 418
 QY 241 aaggaggactggggtccagaaatcgaagccctgtctggaactgcagctgggtgaaccgc 300
 DB 419 aaggaggactggggtccagaaatcgaagccctgtctggaactgcagctgggtgaaccgc 478
 QY 301 ttccagaaggcaaatgttccagccaccagtgtgcccactctgcggggaactgtgtgccagga 360
 DB 479 ttccagaaggcaaatgttccagccaccagtgtgcccactctgcggggaactgtgtgccagga 538
 QY 361 ttttataggaagaagaacttgcggttccagacatgagatgtgtgcttctgtggagac 420
 DB 539 ttttataggaagaagaacttgcggttccagacatgagatgtgtgcttctgtggagac 598
 QY 421 cctctctctcttaacgaacgcactgtgccagcaagtcaacctgtgaagatcgcgtcc 480
 DB 599 cctctctctcttaacgaacgcactgtgccagcaagtcaacctgtgaagatcgcgtcc 658
 QY 481 acggcctccagccacgggacacggcgctggtgcgcttatctgcagcgtctgtggccacc 540
 DB 659 acggcctccagccacgggacacggcgctggtgcgcttatctgcagcgtctgtggccacc 718
 QY 541 gtccgtgtggcctgtctatctctgtgtcattctattgttaagagacagtttatggagaag 600
 DB 719 gtccgtgtggcctgtctatctctgtgtcattctattgttaagagacagtttatggagaag 778
 QY 601 aaaccagctggtctctgcgtcacaggacattcagataacggctctgtgctgtgt 660
 DB 779 aaaccagctggtctctgcgtcacaggacattcagataacggctctgtgctgtgt 838
 QY 661 ctgtgacagacctcagctccacgaatatgccacagagcgtgtgtccagtgccgcgtgtgac 720
 DB 839 ttgtgacagacctcagctccacgaatatgccacagagcgtgtgtccagtgccgcgtgtgac 898
 QY 721 tcagtgcacacctgcggcggt 780
 DB 899 tcagtgcacacctgcggcggt 958
 QY 781 agcccaaccccgcgactcttgggt 840
 DB 959 agcccaaccccgcgactcttgggt 1018
 QY 841 aagcagggcccgccggggagatggtgtgcgacttttcttggtatccctcagcagtcacac 900
 DB 1019 aagcagggcccgccggggagatggtgtgcgacttttcttggtatccctcagcagtcacac 1078
 QY 901 tgtggcgagttttcagatccctgcgtctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 960
 DB 1079 tgtggcgagttttcagatccctgcgtctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1138
 QY 961 tctttttgtgactcttctatctgaactcactgcgagagacattcattctctcaatccagaa 1020
 DB 1139 tctttttgtgactcttctatctgaactcactgcgagagacattcattctctcaatccagaa 1198
 QY 1021 ctgtgaagctcaacgtcttctgtgattcaaatagcagccaagatttgggtgtgtgtgtgtgtgtgt 1080
 DB 1199 ctgtgaagctcaacgtcttctgtgattcaaatagcagccaagatttgggtgtgtgtgtgtgtgtgt 1258
 QY 1081 ccagtcacagctcattctgaaaaactttacagcagctactgatttattctagatataacaac 1140
 DB 1259 ccagtcacagctcattctgaaaaactttacagcagctactgatttattctagatataacaac 1318
 QY 1141 acaactggtagaatcagcatcaactcaggatgcactaactatgagagcagcagctagatcag 1200

Db 1319 acactggttagaatacagcatcaactcagatgcactaactatgagagccagtagatcag 1378
Qy 1201 gagagtgcgtatcatccaccagccactcagacgtccctccaggtta 1248
Db 1379 gagagtgcgtctgtcatccaccagccactcagacgtccctccaggtta 1426

RESULT 6
X59346
ID X59346 standard; cDNA; 987 BP.
XX X59346;
AC X59346;
DT 20-SEP-1999 (first entry)
XX Human NTR-5 cDNA.
XX NTR-5; human; receptor; signal transduction; bone; muscle;
KW diagnosis; therapy; ss.
XX Homo sapiens.
XX
FH Key Location/Qualifiers
FT sig_peptide 1..57
FT /*tag= a
FT mat_peptide 58..987
FT /*tag= b
XX
PN W09933967-A2.
XX
XX 08-JUL-1999.
XX 28-DEC-1998; 98WO-US27688.
XX 29-DEC-1997; 97US-0068925.
XX (REGE-) REGENERON PHARM INC.
XX Valenzuela DM;
XX WPI; 1999-419102/35.
XX P-PSDB; Y06400.
XX
XX New mammalian receptor NTR-5 polypeptides
XX Claim 2a; Page 21-22; 27pp; English.
XX
XX This is the claimed coding region of human cDNA encoding a novel
XX receptor, designated NTR-5 (see Y06400), that shows homology to
XX osteoprotegerin and tumour necrosis factor receptor. The cDNA was
XX isolated from a heart cDNA library using mouse NTR-5 cDNA (see
XX X59345) as probe. Homology to osteoprotegerin suggests that NTR-5
XX is involved in the regulation of bone mass, and may be useful for
XX regulating development, proliferation and death of osteoblast or
XX osteoclast cells or for regulating muscle metabolism, and that it
XX may be implicated in muscle diseases or disorders. A host-vector
XX system for production of NTR-5 is claimed. NTR-5 polypeptides can
XX be used as immunogens and in screening assays to identify NTR-5
XX ligands, agonists and antagonists. The NTR-5 polynucleotide is
XX useful as a diagnostic tool, and as a source of probes and primers.
XX The invention also provides for diagnostic and therapeutic methods
XX based on the interaction of NTR-5 and agents that initiate signal
XX transduction through binding to NTR-5.
XX
XX Sequence 987 BP; 220 A; 251 C; 278 G; 238 T; 0 other;

Query Match .65.8%; Score 835.6; DB 20; Length 987;
Best Local Similarity 99.5%; Pred. No. 7.1e-247;
Matches 838; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 atggttttaaaagtgtactagacaagaagaaacgtttttcactcttttagtattacta 60

Db 1 atggttttaaaagtgtactagacaagaagaaacgtttttcactcttttagtattacta 60
Qy 61 ggcatttgtcatgtataaagtacttgtttaaaccagagagacttagacagacaagaattcagg 120
Db 61 ggcatttgtcatgtataaagtacttgtttaaaccagagagacttagacagacaagaattcagg 120
Qy 121 gatcgggtctggaacctgtgtccctgcacacagatgttggccagagcatggagtgtctctaaag 180
Db 121 gatcgggtctggaacctgtgtccctgcacacagatgttggccagagcatggagtgtctctaaag 180
Qy 181 gaatgtggtctcggtctatggggagagatgcacagtggtgacgtgcggtgcacaggttc 240
Db 181 gaatgtggtctcggtctatggggagagatgcacagtggtgacgtgcggtgcacaggttc 240
Qy 241 aaggaagactgggcttccagaaatgcagccctgtctgcgactgcgagtggtgaaccgc 300
Db 241 aaggaagactgggcttccagaaatgcagccctgtctgcgactgcgagtggtgaaccgc 300
Qy 301 ttccagaaggcaaatgttccagccaccagtgatgcacatctcggggagactgcttgcacaga 360
Db 301 ttccagaaggcaaatgttccagccaccagtgatgcacatctcggggagactgcttgcacaga 360
Qy 361 ttttataggaagaagaaacttgcggttttcaagacatggagtggtgccttgcagagac 420
Db 361 ttttataggaagaagaaacttgcggttttcaagacatggagtggtgccttgcagagac 420
Qy 421 cctcctcctcttaagaaacgcacactgtgccagcaaggccaacctgtgaagatcgcgtcc 480
Db 421 cctcctcctcttaagaaacgcacactgtgccagcaaggccaacctgtgaagatcgcgtcc 480
Qy 481 acggcctccagcccaagggaacagcgctggctgcgttatctgcagcgcctctgcgccacc 540
Db 481 acggcctccagcccaagggaacagcgctggctgcgttatctgcagcgcctctgcgccacc 540
Qy 541 gtccctgtggcctgtcctcctctgtgtcatctatttgaagagacagtttatggagaag 600
Db 541 gtccctgtggcctgtcctcctctgtgtcatctatttgaagagacagtttatggagaag 600
Qy 601 aaacccagctgtctcgtcgttcacagacattcagtaacacgctcagctcgtctgt 660
Db 601 aaacccagctgtctcgtcgttcagagacattcagtaacacgctcagctcgtctgt 660
Qy 661 cttgacagacctcagctccacgaatatgccacagagcctgcctcagtcgcccgtgac 720
Db 661 cttgacagacctcagctccacgaatatgccacagagcctgcctcagtcgcccgtgac 720
Qy 721 taagtgcagacctgcgggcggtgcgttgcctcccatccatgtctgtgagagagcctgc 780
Db 721 taagtgcagacctgcgggcggtgcgttgcctcccatccatgtctgtgagagagcctgc 780
Qy 781 agcccccaacccggcagctcttgggttgggtgcattctgcagccagctcttcaggcaaga 840
Db 781 agcccccaacccggcagctcttgggttgggtgcattctgcagccagctcttcaggcaaga 840
Qy 841 aa 842
Db 841 aa 842

RESULT 7
X23413
ID X23413 standard; DNA; 1678 BP.
XX X23413;
AC X23413;
DT 18-JUN-1999 (first entry)
XX Mouse mAP04-alpha (long) DNA.
XX
XX Tumour necrosis factor receptor; signal transducer molecule; TNF; APO4;
KW developmental abnormality; gestational abnormality; prostate cancer;
KW APO6; APO8; APO9; TNRL-1; TNRL-3; diagnosis; treatment; therapy; disease;

X23414
ID X23414 standard; DNA; 886 BP.
XX
AC X23414;
XX
DT 18-JUN-1999 (first entry)
XX
DE Mouse mAPO4-alpha (short) DNA.
XX
KW Tumour necrosis factor receptor; signal transducer molecule; TNF; APO4;
KW developmental abnormality; gestational abnormality; prostate cancer;
KW APO6; APO8; APO9; TNRL-1; TNRL-3; diagnosis; treatment; therapy; disease;
KW cytoplasmic domain; immunogen; antibody preparation; breast carcinoma;
KW apoptosis; mouse; mAPO4-alpha; ss.
XX
OS Mus sp.
XX
FH Key Location/Qualifiers
FT CDS 72..716
FT /*tag= a
FT /product= "mAPO4-alpha short"
XX
PN WO9911791-A2.
XX
PD 11-MAR-1999.
XX
PF 04-SEP-1998; 98WO-US18393.
XX
PR 05-SEP-1997; 97US-0924634.
XX
PA (UNIW) UNIV WASHINGTON.
XX
PI Chaudhary PM;
XX
PT WPI: 1999-205191/17.
XX
DR P-PSDB; W93580.
XX
DR New Tumor Necrosis Factor family receptor polypeptides and ligands -
PT useful for diagnosis and treatment of prostate cancer and
PT developmental or gestational abnormalities
XX
PS Example IV; Fig 7B; 156pp; English.
XX
CC This invention describes isolated Tumor Necrosis Factor (TNF) family
CC receptor polypeptides: APO4, APO6, APO8 and APO9 or their active
CC fragments, and isolated TNF related ligands 1 and 3 (TNRL1 and TNRL3) or
CC their active fragments. APO4 is useful for diagnosing prostate cancer
CC by determining levels of APO4 in an individual. Prostate cancer can also
CC be treated using APO4 selective binding agents linked to a therapeutic
CC moiety. APO4 polypeptides are also useful for identifying selective
CC binding agents, useful in diagnosis/treatment of disease by binding of
CC agents to the polypeptide/active fragment which is extracellular, or
CC expressed on the cell surface. The binding is preferably performed in
CC vivo. APO4 polypeptides/ active fragments are also useful for screening
CC for agonists and antagonists by binding and observing the change in APO4
CC activity. Effective pharmacological agents useful in diagnosis or
CC treatment of disease are also identified using APO4 polypeptides/active
CC fragments and APO4 signal transducer molecules that specifically interact
CC with a cytoplasmic domain of APO4 and detecting a change in level of APO4
CC activity. The method is performed in vivo or in vitro. APO polypeptides
CC are all useful as immunogens for preparing antibodies. APO4 is also
CC useful for diagnosis/treatment of developmental or gestational
CC abnormalities. APO8 was transfected to human breast carcinoma cell line
CC MCF-7, and induced apoptosis.
XX
SQ Sequence 886 BP; 204 A; 245 C; 247 G; 190 T; 0 other;

Query Match 35.4%; Score 449; DB 20; Length 886;
Best Local Similarity 82.4%; Pred. No. 4.9e-128;
Matches 515; Conservative 0; Mismatches 110; Indels 0; Gaps 0;
Qy 1 atggcttaaaagtgtactactgaacaagagaaacgtttttcactctttttgattacta 60

Db 72 atggcaactcaaggtctctacctctacacagagcggtgtctcttcgtgccatctcttctcta 131
Qy 61 ggctatttgtcatgtataaagtactgtgaacacagagagactgtagacacagaatctcagg 120
Db 132 ctccactggcatgtaaagtgtgtgcaaacggagagattgcaggcagcaggaattcgaag 191
Qy 121 gatcggtctgaaactgtgttccctgcaacacagtgatggccagcgcatggatgtgtctaag 180
Db 192 gatgatctgaaactgtgtctctgtcaaacagtgcggaacctggtgatggatgtgccaaag 251
Qy 181 gaatgtgcttcggctatgggagagatgcacagtgatgtgacgtgcgcgctgcacaggttc 240
Db 252 gaatgtgcttcggctatgggagagatgcacagtgatgtgacgtgcgcgctgcacaggttc 311
Qy 241 aaggagagactggggtctccagaaatgcaagccctgtctggactgcgcagtggtgaaccgc 300
Db 312 aaggagagactggggtctccagaaatgcaagccctgtgctgactgtgcgtgtgtgaaccgc 371
Qy 301 ttccagaagcgaaattgttcagccaccagtgatgccatctgcgggagctgcttgcagga 360
Db 372 ttccagaagcgaaactgtctcacacacagtgatgtctgcgggagctgcttgcagga 431
Qy 361 tttataggaagcgaactgttgcgttctcaagacatggagtggtgcttgcgttgagagac 420
Db 432 tttaccggaagacaaactgtgtgttttcaagacatggagtggtgcttgcgttgagagac 491
Qy 421 cctctctctcttacgaaccgactgtgccagcaaggtcaacctgtgaagatcgcgtcc 480
Db 492 ccactctctctacgaaccacactgtaccagcaaggtgaacctgtgaagatcctctccc 551
Qy 481 acggcctccagccacgggacacggcgctgctgcgttatctgcagcgctctgcccacc 540
Db 552 accgtctccagccctcgggacacggcgctgctgcgttatctgcagcgctctgcccacc 611
Qy 541 gtctgtgctgcccgtctcctctctgtgtcatctattgttaagagacagtttatggagaag 600
Db 612 gtctgtgctgcccgtctcctctctgtgtcatctactgcaagagcgagttcatggagaag 671
Qy 601 aaaccacagctgtctctgcgtcac 625
Db 672 aaaccacagctgttaagctccatccc 696

RESULT 9
X24977
ID X24977 standard; cDNA; 942 BP.
XX
AC X24977;
XX
DT 05-JUL-1999 (first entry)
XX
DE Mouse TRAIN-R (long form) cDNA.
XX
KW TRAIN-R; receptor; mouse; tumour necrosis factor receptor;
KW agonist; antagonist; cancer; immunological disease; therapy;
XX cytosolic; ss.
XX
OS Mus musculus.
XX
FH Key Location/Qualifiers
FT CDS 101..745
FT /*tag= a
XX
PN WO9913078-A1.
XX
PD 18-MAR-1999.
XX
PF 11-SEP-1998; 98WO-US19030.
XX
PR 06-MAY-1998; 98US-0084422.
XX
PR 12-SEP-1997; 97US-0058631.
XX

2 Splice forms of murine STRIFE have been identified, one that is predicted to be membrane-bound (STRIFE1) and one that is secreted (STRIFE2, see Y06523). STRIFE was identified as a TNFR homologue by a computer-based search of public EST databases. The invention provides STRIFE1 and STRIFE2 polynucleotides and polypeptides, as well as fusion proteins, antigenic peptides and antibodies. It also provides expression vectors, host cells and transgenic animals, as well as diagnostic, screening and therapeutic methods. STRIFE I and STRIFE II may play a role in mediating inflammatory, immune and host defense functions and may play a role in various neoplastic disease states. They may be useful as targets for developing novel diagnostic and therapeutic agents for TNF- and TNFR-associated disorders. Examples include sepsis syndrome, circulatory collapse and shock resulting from bacterial infection, acute and chronic parasitic or infectious processes, acute and chronic immune and autoimmune pathologies, alcohol-induced hepatitis, chronic inflammatory pathologies, vascular inflammatory pathologies, graft-versus-host pathology, malignant pathologies involving TNF-secreting tumors, cerebral malaria and multiple sclerosis.

Sequence 981 BP; 247 A; 270 C; 264 G; 200 T; 0 other;

Query Match 35.4%; Score 449; DB 20; Length 981;
Best Local Similarity 82.4%; Pred. No. 5.2e-128;
Matches 515; Conservative 0; Mismatches 110; Indels

[illegible]

RESULT	11	
X84622		
ID	X84622	standard; DNA; 893 BP.
XX		
AC	X84622;	
XX		
DT	16-SEP-1999	(first entry)
XX		
XX	Human TNFR superfamily soluble receptor coding sequence.	
XX		
KW	TNFL1; human; TNFR superfamily; tumour necrosis factor ligand; TNF;	
KW	tumour necrosis factor receptor; TNFR superfamily; cell proliferation;	
KW	cell differentiation; cytokine production; immunoglobulin; hyperplasia;	
KW	apoptosis inducer; activated T cell; autoimmune disease; inhibitor;	
KW	myasthenia gravis; insulin-dependent diabetes mellitus; endotoxic shock;	
KW	rheumatoid arthritis; multiple sclerosis; systemic lupus erythematosus;	
KW	tumour; proliferative disorder; dysplasia; dysplasia; immunocompetence;	
KW	lymphoid organogenesis; bacterial resistance; contact hypersensitivity;	
KW	delayed type sensitivity; therapy; ss.	
XX		
OS	Homo sapiens.	
XX		
PN	W09933980-A2.	
XX		
PD	08-JUL-1999.	
XX		
PF	22-DEC-1998; 98WO-US27474.	
XX		
PR	16-DEC-1998; 98US-0212270.	
PR	30-DEC-1997; 97US-0068959.	
XX		
PA	(CHIR) CHIRON CORP.	
XX		
PI	Kassam A, Lamson G, Pot D, Tribouley C;	
XX		
DR	WPI; 1999-405508/34.	
DR	P-PSDB; Y22223.	
XX		
PT	New tumour necrosis factor ligands, useful for induction of cell	
PT	death and/or proliferation of cells	
XX		
PS	Claim 15; Page 65-66; 69pp; English.	
XX		
CC	This sequence encodes a tumour necrosis factor receptor (TNFR)	
CC	superfamily soluble protein of the invention. The invention also relates	
CC	to tumour necrosis factor (TNF) ligand (TNFL) family proteins. The TNFL	
CC	proteins play regulatory roles in cell proliferation and/or	
CC	differentiation, e.g. they can induce production of cytokines,	
CC	immunoglobulins, etc. A variety of diseases can be treated by modulating	
CC	the activity of TNFL proteins, e.g. they can induce apoptosis of	
CC	activated T cells but rescue resting T cell from apoptosis. TNFL	
CC	polypeptides can therefore be used to treat autoimmune diseases, such as	
CC	myasthenia gravis, insulin-dependent diabetes mellitus, rheumatoid	
CC	arthritis, multiple sclerosis, and systemic lupus erythematosus. TNFL	
CC	proteins also have tumour stimulating properties, so tumours can be	
CC	treated by inhibiting the expression or activity of TNFL. Other	
CC	proliferative disorders, such as neoplasias, dysplasias, and hyperplasias	
CC	can also be treated using TNFL inhibitors. The TNFL polypeptides and	
CC	polynucleotides can also be used to enhance or decrease TNF activity,	
CC	thus providing therapeutic benefits such as induction of cell death,	
CC	lymphoid organogenesis, or host bacterial resistance, and inhibition of	
CC	endotoxic shock, contact hypersensitivity, delayed type sensitivity or	
CC	immunocompetence of a transplant recipient. TNF and its receptors play a	
CC	major role in host defence and immunosurveillance. As such, there is a	
CC	need to identify new members of TNFR families. This invention provides	
CC	this need.	

Query Match	34.3%	Score 435.4;	DB 20;	Length 893;
Best Local Similarity	82.1%	Pred. No. 7.4e-124;		
Matches 513: Conservative	0;	Mismatches 111;	Indels 1;	Gaps 1;

Best Local Similarity 82.1%; PRED: NO: 7.4e-124;
Matches 513; Conservative 0; Mismatches 111; Indels 1; Gaps 1;


```

ID V11422 standard; cDNA; 371 BP.
XX V11422;
AC
DT 23-JUL-1998 (first entry)
XX
DE Human secreted protein clone AX92_3 cDNA 5'-end.
XX
KW Secreted protein; prevention; treatment; gene therapy; ds.
XX
OS Homo sapiens.
XX
PN W09801554-A2.
XX
PD 15-JAN-1998.
XX
PF 07-JUL-1997; 97WO-US11876.
XX
PR 09-JUL-1996; 96US-0677231.
XX
PA (GEMY ) GENETICS INST INC.
XX
PI Bowman M, Evans C, Jacobs K, LaVallie ER, McCoy JM;
PI Merberg D, Racine LA, Spaulding V, Treacy M;
XX
DR WI; 1998-110230/10.
XX
PS P-PSDB; W58844.
XX
PT Secreted proteins and polynucleotides encoding them - useful to
PT prevent, treat and ameliorate medical conditions
XX
PS Claim 15; Page 57; 93pp; English.
XX
CC V11422-V11424 encode fragments of a novel secreted protein derived from
CC clone AX92_3 which was isolated from a human adult testes cDNA library.
CC The protein can be used to prevent, treat or ameliorate a medical
CC condition, while the polynucleotides can be used for gene therapy.
XX
SQ Sequence 371 BP; 83 A; 96 C; 107 G; 82 T; 3 other;

Query Match 28.5%; Score 361.6; DB 19; Length 371;
Best Local Similarity 98.1%; Pred. No. 2.2e-101;
Matches 364; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 128 ctggaactgtgtccctgcaaccagtgtggccaggcatggagtgtctaaaggaaatgtg 187
Db |||||
OY 188 gcttcggctatgggagatgcacagtgtgtgacgtgcgcgctgcacaggttcaaggagg 247
Db |||||
OY 248 actgggggttcagaaatgcagccctgtctgactgcgagtggtgaacgcctttcaga 307
Db |||||
OY 308 aggcgaattgttcagccaccagtgtgcatctgcgggactgttgcaggattttata 367
Db |||||
OY 368 ggaagacgaacttgcggttccttcagacatgagtggtgctgtgagacccctc 427
Db |||||
OY 428 ctcttaagaaaccgactgtgcccaggaaggtcaacctgtgaagatcgcgtccacgacct 487
Db |||||
OY 488 ccagccacagg 498
Db |||||
OY 361 ccagccacagg 371
Db |||||

RESULT 14
X23417
ID X23417 standard; DNA; 591 BP.
XX
AC X23417;
XX
DT 18-JUN-1999 (first entry)
XX
DE Mouse mAPO4-gamma DNA.
XX
KW Tumour necrosis factor receptor; signal transducer molecule; TNF; APO4;
KW developmental abnormality; gestational abnormality; prostate cancer;
KW APO6; APO8; TNRL-1; TNRL-3; diagnosis; treatment; therapy; disease;
KW cytoplasmic domain; immunogen; antibody preparation; breast carcinoma;
KW apoptosis; mouse; APO4-gamma; ss.
XX
OS Mus sp.
XX
FH Key Location/Qualifiers
FT CDS 95..547
FT /*tag= a
FT /product= "mAPO4-gamma"
XX
PN W09911791-A2.
XX
PD 11-MAR-1999.
XX
PF 04-SEP-1998; 98WO-US18393.
XX
PR 05-SEP-1997; 97US-0924634.
XX
PA (UNIW ) UNIV WASHINGTON.
XX
PI Chaudhary PM;
XX
DR WI; 1999-205191/17.
XX
PS P-PSDB; W93583.
XX
PT New Tumor Necrosis Factor family receptor polypeptides and ligands -
PT useful for diagnosis and treatment of prostate cancer and
PT developmental or gestational abnormalities
XX
PS Disclosure; Fig 7E; 156pp; English.
XX
CC This invention describes isolated Tumor Necrosis Factor (TNF) family
CC receptor polypeptides: APO4, APO6, APO8 and APO9 or their active
CC fragments, and isolated TNF related ligands 1 and 3 (TNRL1 and TNRL3) or
CC their active fragments. APO4 is useful for diagnosing prostate cancer
CC by determining levels of APO4 in an individual. Prostate cancer can also
CC be treated using APO4 selective binding agents linked to a therapeutic
CC moiety. APO4 polypeptides are also useful for identifying selective
CC binding agents, useful in diagnosis/treatment of disease by binding of
CC agents to the polypeptide/active fragment which is extracellular, or
CC expressed on the cell surface. The binding is preferably performed in
CC vivo. APO4 polypeptides/ active fragments are also useful for screening
CC for agonists and antagonists by binding and observing the change in APO4
CC activity. Effective pharmacological agents useful in diagnosis or
CC treatment of disease are also identified using APO4 polypeptides/active
CC fragments and APO4 signal transducer molecules that specifically interact
CC with a cytoplasmic domain of APO4 and detecting a change in level of APO4
CC activity. The method is performed in vivo or in vitro. APO polypeptides
CC are all useful as immunogens for preparing antibodies. APO4 is also
CC useful for diagnosis/treatment of developmental or gestational cell line
CC abnormalities. APO8 was transfected to human breast carcinoma cell line
CC MCF-7, and induced apoptosis.
XX
SQ Sequence 591 BP; 148 A; 145 C; 175 G; 123 T; 0 other;

Query Match 24.7%; Score 314; DB 20; Length 591;
Best Local Similarity 78.9%; Pred. No. 1.2e-86;
Matches 374; Conservative 0; Mismatches 100; Indels 0; Gaps 0;

```


GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 2, 2001, 03:51:51 ; Search time 217.59 Seconds

(without alignments)

939,898 Million cell updates/sec

Title: US-09-380-276A-1

Perfect score: 1269

Sequence: 1 atggcttaaaagtctact.....ggcagcgactgggttccttg 1269

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 280836 seqs, 80580151 residues

Total number of hits satisfying chosen parameters: 561672

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_NA.*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq.*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq.*
3: /cgn2_6/ptodata/1/ina/6_COMB.seq.*
4: /cgn2_6/ptodata/1/ina/PTCUS_COMB.seq.*
5: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	36.4	2.9	1601	1 US-08-722-001-7	Sequence 7, Appli
2	36.4	2.9	1987	1 US-08-722-001-26	Sequence 26, Appl
3	36.4	2.9	1997	1 US-08-722-001-27	Sequence 27, Appl
4	36.4	2.9	2004	1 US-08-722-001-11	Sequence 11, Appl
5	36.2	2.9	2485	1 US-08-424-424B-1	Sequence 1, Appli
6	36.2	2.9	2486	4 PCT-US94-05363A-1	Sequence 1, Appli
7	34.8	2.7	1639	1 US-08-334-698-5	Sequence 5, Appli
8	34.8	2.7	1639	1 US-08-228-932-5	Sequence 5, Appli
9	34.8	2.7	1639	1 US-08-468-935-5	Sequence 5, Appli
10	34.8	2.7	1639	2 US-08-406-855A-5	Sequence 5, Appli
11	34.8	2.7	1639	2 US-08-722-190-5	Sequence 5, Appli
12	34.8	2.7	1639	3 US-08-244-354-5	Sequence 5, Appli
13	34.8	2.7	1639	3 US-09-206-899-5	Sequence 5, Appli
14	34.8	2.7	1639	4 PCT-US95-04203-5	Sequence 5, Appli
15	34.6	2.7	5962	5 5386025-5	Patent No. 5386025
16	34.6	2.7	7218	1 US-08-232-463-14	Sequence 14, Appli
17	33.6	2.6	800	2 US-08-416-603-11	Sequence 11, Appli
18	33.4	2.6	4360	1 US-08-470-350B-1	Sequence 1, Appli
19	33	2.6	9472	1 US-08-325-547-9	Sequence 9, Appli
20	32.8	2.6	2230	1 US-08-200-512-1	Sequence 1, Appli
21	32.6	2.6	1593	2 US-08-524-828-2	Sequence 2, Appli
22	32.6	2.6	1593	2 US-08-975-114A-2	Sequence 2, Appli
23	32.6	2.6	1593	3 US-08-849-281A-2	Sequence 2, Appli
24	32.6	2.6	2247	2 US-08-524-828-1	Sequence 1, Appli
25	32.6	2.6	2247	2 US-08-975-114A-1	Sequence 1, Appli
26	32.6	2.6	3891	1 US-08-480-604A-27	Sequence 27, Appl
27	32.6	2.6	3891	2 US-08-405-496A-27	Sequence 27, Appl
28	32.4	2.6	1167	1 US-07-960-985-1	Sequence 1, Appli

29 32.4 2.6 1167 2 US-08-496-671-1 Sequence 1, Appli
30 32.4 2.6 1690 2 US-08-461-812-3 Sequence 3, Appli
31 32.4 2.6 3083 2 US-08-480-994-36 Sequence 36, Appl
32 32.4 2.6 3083 2 US-08-616-844-36 Sequence 36, Appl
33 32.4 2.6 3083 2 US-08-599-654-36 Sequence 36, Appl
34 32.4 2.6 3083 2 US-08-485-573-36 Sequence 36, Appl
35 32.4 2.6 3083 3 US-08-944-868A-36 Sequence 36, Appl
36 32.4 2.6 3083 3 US-08-944-423A-36 Sequence 36, Appl
37 32.4 2.6 3083 3 US-08-925-743-36 Sequence 36, Appl
38 32.4 2.6 3083 3 US-08-944-496-36 Sequence 36, Appl
39 32.4 2.6 3084 3 US-08-826-246-11 Sequence 11, Appl
40 32.4 2.6 3084 3 US-08-944-495-11 Sequence 11, Appl
41 32.4 2.6 3084 3 US-09-126-640-6 Sequence 6, Appli
42 32.4 2.6 28804 3 US-08-592-874-1 Sequence 1, Appli
43 32.4 2.6 28804 3 US-09-096-942-2 Sequence 2, Appli
44 32.4 2.6 28804 3 US-09-096-867-2 Sequence 2, Appli
45 32.2 2.5 953 1 US-08-197-793-1 Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-08-722-001-7
; Sequence 7, Application US/08722001
; Patent No. 5760054
; GENERAL INFORMATION:
; APPLICANT: Thompson, Wayne J.
; APPLICANT: Huff, Joel R.
; APPLICANT: Nerenberg, Jennie B.
; APPLICANT: Lee, Hee-Yoon
; APPLICANT: Bell, Ian M.
; TITLE OF INVENTION: ALPHALC ADRENERGIC RECEPTOR ANTAGONISTS
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: 126 Lincoln Avenue
; CITY: Rahway
; STATE: New Jersey
; COUNTRY: United States of America
; ZIP: 07065

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/722,001
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/229,276
FILING DATE: 14-APR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Apollina, Mary A.
REGISTRATION NUMBER: 34,087
REFERENCE/DOCKET NUMBER: 19169Y
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908)594-3462
TELEFAX: (908)594-4720
TELEX: 138825
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1601 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-722-001-7

```

Query Match      2.9%; Score 36.4; DB 1; Length 1601;
Best Local Similarity 52.7%; Pred. No. 0.18; 71; Indels 0; Gaps 0;
Matches 79; Conservative 0; Mismatches 71; Indels 0; Gaps 0;

QY 474 cgggtccacggcctccagccacgggagacacggcgctgctgctgtatctgacgcgtct 533
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1107 CGAGGAGGAGACCATCTGCCAGATCAACAGGAGCGCGGCTACGTCTTCTCGGCTCT 1166

QY 534 ggcacgcctctgctgctcctctcctctgctgctatctattgtaagagacagtttat 593
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1167 GGCTCTCTTACTGCTCTGCCCATCATCTGGTCTACTGCTCGCGGCTCTACGTGGT 1226

QY 594 ggagaagaacccagctggtctctcggtc 623
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1227 GGCAAGAGGAGAGCGCGGCTCAAGTC 1256

RESULT 2
US-08-722-001-26
; Sequence 26, Application US/08722001
; Patent No. 5760054
; GENERAL INFORMATION:
; APPLICANT: Thompson, Wayne J.
; APPLICANT: Huff, Joel R.
; APPLICANT: Nerenberg, Jennie B.
; APPLICANT: Lee, Hee-Yoon
; APPLICANT: Bell, Ian M.
; TITLE OF INVENTION: ALPHAIC ADRENERGIC RECEPTOR ANTAGONISTS
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: 126 Lincoln Avenue
; CITY: Rahway
; STATE: New Jersey
; COUNTRY: United States of America
; ZIP: 07065
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/722,001
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/229,276
; FILING DATE: 14-APR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Appollina, Mary A.
; REGISTRATION NUMBER: 34,087
; REFERENCE/DOCKET NUMBER: 19169Y
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908)594-3462
; TELEFAX: (908)594-4720
; TELEX: 138825
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1987 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: CDNA
; HYPOTHEetical: NO
; ANTI-SENSE: NO
; US-08-722-001-26

Query Match      2.9%; Score 36.4; DB 1; Length 1987;
Best Local Similarity 52.7%; Pred. No. 0.21; 71; Indels 0; Gaps 0;
Matches 79; Conservative 0; Mismatches 71; Indels 0; Gaps 0;

QY 474 cgggtccacggcctccagccacgggagacacggcgctgctgctgtatctgacgcgtct 533
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

```

Db 1112 CGAGGAGGAGACCATCTGCCAGATCAACAGGAGCGCGGCTACGTCTTCTCGGCTCT 1171

QY 534 ggcacgcctctgctgctcctctcctctgctgctatctattgtaagagacagtttat 593
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1172 GGGTCTCTTACTGCTCTGCCCATCATCTGGTCTACTGCTCGCGGCTCTACGTGGT 1231

QY 594 ggagaagaacccagctggtctctcggtc 623
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1232 GGCAAGAGGAGAGCGCGGCTCAAGTC 1261

RESULT 3
US-08-722-001-27
; Sequence 27, Application US/08722001
; Patent No. 5760054
; GENERAL INFORMATION:
; APPLICANT: Thompson, Wayne J.
; APPLICANT: Huff, Joel R.
; APPLICANT: Nerenberg, Jennie B.
; APPLICANT: Lee, Hee-Yoon
; APPLICANT: Bell, Ian M.
; TITLE OF INVENTION: ALPHAIC ADRENERGIC RECEPTOR ANTAGONISTS
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: 126 Lincoln Avenue
; CITY: Rahway
; STATE: New Jersey
; COUNTRY: United States of America
; ZIP: 07065
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/722,001
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/229,276
; FILING DATE: 14-APR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Appollina, Mary A.
; REGISTRATION NUMBER: 34,087
; REFERENCE/DOCKET NUMBER: 19169Y
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908)594-3462
; TELEFAX: (908)594-4720
; TELEX: 138825
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1997 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: CDNA
; HYPOTHEtical: NO
; ANTI-SENSE: NO
; US-08-722-001-27

Query Match      2.9%; Score 36.4; DB 1; Length 1997;
Best Local Similarity 52.7%; Pred. No. 0.21; 71; Indels 0; Gaps 0;
Matches 79; Conservative 0; Mismatches 71; Indels 0; Gaps 0;

QY 474 cgggtccacggcctccagccacgggagacacggcgctgctgctgtatctgacgcgtct 533
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1106 CGAGGAGGAGACCATCTGCCAGATCAACAGGAGCGCGGCTACGTCTTCTCGGCTCT 1165

QY 534 ggcacgcctctgctgctcctctcctctgctgctatctattgtaagagacagtttat 593
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

Db 1166 GGGCTCTTCTACCTGCGCTCTGGCCATCATCTCTGTCTACTGTCGCCGCTCTACGTGCT 1225

Qy 594 ggagaagaaccagctggtctctcggtc 623

Db 1226 GCCCAAGAGGAGACCGGGGCTCAAGTC 1255

RESULT 4

US-08-722-001-11

; Sequence 11, Application US/08722001

; Patent No 5760054

; GENERAL INFORMATION:

; APPLICANT: Thompson, Wayne J.

; APPLICANT: Huff, Joel R.

; APPLICANT: Nerenberg, Jennie B.

; APPLICANT: Lee, Hee-Yoon

; APPLICANT: Bell, Ian M.

; TITLE OF INVENTION: ALPHALC ADRENERGIC RECEPTOR ANTAGONISTS

; NUMBER OF SEQUENCES: 35

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Merck & Co., Inc.

; STREET: 126 Lincoln Avenue

; CITY: Rahway

; STATE: New Jersey

; COUNTRY: United States of America

; ZIP: 07065

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/722,001

; FILING DATE:

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/229,276

; FILING DATE: 14-APR-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Appollina, Mary A.

; REGISTRATION NUMBER: 34,087

; REFERENCE/DOCKET NUMBER: 19169Y

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (908)594-3462

; TELEFAX: (908)594-4720

; TELEX: 138825

; INFORMATION FOR SEQ ID NO: 11:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 2004 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: both

; TOPOLOGY: both

; MOLECULE TYPE: cDNA

; HYPOTHETICAL: NO

; ANTI-SENSE: NO

US-08-722-001-11

Query Match

Best Local Similarity 52.7%; Score 36.4; DB 1; Length 2004;

Matches 79; Conservative 0; Mismatches 71; Indels 0; Gaps 0;

Qy 474 cgcgtccagcgctccagcccgagacggcgctggtcgctgtatctgagcgctct 533

Db 1107 CGAGGACGAGACCATCTGCCATCAACGAGGAGCGGCTACGTGCTCTTCGGCTCT 1166

Qy 534 ggccaccgctgctggccctgctcatctctgtgtcatctattgtaagagacagttat 593

Db 1167 GGGCTCTTCTACCTGCGCTCTGGCCATCATCTGTGTCATGTACTGCCGGCTACGTGCT 1226

Qy 594 ggagaagaaccagctggtctctcggtc 623

Db 1227 GCCCAAGAGGAGACCGGGGCTCAAGTC 1256

RESULT 5

US-08-424-424B-1

; Sequence 1, Application US/08424424B

; Patent No. 5759854

; GENERAL INFORMATION:

; APPLICANT: LI, ET AL.

; TITLE OF INVENTION: Neurotransmitter Transporter

; NUMBER OF SEQUENCES: 6

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,

; STREET: 6 BECKER FARM ROAD

; CITY: ROSELAND

; STATE: NEW JERSEY

; COUNTRY: USA

; ZIP: 07068

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 INCH DISKETTE

; COMPUTER: IBM PS/2

; OPERATING SYSTEM: MS-DOS

; SOFTWARE: WORD PERFECT 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/424,424B

; FILING DATE: APRIL 21, 1995

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/US94/05363

; FILING DATE: MAY 25, 1996

; ATTORNEY/AGENT INFORMATION:

; NAME: MULLINS, J.G.

; REGISTRATION NUMBER: 33,073

; REFERENCE/DOCKET NUMBER: 325800-308

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 201-994-1700

; TELEFAX: 201-994-1744

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 2485 BASE PAIRS

; TYPE: NUCLEIC ACID

; STRANDEDNESS: SINGLE

; TOPOLOGY: LINEAR

; MOLECULE TYPE: CDNA

US-08-424-424B-1

Query Match

Best Local Similarity 56.2%; Score 36.2; DB 1; Length 2485;

Matches 68; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

Qy 453 caaggtcaacctcgtgaagatcgctccacggcctccagcccaacgggacacggcgctggc 512

Db 2023 CAGCATCATCCAGCTGGGGGTACCGCCCCGGCTACAGCCTGGATCAAGGAGAGGC 2082

Qy 513 tgcgcttatctgcagcgctctgcccacgcgtctgctggccctgctcatctctgtgtcat 572

Db 2083 TGCCGAGGCGTACCTGTATTTCCCAACTGGCCCATGGCACTCCTCATCATCGT 2142

Qy 573 c 573

Db 2143 C 2143

RESULT 6

PCT-US94-05363A-1

; Sequence 1, Application PC/TUS9405363A

; GENERAL INFORMATION:

; APPLICANT: LI, ET AL.

; TITLE OF INVENTION: Neurotransmitter Transporter

; NUMBER OF SEQUENCES: 2

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,

Query Match	2.7%	Score 34.8;	DB 1;	Length 1639;
Best Local Similarity	52.0%	Pred. No. 0.59;		
Matches 78;	Conservative	0;	Mismatches 72;	Indels 0;
Gaps				

Qy	474	cgcgctccacggcctccagcccaaggagacacggcgcgctggctgcggttatctctgacgcgctct	533
Db	635	CGAGGACGAGACCATCTGCCAGATCAACAGAGGACCGGGGCTACGCTGCTCTTCACGCGCT	694
Qy	534	ggcacccgctcctgctggccctgcgtcatcctctctgctcatctatgttaagagacagtttat	593
Db	695	GGGCTCCTCTTACGCTGCTCTGGCCATCATCCTGGTCATGTACTGGCGGCTCACGTGCT	754
Qy	594	ggagaagaacccagctgggtctctcgggtc	623
Db	755	GGCAAGAGAGGAGAGCGGGGCTCAAGTC	784

RESULT 8
US-08-228-932-5
; Sequence 5, Application US/08228932
; Patent No. 5578611
; GENERAL INFORMATION:
; APPLICANT: Charles Gluchowski, Carlos C. Forray, George Chiu,
; APPLICANT: Theresa A. Branchek, John M. Wetzel and Paul R. Hartig
; TITLE OF INVENTION: USE OF ALPHA-1C SPECIFIC COMPOUNDS TO TREAT BENIGN
; TITLE OF INVENTION: PROSTATIC HYPERPLASIA
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: COOPER & DUNHAM
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/228,932
; FILING DATE: 13-APR-1994

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 16, 2001, 21:09:00 ; Search time 53.31 Seconds
(without alignments)
930.012 Million cell updates/sec

Title: US-09-380-276a-8
Perfect score: 2283
Sequence: 1 MALKVLEQEKTFFTLLVLL.....AIHPATQTSLQVRQLGSL 423

Scoring table: BLOSUM62
Gapop 10.0 ; Gapext 0.5

Searched: 374700 seqs, 117207915 residues
Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_15.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phase.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2274	99.6	423	Q9NS68	Q9ns68 homo sapien
2	2258	98.9	423	Q9NZV2	Q9nzv2 homo sapien
3	1559.5	68.3	416	Q9JUH6	Q9jih6 mus musculus
4	1557.5	68.2	416	Q9JUL3	Q9jil3 mus musculus
5	1472.5	64.5	348	Q9QXW7	Q9qxw7 mus musculus
6	977	42.8	214	Q9JHF1	Q9jhf1 mus musculus
7	725	31.8	150	Q9JUL2	Q9jil2 mus musculus
8	197	8.6	448	Q9RI87	Q9ri87 mus musculus
9	191	8.4	448	Q9UNE0	Q9une0 homo sapien
10	191	8.4	448	Q9UND9	Q9und9 homo sapien
11	170.5	7.5	387	Q9PVD4	Q9pvd4 xenopus lae
12	144.5	6.3	430	Q9N092	Q9n092 macaca fasc
13	142	6.2	417	Q9Z0W1	Q9z0w1 mus musculus
14	142	6.2	426	O14865	O14865 homo sapien
15	137.5	6.0	186	O12735	O12735 cowpox viru
16	136	6.0	625	O135305	O135305 mus musculus
17	134.5	5.9	3396	Q9VM55	Q9vm55 drosophila
18	134	5.9	186	Q9YP87	Q9yp87 cowpox viru
19	134	5.9	277	O14866	O14866 homo sapien

20	134	5.9	348	12	O57277	057277 monkeypox v
21	134	5.9	348	12	O57103	057103 monkeypox v
22	134	5.9	348	12	O57108	057108 monkeypox v
23	133.5	5.8	350	12	O57123	057123 cowpox viru
24	133	5.8	543	5	Q9VJU5	Q9vjU5 drosophila
25	133	5.8	620	5	Q9NKD8	Q9nkd8 drosophila
26	132.5	5.8	3680	5	Q9VR08	Q9vr08 drosophila
27	131.5	5.8	349	12	O57291	057291 monkeypox v
28	131.5	5.8	349	12	O57099	057099 monkeypox v
29	131.5	5.8	349	12	O57100	057100 monkeypox v
30	131.5	5.8	349	12	O57101	057101 monkeypox v
31	131.5	5.8	349	12	O57102	057102 monkeypox v
32	130	5.7	186	12	Q9WJB4	Q9wjB4 vaccinia vl
33	129.5	5.7	1254	13	Q9VHU2	Q9yhu2 brachydanio
34	128	5.6	347	12	O57115	057115 cowpox viru
35	128	5.6	355	12	O85308	O85308 cowpox viru
36	128	5.6	401	13	Q9PRG7	Q9prg7 xenopus lae
37	127.5	5.6	349	12	O57111	057111 variola vir
38	127	5.6	1114	11	Q9JKW7	Q9jkw7 mus musculus
39	127	5.6	1650	11	Q9QVT6	Q9qvt6 rattus sp.
40	127	5.6	1792	13	O57484	O57484 gallus gall
41	127	5.6	1827	5	O20535	O20535 caenorhabdi
42	126.5	5.5	380	4	O00280	O00280 homo sapien
43	126.5	5.5	1394	5	Q9VS89	Q9vs89 drosophila
44	126	5.5	349	12	O57305	O57305 cowpox viru
45	126	5.5	350	12	O57116	O57116 cowpox viru

ALIGNMENTS

RESULT 1						
Q9NS68						
ID	Q9NS68	PRELIMINARY;	PRT;	423 AA.		
AC	Q9NS68;					
DT	01-OCT-2000	(TReMBLrel. 15, Created)				
DT	01-OCT-2000	(TReMBLrel. 15, Last sequence update)				
DT	01-OCT-2000	(TReMBLrel. 15, Last annotation update)				
DE	HTROX.					
GN	HTROX.					
OS	Homo sapiens (Human).					
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
OX	NCBI_TaxID=9606;					
RP	SEQUENCE FROM N.A.					
RA	Kojima T., Morikawa Y., Copeland N.G., Gilbert D.J., Jenkins N.A.,					
RA	Senba E., Kitamura T.;					
RT	"TROX, a newly identified member of the tumor necrosis factor receptor					
RT	superfamily, exhibits a homology with edar and is expressed in					
RT	embryonic skin and hair follicles."					
RL	J. Biol. Chem. 275:20742-20747(2000).					
DR	EMBL; AB040434; BAB03269.1; -					
SQ	SEQUENCE 423 AA; 46015 MW; B5891CEA9ED45361 CRC64;					

Query Match	99.6%	Score 2274;	DB 4;	Length 423;
Best Local Similarity	99.3%	Pred. No. 5.6e-202;		
Matches 420;	Conservative 2;	Mismatches 1;	Indels 0;	Gaps 0;
Qy	1	MALKVLEQEKTFFTLLVLLGLYLSCKVTCETGDCRQBFDRSGNCVPCNCGPGMELSK	60	
Db	1	MALKVLEQEKTFFTLLVLLGLYLSCKVTCESGDCRQBFDRSGNCVPCNCGPGMELSK	60	
Qy	61	ECGFGYGDAQCVCRLHFRFEDWGFKCPCLDCAVNVRFQKNCATSATSDAICGDLPG	120	
Db	61	ECGFGYGDAQCVCRLHFRFEDWGFKCPCLDCAVNVRFQKNCATSATSDAICGDLPG	120	
Qy	121	FYRKTGLVGFQDMCVPCGDDPPPPYEPHCASKVNLVKIATASSPRDTALAIVICSALAT	180	
Db	121	FYRKTGLVGFQDMCVPCGDDPPPPYEPHCASKVNLVKIATASSPRDTALAIVICSALAT	180	
Qy	181	VLLALLILCVIYCKRFQMEKKPSWSLRSQDIQYNGSELSCSLDRPOLHEYAHRAACQCRRD	240	

```
Db 181 VLLALLILCVYKROFMKKPSWLSRSODIQYNGSELSCFDRPQLHEYAHRAACCCRRD 240
QY 241 SVOTCGPVRLLPSMCCCEACSPNATLGGCVHSAASLQARNAGPAGEMVPTFGSLTQSI 300
Db 241 SVOTCGPVRLLPSMCCCEACSPNATLGGCVHSAASLQARNAGPAGEMVPTFGSLTQSI 300
QY 301 CGEFSDAWPLMQNPMGDDNISFCDSYPETLGTEDIHSLNPELESSTSLDSSODLVGGAV 360
Db 301 CGEFSDAWPLMQNPMGDDNISFCDSYPETLGTEDIHSLNPELESSTSLDSSODLVGGAV 360
QY 361 PVOSHENFTAAATDLRYNNLTVESASTQDALTMRSQLDOESGAIHPATQTSLOVRQRL 420
Db 361 PVOSHENFTAAATDLRYNNLTVESASTQDALTMRSQLDOESGAIHPATQTSLOVRQRL 420
QY 421 GSL 423
Db 421 GSL 423

RESULT 2
Q9NZV2
ID Q9NZV2 PRELIMINARY; PRT; 423 AA.
AC Q9NZV2;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DE TAJ-ALPHA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Eby M.T., Jasmin A., Kumar A., Sharma K., Chaudhary P.M.;
RT "TAJ, a Novel Member of the Tumor Necrosis Factor Receptor Family,
RT Activates the c-Jun N-terminal Kinase Pathway and Mediates Caspase-
RT Independent Cell Death.";
RL J. Biol. Chem. 275:15336-15342(2000).
DR EMBL; AF167555; AAF71828.1; -.
SQ SEQUENCE 423 AA; 46071 MW; BB7C9917132A4B2F CRC64;

Query Match 98.9%; Score 2258; DB 4; Length 423;
Best Local Similarity 98.6%; Pred. No. 1.7e-200;
Matches 417; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 MALKVLEQEKFTFTLLVLLGYLSCKVTCTGDCRQOEFRDRSGNCVPCNQCQPGMELSK 60
Db 1 MALKVLEQEKFTFTLLVLLGYLSCKVTCTGDCRQOEFRDRSGNCVPCNQCQPGMELSK 60
QY 61 ECGFGYGEDAQCVTCRLHREFKEDWGQCKPCLDCAVAVNRFOKANCATSATSDAICGCLPG 120
Db 61 ECGFGYGEDAQCVTCRLHREFKEDWGQCKPCLDCAVAVNRFOKANCATSATSDAICGCLPG 120
QY 121 FYRKTLLVGFQDMQECVPCGDDPPPEPHCASKVNLVKIASTASSPRDTALAAVICSALAT 180
Db 121 FYRKTLLVGFQDMQECVPCGDDPPPEPHCASKVNLVKIASTASSPRDTALAAVICSALAT 180
QY 181 VLLALLILCVYKROFMKKPSWLSRSODIQYNGSELSCFDRPQLHEYAHRAACCCRRD 240
Db 181 VLLALLILCVYKROFMKKPSWLSRSODIQYNGSELSCFDRPQLHEYAHRAACCCRRD 240
QY 241 SVOTCGPVRLLPSMCCCEACSPNATLGGCVHSAASLQARNAGPAGEMVPTFGSLTQSI 300
Db 241 SVOTCGPVRLLPSMCCCEACSPNATLGGCVHSAASLQARNAGPAGEMVPTFGSLTQSI 300
QY 301 CGEFSDAWPLMQNPMGDDNISFCDSYPETLGTEDIHSLNPELESSTSLDSSODLVGGAV 360
Db 301 CGEFSDAWPLMQNPMGDDNISFCDSYPETLGTEDIHSLNPELESSTSLDSSODLVGGAV 360
QY 361 PVOSHENFTAAATDLRYNNLTVESASTQDALTMRSQLDOESGAIHPATQTSLOVRQRL 420
Db 361 PVOSHENFTAAATDLRYNNLTVESASTQDALTMRSQLDOESGAIHPATQTSLOVRQRL 420
QY 421 GSL 423
Db 421 GSL 423
```

```
Db 361 PVOSHENFTAAATDLRYNNLTVESASTQDALTMRSQLDOESGAIHPATQTSLOVRQRL 420
QY 421 GSL 423
Db 421 GSL 423

RESULT 3
Q9JJH6
ID Q9JJH6 PRELIMINARY; PRT; 416 AA.
AC Q9JJH6;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TReMBLrel. 15, Last annotation update)
DE TROY.
GN TROY.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Kojima T., Morikawa Y., Copeland N.G., Gilbert D.J., Jenkins N.A.,
RA Senba E., Kitamura T.;
RT "TROY, a newly identified member of the tumor necrosis factor receptor
RT superfamily, exhibits a homology with Edar and is expressed in
RT embryonic skin and hair follicles";
RL J. Biol. Chem. 275:20742-20747(2000).
DR EMBL; AB040432; BAB03267.1; -.
SQ SEQUENCE 416 AA; 45265 MW; 9BDC7C7A2D6A9C47 CRC64;

Query Match 68.3%; Score 1559.5; DB 11; Length 416;
Best Local Similarity 70.5%; Pred. No. 5.5e-136;
Matches 294; Conservative 34; Mismatches 84; Indels 5; Gaps 3;

QY 1 MALKVLEQEKFTFTLLVLLGYLSCKVTCTGDCRQOEFRDRSGNCVPCNQCQPGMELSK 60
Db 1 MALKVLEQEKFTFTLLVLLGYLSCKVTCTGDCRQOEFRDRSGNCVPCNQCQPGMELSK 60
QY 61 ECGFGYGEDAQCVTCRLHREFKEDWGQCKPCLDCAVAVNRFOKANCATSATSDAICGCLPG 120
Db 61 ECGFGYGEDAQCVTCRLHREFKEDWGQCKPCLDCAVAVNRFOKANCATSATSDAICGCLPG 120
QY 121 FYRKTLLVGFQDMQECVPCGDDPPPEPHCASKVNLVKIASTASSPRDTALAAVICSALAT 180
Db 121 FYRKTLLVGFQDMQECVPCGDDPPPEPHCASKVNLVKIASTASSPRDTALAAVICSALAT 180
QY 181 VLLALLILCVYKROFMKKPSWLSRSODIQYNGSELSCFDRPQLHEYAHRAACCCRRD 240
Db 181 VLLALLILCVYKROFMKKPSWLSRSODIQYNGSELSCFDRPQLHEYAHRAACCCRRD 240
QY 241 SVOTCGPVRLLPSMCCCEACSPNATLGGCVHSAASLQARNAGPAGEMVPTFGSLTQSI 300
Db 241 SVOTCGPVRLLPSMCCCEACSPNATLGGCVHSAASLQARNAGPAGEMVPTFGSLTQSI 300
QY 301 CGEFSDAWPLMQNPMGDDNISFCDSYPETLGTEDIHSLNPELESSTSLDSSODLVGGAV 360
Db 301 CGEFSDAWPLMQNPMGDDNISFCDSYPETLGTEDIHSLNPELESSTSLDSSODLVGGAV 360
QY 361 PVOSHENFTAAATDLRYNN--TLVESASTQDALTMRSQLDOESGAIHPATQTSLO 415
Db 359 -ALESSGNVSEKTSRPHGDTGTGTWETLQAQARTPSOGGREDRENLANMPTAQ 414

RESULT 4
Q9JLL3
ID Q9JLL3 PRELIMINARY; PRT; 416 AA.
AC Q9JLL3;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TReMBLrel. 15, Last annotation update)
DE TAJ-ALPHA LONG.
```

OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Eby M.T., Jasmin A., Kumar A., Sharma K., Chaudhary P.M.;
 RT "TAJ, a Novel Member of the Tumor Necrosis Factor Receptor Family,
 RT Activates the c-Jun N-terminal Kinase Pathway and Mediates Caspase-
 RT Independent Cell Death.";
 RL J. Biol. Chem. 275:15336-15342(2000).
 DR EMBL; AF167552; AAF1825.1; -;
 SQ SEQUENCE 416 AA; 45294 MW; 19CA2F75DD7B9D49 CRC64;

Query Match 68.2%; Score 1557.5; DB 11; Length 416;
 Best Local Similarity 70.5%; Pred. No. 8.4e-136;
 Matches 294; Conservative 33; Mismatches 85; Indels 5; Gaps 3;

Qy 1 MALKVLEQEKTFFTLVLLGYLSCKVTCETGDCRQEQFRDRSGNCVPCNQCQPGMELSK 60
 Db 1 MALKVLPPLHRTVLFPAAILFLLHLACKVSCETGDCRQEQFRDRSGNCVLCQCGPGMELSK 60

Qy 61 ECGFGYGEDAQCQVTCRLHRFKEDWGFKCPCLDCAVNRFKANCATSDAICGDCPLG 120
 Db 61 ECGFGYGEDAQCQVPCPRHFRFKEDWGFKCPKPCADCALVNRFORANCSTSDAVCGDCPLG 120

Qy 121 FYRKTGLVGFQDMECVPCGDPDPPEPHCASKVNLVKIATSTASSPRDATALAAVICSALAT 180
 Db 121 FYRKTGLVGFQDMECVPCGDPDPPEPHCTSKVNLVKISSTVSSPRDATALAAVICSALAT 180

Qy 181 VLLALLILCVYCKRQFMKPSWLSRSDIOYNGSELSCLDRLPQLHEYAHRAQCQRRD 240
 Db 181 VLLALLILCVYCKRQFMKPSWLSRSDIOYNGSELSCFDQPRLRHCAHRAQCQYHRD 240

Qy 241 SVQTCGPVRLPSPMCCEACSPNATLGGVHSAASLQARNAGPAGEMVPTFGSLTQSI 300
 Db 241 SAPMTGPVHLIPSLCCEARSAARAVLGGCLRSPTTLQERNPASVGNTPAPFGSVRSI 300

Qy 301 CGEFS DAMPLMONGGDNISFCDSPYELTGEDIHSLNPEL 341
 Db 301 CAEFS DAMPLMONGGDNISFCDSPYELTGEDIHSLNPEM 340

Qy 181 VLLALLILCVYCKRQFMKPSWLSRSDIOYNGSELSCLDRLPQLHEYAHRAQCQRRD 240
 Db 181 VLLALLILCVYCKRQFMKPSWLSRSDIOYNGSELSCFDQPRLRHCAHRAQCQYHRD 240

Qy 241 SVQTCGPVRLPSPMCCEACSPNATLGGVHSAASLQARNAGPAGEMVPTFGSLTQSI 300
 Db 241 SAPMTGPVHLIPSLCCEARSAARAVLGGCLRSPTTLQERNPASVGNTPAPFGSVRSI 300

Qy 301 CGEFS DAMPLMONGGDNISFCDSPYELTGEDIHSLNPEL 341
 Db 301 CAEFS DAMPLMONGGDNISFCDSPYELTGEDIHSLNPEM 340

Qy 361 PVQSHENFTATDLRSYNN--TLVESASTQDALTMRSQLDQESGAIHPATQTSILQ 415
 Db 359 -ALESSGNVSESTDSPRHGDTGVWEQTLAQDARTPSGGWEDRENLMPTAFQ 414

RESULT 5
 Q90XW7
 ID Q90XW7 PRELIMINARY; PRT; 348 AA.
 AC Q90XW7
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
 DE TNFRSF19.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Hu S., Tamada K., Ni J., Vincenz C., Chen L.;
 RT "Characterization of TNFRSF19, a novel member of tumor necrosis factor
 RT receptor superfamily.";
 RL Genomics 62:103-107(1999).
 DR EMBL; AF173166; AAF19795.1; -;
 DR INTERPRO; IPR001368; -;
 DR PFAM; PF00020; TNFR_C6; 2.
 DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_2.
 DR PROSITE; PS50050; TNFR_NGFR_2; 1.
 SQ SEQUENCE 348 AA; 38450 MW; 013C799638F8E333 CRC64;

Query Match 42.8%; Score 977; DB 11; Length 214;
 Best Local Similarity 84.6%; Pred. No. 1.6e-82;
 Matches 176; Conservative 10; Mismatches 22; Indels 0; Gaps 0;

Qy 1 MALKVLEQEKTFFTLVLLGYLSCKVTCETGDCRQEQFRDRSGNCVPCNQCQPGMELSK 60
 Db 1 MALKVLPPLHRTVLFPAAILFLLHLACKVSCETGDCRQEQFRDRSGNCVLCQCGPGMELSK 60

Qy 61 ECGFGYGEDAQCQVTCRLHRFKEDWGFKCPCLDCAVNRFKANCATSDAICGDCPLG 120
 Db 61 ECGFGYGEDAQCQVPCPRHFRFKEDWGFKCPKPCADCALVNRFORANCSTSDAVCGDCPLG 120

Query Match 42.8%; Score 977; DB 11; Length 214;
 Best Local Similarity 84.6%; Pred. No. 1.6e-82;
 Matches 176; Conservative 10; Mismatches 22; Indels 0; Gaps 0;

Qy 1 MALKVLEQEKTFFTLVLLGYLSCKVTCETGDCRQEQFRDRSGNCVPCNQCQPGMELSK 60
 Db 1 MALKVLPPLHRTVLFPAAILFLLHLACKVSCETGDCRQEQFRDRSGNCVLCQCGPGMELSK 60

Qy 61 ECGFGYGEDAQCQVTCRLHRFKEDWGFKCPCLDCAVNRFKANCATSDAICGDCPLG 120
 Db 61 ECGFGYGEDAQCQVPCPRHFRFKEDWGFKCPKPCADCALVNRFORANCSTSDAVCGDCPLG 120

Db 61 ECGFGYGEDAQCPCPRHRFKEDWGQKCKPCADCALVNRFRQANCSTHTSDAVCGDCLPG 120
QY 121 FYRKTCLVGFQDMCEVPCGPPPPYEPHCASKVNLVKIATSTASSPRDTALAAYICSALAT 180
Db 121 FYRKTCLVGFQDMCEVPCGPPPPYEPHCASKVNLVKIATSTASSPRDTALAAYICSALAT 180
QY 181 VLLALLILCVIYCKRQFMKKPSWSLRS 208
Db 181 VLLALLILCVIYCKRQFMKKPSKCLPS 208
RESULT 7
Q9JLL2 PRELIMINARY; PRT; 150 AA.
AC Q9JLL2
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TReMBLrel. 15, Last annotation update)
DE TAJ-BETAL.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Eby M.T., Jasmin A., Kumar A., Sharma K., Chaudhary P.M.;
RT "TAJ, a Novel Member of the Tumor Necrosis Factor Receptor Family,
RT Activates the c-Jun N-terminal Kinase Pathway and Mediates Caspase-
RT Independent Cell Death.";
RL J. Biol. Chem. 275:15336-15342(2000).
DR EMBL; AF167554; AAF1827.1; -.
SQ SEQUENCE 150 AA; 16728 MW; 4A1B2E93AEF7FF43 CRC64;

Query Match 31.8%; Score 725; DB 11; Length 150;
Best Local Similarity 82.6%; Pred. No. 2.1e-59;
Matches 123; Conservative 9; Mismatches 17; Indels 0; Gaps 0;
QY 1 MALKVLEQEKTFLLVLLGLYSCKVTCETGDCRQOEFRDRSGNCVPCNOCGPMGELSK 60
Db 1 MALKVPLHRTVLFALFLHLLACKVSCETGDCRQOEFRDRSGNCVLCQCGPMGELSK 60
QY 61 ECGFGYGEDAQCPCPRHRFKEDWGQKCKPCADCALVNRFRQANCSTHTSDAVCGDCLPG 120
Db 61 ECGFGYGEDAQCPCPRHRFKEDWGQKCKPCADCALVNRFRQANCSTHTSDAVCGDCLPG 120
QY 121 FYRKTCLVGFQDMCEVPCGPPPPYEPHC 149
Db 121 FYRKTCLVGFQDMCEVPCGPPPPYEPHC 149

RESULT 8
Q9R187 PRELIMINARY; PRT; 448 AA.
AC Q9R187
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-OCT-2000 (TReMBLrel. 15, Last annotation update)
DE ECTODERMAL DYSPLASIA RECEPTOR.
GN EDAR OR DL.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Headon D.J., Overbeek P.A.;
RT "Involvement of a novel Tnf receptor homologue in hair follicle
RT induction";
RL Nat. Genet. 22:370-374(1999).
DR EMBL; AF160502; AAD50425.1; -.
DR MGI; 1343498; Edar.

KW Receptor.
SQ SEQUENCE 448 AA; 48434 MW; FCCAF38F3D6BB971 CRC64;
Query Match 8.6%; Score 197; DB 11; Length 448;
Best Local Similarity 28.2%; Pred. No. 4.2e-10;
Matches 61; Conservative 32; Mismatches 83; Indels 40; Gaps 11;
QY 16 LVLVLLGLYSCKVTCETGDCRQOEFRDR-SGNCVPCNOCGPMGELSKCEGFG-YGEDAQC 73
Db 13 LPVLVLSLMSARAEDSNCGENYHNQTTGLCQCCPCPRGPEEPYMSCGYGTDDYGC 72
QY 74 TCRHFRFKEDWGQKCKPCDCLDCAVAVNRQKANC-----SATSDAICGDCPLPGFY-----RKT 125
Db 73 PCPAEFKSG-GYOICRRHKDC---EGFFRATVLTPCDMENDAECGCLPGYYMLNRP 128
QY 126 KLGVFQDMCEVPCGPPPPYEPHCASKVNLVKIATSTASSPRDTA-----L 170
Db 129 NIYG---MVCYSC-LLAPPNTKECVGATSGVSAHSSSTSGGSTLSPFQHAHKELSGO 184
QY 171 AAVICSALATVL---LALLILCVIYCKRQFMKKPS 203
Db 185 ATALIATMSTIFIMATAIVLIIMFY----IMTKPS 216

RESULT 9
Q9UNE0 PRELIMINARY; PRT; 448 AA.
AC Q9UNE0
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TReMBLrel. 13, Last annotation update)
DE ECTODYSPLASIN-A RECEPTOR PROTEIN.
GN EDAR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99364416; PubMed=10431241;
RA Monreal A.W., Ferguson B.M., Headon D.J., Street S.L., Overbeek P.A.,
RA Zonana J.;
RT "Mutations in the human homologue of mouse dl cause autosomal
RT recessive and dominant hypohidrotic ectodermal dysplasia";
RL Nat. Genet. 22:366-369(1999).
DR EMBL; AF130988; AAD50076.1; -.
KW Receptor.
SQ SEQUENCE 448 AA; 48582 MW; AC8D61249D608439 CRC64;

Query Match 8.4%; Score 191; DB 4; Length 448;
Best Local Similarity 28.7%; Pred. No. 1.5e-09;
Matches 62; Conservative 30; Mismatches 84; Indels 40; Gaps 12;
QY 16 LVLVLLGLYSCKVTCETGDCRQOEFRDR-SGNCVPCNOCGPMGELSKCEGFG-YGEDAQC 73
Db 13 LPVLVLSLMSARAEDSNCGENYHNQTTGLCQCCPCPRGPEEPYMSCGYGTDDYGC 72
QY 74 TCRHFRFKEDWGQKCKPCDCLDCAVAVNRQKANC-----SATSDAICGDCPLPGFY-----RKT 125
Db 73 PCPAEFKSG-GYOICRRHKDC---EGFFRATVLTPCDMENDAECGCLPGYYMLNRP 128
QY 126 KLGVFQDMCEVPCGPPPPYEPHCASKVNLVKI-----ASTASSPRDTA-----L 170
Db 129 NIYG---MVCYSC-LLAPPNTKECVGATSGASANFFGTSGSTLSPFQHAHKELSGO 184
QY 171 AAVICSALATVL---LALLILCVIYCKRQFMKKPS 203
Db 185 ATALIATMSTIFIMATAIVLIIMFY----IMTKPS 216
RESULT 10

Db	134	VAGASSGGTETQPGNGTRAGGPEETAAYAVI--AIVPVFCLMGLLGLVC-----	183
QY	202	PSWSLRSDIQYNGSLSCLDRPQLHEYAHACCOCRRDSVTCGPVRLPLSMCCEACS	261
Db	184	-----NLLKRGYHCTAHK-----	EVG 200
QY	262	PNPATIGCGVHSNASLQARNAGPAGEMV	289
Db	201	PGPGGGGGINPAYRTEDVNEDTIGVLV	228
RESULT	13		
Q920W1			
ID	Q920W1	PRELIMINARY;	PRT; 417 AA.
AC	Q920W1		
DT	01-MAY-1999	(TREMBLrel. 10, Created)	
DT	01-MAY-1999	(TREMBLrel. 10, Last sequence update)	
DT	01-MAY-2000	(TREMBLrel. 13, Last annotation update)	
DE	NERVE GROWTH FACTOR RECEPTOR.		
OS	Mus musculus (Mouse)		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
NCBI_Taxid	10090;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=A;		
RA	MEDLINE=99077793; PubMed=9857182;		
RT	Tuffreau C., Benjean J., Blondel D., Kieffer B., Flamand A.;		
RT	"Low-affinity nerve-growth factor receptor (P75NTR) can serve as a		
RL	receptor for rabies virus.";		
RL	EMBO J. 17:7250-7259(1998)."		
DR	EMBL; AF105292; AAD17943.1; -.		
DR	HSSP; P07174; INGR.		
DR	INTERPRO; IPR000488; -.		
DR	INTERPRO; IPR000561; -.		
DR	INTERPRO; IPR000734; -.		
DR	INTERPRO; IPR001368; -.		
DR	PFAM; PF000020; TNFR_c6; 4.		
DR	PFAM; PF00531; death; 1.		
DR	PROSITE; PS00120; LIPASE_SER; UNKNOWN_1.		
DR	PROSITE; PS00652; TNFR_NGFR_1; 3.		
DR	PROSITE; PS01186; EGF_2; UNKNOWN_1.		
DR	PROSITE; PS50017; DEATH_DOMAIN; 1.		
DR	PROSITE; PS50050; TNFR_NGFR_2; 4.		
DR	Receptor.		
Q920W1			
SEQUENCE	417 AA; 44686 MW; 5D7AA4510DB8AF9B2	CRG64;	

Query Match	6.2%	Score 142;	DB 11;	Length 417;
Best Local Similarity	22.4%;	Pred. No. 4.7e-05;		
Matches	93;	Conservative 50;	Mismatches 178;	Indels 94; Gaps 23;
QY	7	LEBEKTEFTLLVLVG--YLSCKVTCETGDCRQRQEFDRSRSCVPCNOCGGPOMELUSKECGF	64	
Db	:	::: : ::::: :	:	
1	MDRLRLLLLLLGVSGGAKETCSTG-----MYTHSGEC--CKACNLGEGVAQPGC-	51		
QY	65	GYGEDAOCVTCRLHRFKED--WGFQKCPCLDCAVANRFQKANCATS DATCGDCLPGFY	122	
Db	52	--ANQTVCPECLDSVTFSDDVSATEPKCPCTEGLGL-QSMSAPCVEADAVC-RCSTGYI	107	
QY	123	RKTKLVGFQDWE-----CVPCGDPPPYEPHFCASKNVLV-----KIATASSPROTAL	170	
Db	108	-----QBETGRCEACSVCG-VGSGLVFSCODKONTVCEECPGTYSDEAHNVDPCL	158	
QY	171	AAVTCSALATVLLALLILCYIKRQPMEXKPSLSRSDIQNGSELSCLDLRPQLHEYA	230	
Db	159	PCTVCEDTEROLRE---CTPWADAEECIIPGRWITRSTTPE--GSDVT---TFSTQE--	207	
QY	231	HRACCQCRRDSVQTCGPVR-LLPSPMCSEECASPNATLGCGVHSAASLQARNAGPAGEMV	289	
Db	208	-----PEAPERDLIASTVAD-----TWTTVMGSSOPVVTR--GTADNLI	245	

Qy	290	PTPFGSLQTSGICEFS-----DAPLMPQNPMGCDNISFCDSYPELTGEDIHSLNPELESST	34
		: :	
Db	246	PVYSICILAAVVVLGVAYIAFKRMNSCKNQKQANSRPVNQTPPEGEKKLHS-----DSGI	300
		: :	
Qy	346	SLDNSSQDLVGGAVPVQSHSENFATATDLSRYNNNTLVESASTQDALTWRSOLDQ	400
		: :	
Db	301	SVDSQSLLHD-----QQTHTQ--TASAQALKGDGNLYSSL---PLTKREEVEK	342
		: :	
 RESULT 14			
ID	O14865	PRELIMINARY; PRT; 426 AA.	
AC	O14865;		
DT	01-JAN-1998 (TREMBLrel. 05, Created)		
DT	01-JAN-1998 (TREMBLrel. 05, Last sequence update)		
DT	01-OCT-2000 (TREMBLrel. 15, Last annotation update)		
DE	DEATH RECEPTOR 3 BETA.		
GN	DR3.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
CC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=98113360; PubMed=9446802;		
RA	Marzocha K., Ribeiro P., Charlot C., Renard N., Coiffier B.,		
SA	Salles G.;		
RT	"A new death receptor 3 isoform: expression in human lymphoid cell		
RL	lines and non-Hodgkin's lymphomas";		
BL	Biochem. Biophys. Res. Commun. 242:376-379(1998).		
EMBL	AF026070; AAC39556.1; -		
DR	HSSP; P19438; INCF.		
DR	INTERPRO; IPR000488; -		
DR	INTERPRO; IPR000561; -		
DR	INTERPRO; IPR001368; -		
DR	PFAM; PF00020; TNFR_c6; 2.		
DR	PFAM; PF00531; death_1.		
DR	PROSITE; PS00652; TNFR_NGFR_1; 2.		
DR	PROSITE; PS01186; EGF_2; UNKNOWN_1.		
DR	PROSITE; PSS0017; DEATH_DOMAIN; 1.		
DR	PROSITE; PSS0050; TNFR_NGFR_2; 1.		
SO	SEQUENCE 426 AA; 43950 MW; 371AA7F16AD29C16 CRC64;		

```

Query Match      6.2%; Score 142; DB 4; Length 426;
Best Local Similarity 25.2%; pred. No. 4.8e-05;
Matches 66; Conservative 26; Mismatches 70; Indels 100; Gaps 14;

Qy 34 CRQEFDRSGNC--VPCNQCG--PGMBLSKECGFGYGEDAQCVCRLUHRFKEDWGFOKC 89
   | | | | | : | | | | | : | | | | | : | | | | |
Db 95 CDEQASQVALENCASAVATRCCKPGWFW--EC-----QVSQCVSSSPF-----YC 138

Qy 90 KPCLDCAVVNRQKANCSATSDAICGDCCLPGFYRKTKLVGFQDMBCVPCGDPDPPEPHC 149
   : | | | | : | | | | | : | | | | | : | | | | |
Db 139 QPCLDCGALHRRHTRLLCS--RRDTCGTCCLPGFYE-----HGDGCVSCPTPPP----- 184

Qy 150 ASKYNLVKIASTASSPRDTALAAVCSAL-----ATVLLALLILCVICKRQFMKK 201
   | | | | | : | | | | | : | | | | | : | | | | |
Db 185 -----SLAGAPGAVOSAPVSLVAGGRGVGVQVLLAGLVVPLLL----- 225

Qy 202 PSWLSRSODIQYNGSELSCLDRLPQLUHEYAHRACCCRRDSVQTQCGPVRLLSMCCE--- 257
   | | | | | : | | | | | : | | | | | : | | | | |
Db 236 -----GATL-----YTYRH-----CWPHK--PLVTTADEAGM 250

Qy 238 EACSPNPATLGGCVHSAASLOA 279
   || : | | | | | : | | | | |
Db 251 EALTTPPPTHSLPDSHTLLA 272

RESULT 15
OT2735
ID OT2735 PRELIMINARY; PRT; 186 AA.
AC OT2735;

```

```
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE A53R PROTEIN.
GN A53R.
OS Cowpox virus (CPV).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_TaxID=10243;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GRI-90;
RX MEDLINE=98229462; PubMed=9568042;
RA Shchelkunov S.N., Saifonov P.F., Totmenin A.V., Petrov N.A.,
RA Ryazankina O.I., Gutorov V.V., Kotwal G.J.;
RT "The genomic sequence analysis of the left and right species-specific
RT terminal region of a cowpox virus strain reveals unique sequences and
RT a cluster of intact ORFs for immunomodulatory and host range
RT proteins."
RL Virology 243:432-460(1998).
DR EMBL; Y15035; CAA75273.1; -.
DR HSSP; P25942; 1CDF.
DR INTERPRO; IPR001368; -.
DR PFAM; PF00020; TNFR_C6; 2.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_2.
DR PROSITE; PS00050; TNFR_NGFR_2; 2.
DR PRODOM; PD000771; -. 1.
SQ SEQUENCE 186 AA; 20482 MW; D2342F1040A00AE3 CRC64;
```

Query Match 6.0%; Score 137.5; DB 12; Length 186;
Best Local Similarity 28.0%; Pred. NO. 4.8e-05;
Matches 46; Conservative 18; Mismatches 69; Indels 31; Gaps 11;

```
Qy 11 KTFFTLLVLGLVLSCKVTCE-----TGDCRQOEFRDRSGN-CVPCNQCQGMEL 58
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 4 KSLLA VCTIL-YITLTVTADITPLPPHAPVNGSCDEGEYLDKRHNQC--CNQCPGGEFA 60
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 59 SKECGFYGYGED-AQCVTCLRLHRFKEDWGFOK-CKPCLDCAVVNRQKANCATSDAICGD 116
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 61 KVRCS---GSDNTKCEPCPPHTYTAIPNYSNGCHQCKCP-TGSFQKVKCTGTQNSKC-S 115
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 117 CLPGFYRKTGLVGFD-MECVPCGDP PPPY-----EPHCAS 151
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 116 CLPGWYCATDSSQTEDCRDCVPKSRCPGCGYGGIDEQGNPICKS 159
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : ~~~~~~
```

THIS PAGE BLANK (USPTO)

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 16, 2001, 21:06:00 ; Search time 30.21 Seconds

(without alignments)
478.781 Million cell updates/sec

Title: US-09-380-276A-8

Perfect score: 2283

Sequence: 1 MALKVLEGEKFTLLVLL.....AIHPATQTSQVORRLGSL 423

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 268485 seqs, 34193795 residues

Total number of hits satisfying chosen parameters: 268485

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_36:*

- 1: /SIDSL/gcgdata/geneseq/geneseq/AA1980.DAT:*
- 2: /SIDSL/gcgdata/geneseq/geneseq/AA1981.DAT:*
- 3: /SIDSL/gcgdata/geneseq/geneseq/AA1982.DAT:*
- 4: /SIDSL/gcgdata/geneseq/geneseq/AA1983.DAT:*
- 5: /SIDSL/gcgdata/geneseq/geneseq/AA1984.DAT:*
- 6: /SIDSL/gcgdata/geneseq/geneseq/AA1985.DAT:*
- 7: /SIDSL/gcgdata/geneseq/geneseq/AA1986.DAT:*
- 8: /SIDSL/gcgdata/geneseq/geneseq/AA1987.DAT:*
- 9: /SIDSL/gcgdata/geneseq/geneseq/AA1988.DAT:*
- 10: /SIDSL/gcgdata/geneseq/geneseq/AA1989.DAT:*
- 11: /SIDSL/gcgdata/geneseq/geneseq/AA1990.DAT:*
- 12: /SIDSL/gcgdata/geneseq/geneseq/AA1991.DAT:*
- 13: /SIDSL/gcgdata/geneseq/geneseq/AA1992.DAT:*
- 14: /SIDSL/gcgdata/geneseq/geneseq/AA1993.DAT:*
- 15: /SIDSL/gcgdata/geneseq/geneseq/AA1994.DAT:*
- 16: /SIDSL/gcgdata/geneseq/geneseq/AA1995.DAT:*
- 17: /SIDSL/gcgdata/geneseq/geneseq/AA1996.DAT:*
- 18: /SIDSL/gcgdata/geneseq/geneseq/AA1997.DAT:*
- 19: /SIDSL/gcgdata/geneseq/geneseq/AA1998.DAT:*
- 20: /SIDSL/gcgdata/geneseq/geneseq/AA1999.DAT:*
- 21: /SIDSL/gcgdata/geneseq/geneseq/AA2000.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2278	99.8	423	20 W85724	Novel protein (Clo
2	2267	99.3	423	19 W0387	Amino acid sequenc
3	2258	98.9	423	20 W93581	Human HAPO4-alpha
4	2237	98.0	417	20 W98146	Human TRAIN-R. Ho
5	2230	97.7	417	19 W0386	Amino acid sequenc
6	1557.5	68.2	416	20 W93579	Mouse HAPO4-alpha
7	1544.5	67.7	328	20 Y06400	Human NTR-5 recept
8	977	42.8	214	20 Y06522	Mouse STRIP1 (Tan
9	977	42.8	214	20 W98145	Mouse TRAIN-R (lon
10	977	42.8	214	20 W93580	Mouse HAPO4-alpha
11	869	38.1	210	20 Y22223	Human TNFR superfa
12	854	37.4	150	20 W98148	TRAIN-R short, sol

13	783	34.3	160	20	Y06399	Mouse NTR-5 recept
14	725	31.8	150	20	Y06523	Mouse STRIFE2 (Tan
15	725	31.8	150	20	Y22224	Mouse TNFR superfa
16	725	31.8	150	20	W98144	Mouse TRAIN-R (Sho
17	725	31.8	150	20	W93583	Mouse HAPO4-gamma
18	725	31.8	150	21	Y77465	Murine Rank-like p
19	480	21.0	231	21	Y77468	Human Rank-like pr
20	261.5	11.5	109	20	W93582	Rat RAPO4-alpha pr
21	244	10.7	77	21	Y77467	Human Rank-like pr
22	192.5	8.4	132	21	Y77466	Human Rank-like pr
23	179	7.8	30	20	W98147	TRAIN-R secreted f
24	159	7.0	438	16	R81882	Plasmid pDC406/OX4
25	159	7.0	438	19	W48976	OX40/FC mutein. C
26	150	6.6	206	16	R81881	Mouse type-II memb
27	150	6.6	206	19	W48977	Mouse OX40 extrace
28	146.5	6.4	1801	19	W50895	Rat laminin B2 cha
29	144	6.3	1104	17	R94957	NF-X1 DNA-binding
30	142	6.2	95	20	W93584	Mouse HAPO4-beta p
31	140.5	6.2	408	20	Y41111	Human TANGO 129 (T
32	140.5	6.2	430	20	Y41110	Human TANGO 129 (T
33	140.5	6.2	430	21	Y70785	Human tumour necro
34	140	6.1	425	21	Y92370	p75-NTR (neurotrop
35	137	6.0	1798	19	W50896	Human laminin B2 c
36	136	6.0	625	19	W83200	Murine osteoclast
37	136	6.0	625	19	W69958	Murine NF-KB recep
38	136	6.0	625	19	W68294	Murine NF-KB recep
39	136	6.0	625	21	Y59509	OBM binding protei
40	136	6.0	625	21	Y53649	A mouse receptor a
41	134	5.9	186	15	R62655	Cowpox virus pst I
42	134	5.9	307	18	W33358	TBP(20-161)/hcg-be
43	134	5.9	1764	10	P91672	Primary amino acid
44	134	5.9	1776	19	W50894	Mouse laminin B1 c
45	133.5	5.8	2050	20	W73499	Von Willebrand fac

ALIGNMENTS

RESULT 1

W85724

ID W85724 standard; Protein; 423 AA.

XX W85724;

XX AC

XX DT 27-SEP-1999 (first entry)

XX DE Novel protein (Clone AX92_3).

XX KW Polynucleotide; protein; nutrition; cytokine; cell proliferation;

XX KW cell differentiation; immunostimulation; immunosuppression;

XX KW haematopoiesis regulation; tissue growth; activin; inhibin;

XX KW chemotaxis; chemokinesis; haemostasis; thrombolysis; receptor;

XX KW ligand; anti-inflammatory; tumour suppression; gene therapy.

XX OS Homo sapiens.

XX PN W09920644-A1.

XX PD 29-APR-1999.

XX PF 16-OCT-1998; 98WO-US22034.

XX PR 18-OCT-1997; 97US-0955557.

XX PA (GEMY) GENETICS INST INC.

XX PI Agostino MJ, Bowman MR, Evans C, Jacobs K, Lavallie ER;

XX PI McCoy JM, Merberg D, Racie LA, Spaulding V, Treacy M;

XX XX WPI; 1999-288272/24.

XX DR N-PSDB; X08689.

XX PT New polynucleotides encoding secreted human proteins

XX PS Claim 32: Page 117-118; 136pp; English.

XX CC The new human secreted proteins are encoded by polynucleotides

CC obtained from human placenta, adult testes, fetal kidney, fetal

CC brain, adult brain, adult brain and adult blood cDNA libraries.

CC The polynucleotides and proteins are predicted to have biological

CC activities which would make them suitable for treating, preventing or

CC ameliorating medical conditions in humans and animals. Suggested

CC activities include nutritional activity, cytokine and cell

CC proliferation/differentiation activity, immune stimulating (e.g. as

CC vaccines) or suppressing activity, haematopoiesis regulating

CC activity, tissue growth activity, activin/inhibin activity,

CC chemotactic/chemokinetic activity, haemostatic and thrombolytic

CC activity, receptor/ligand activity, anti-inflammatory activity,

CC cadherin/tumour invasion suppressor activity, and tumour inhibition

CC activity. The polynucleotides are also stated to be useful for gene

CC therapy. The sequences identified by a secretory leader

CC sequence motif in the polynucleotide and it is thought that the

CC encoded proteins have biological activity by virtue of their secreted

CC nature. This polypeptide was encoded by a clone designated AX92_3

CC (See X08689).

XX SQ Sequence 423 AA;

Query Match 99.8%; Score 2278; DB 20; Length 423;

Best Local Similarity 99.8%; Pred. No. 2.1e-201;

Matches 422; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MALKVLEQEKFTFTLLVLLGYLSCKVTCTGDCRQOEFRDRSGNCVPCNQCQPGMELSK 60

DB 1 malkvleqeektfttllvllglylsckvtcetgdcrgqefdrsgncvpcnqcpgmelsk 60

QY 61 ECGFGYGEDAQCVTCRLHRFKEDWGQKPCLDCAVAVNRQKANCSDATCGDCLPG 120

DB 61 ecgfygedaqcvctclhrfkedwgfqckpcldcavavnrqkancsatsdaicgdcclpg 120

QY 121 FYRKTCLVGFQDMECVPCGPPPPYEPHCASKVNLVKIASTASSPRDTALAAVICSALAT 180

DB 121 fyrktclvlgfmdmecvpcgppppypchcaskvnlvkiastassprdtalaavicsalat 180

QY 181 VLLALLILCVYCKRQFMKKPSWSLRSODIQYNGSELSCDRPQLHEYAHRACCCRRD 240

DB 181 vllallilcvyckrmekppswslrsodiqyngselscldrpqlheyahracccrrd 240

QY 241 SVQTCGPVRLPSPMCCEACSPNPATLGGCVHSAASLQARNAGPAGEMVPTFFGSLTQSI 300

DB 241 svtcgvpvrlpsmcceacspnpatlggcvhsaaslqarnagpagemvptffgsltqsi 300

QY 301 CGEFSDAWPLMQNPMGMDNISFCDSYPELTGEDIHSLNPELESSTSLDSNSODLVGGAV 360

DB 301 cgefswdaplmgpnmggdnisfcdsyeltdgedihslnpelesstslsnsodlvvgav 360

QY 361 PVQSHSENFTAAATDLRYNNLTVESASTQDALTMRSQDQESGAIHPATQTSLOVRQL 420

DB 361 pvqshsenftaatdlrynnltvesastqdaltmrsqdqesgaiihpatqtslvrql 420

RESULT 2

ID W70387

AC W70387 standard; Protein: 423 AA.

XX AC W70387;

XX DT 02-DEC-1998 (first entry)

XX DE Amino acid sequence of human beta-OAF065.

XX

KW Human; beta-OAF065; stroma cell; antibody; inflammatory;

XX cytokine-mediated disease; rheumatism; ulcerative colitis.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT Misc-difference 223

FT /note= "encoded by AGA"

FT Misc-difference 224

FT /note= "encoded by CCT"

XX PN W09838304-A1.

XX PD 03-SEP-1998.

XX PF 26-FEB-1998; 98WO-JP00799.

XX PR 27-FEB-1997; 97JP-0043143.

XX PA (ONOV) ONO PHARM CO LTD.

XX PI Fukushima D, Konishi M, Tada H;

XX DR WPI; 1998-481205/41.

XX DR N-PSDB; V33362.

XX PT Membrane polypeptide expressed by human stroma cells, and antibodies

PT recognising it - for treatment of inflammatory and other

PT cytokine-mediated diseases.

XX PS Disclosure; Pages 37-49; 54pp; Japanese.

XX CC This is the amino acid sequence of the human beta-OAF065, used in

CC the method of the invention. The process involves the use of peptides

CC expressed by stroma cells, and its antibodies are used for in the

CC prevention and treatment of inflammatory and other cytokine-mediated

CC diseases such as rheumatism, ulcerative colitis.

XX SQ Sequence 423 AA;

Query Match 99.3%; Score 2267; DB 19; Length 423;

Best Local Similarity 99.5%; Pred. No. 2.2e-200;

Matches 421; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MALKVLEQEKFTFTLLVLLGYLSCKVTCTGDCRQOEFRDRSGNCVPCNQCQPGMELSK 60

DB 1 malkvleqeektfttllvllglylsckvtcetgdcrgqefdrsgncvpcnqcpgmelsk 60

QY 61 ECGFGYGEDAQCVTCRLHRFKEDWGQKPCLDCAVAVNRQKANCSDATCGDCLPG 120

DB 61 ecgfygedaqcvctclhrfkedwgfqckpcldcavavnrqkancsatsdaicgdcclpg 120

QY 121 FYRKTCLVGFQDMECVPCGPPPPYEPHCASKVNLVKIASTASSPRDTALAAVICSALAT 180

DB 121 fyrktclvlgfmdmecvpcgppppypchcaskvnlvkiastassprdtalaavicsalat 180

QY 181 VLLALLILCVYCKRQFMKKPSWSLRSODIQYNGSELSCDRPQLHEYAHRACCCRRD 240

DB 181 vllallilcvyckrmekppswslrsodiqyngselscldrpqlheyahracccrrd 240

QY 241 SVQTCGPVRLPSPMCCEACSPNPATLGGCVHSAASLQARNAGPAGEMVPTFFGSLTQSI 300

DB 241 svtcgvpvrlpsmcceacspnpatlggcvhsaaslqarnagpagemvptffgsltqsi 300

QY 301 CGEFSDAWPLMQNPMGMDNISFCDSYPELTGEDIHSLNPELESSTSLDSNSODLVGGAV 360

DB 301 cgefswdaplmgpnmggdnisfcdsyeltdgedihslnpelesstslsnsodlvvgav 360

QY 361 PVQSHSENFTAAATDLRYNNLTVESASTQDALTMRSQDQESGAIHPATQTSLOVRQL 420

DB 361 pvqshsenftaatdlrynnltvesastqdaltmrsqdqesgaiihpatqtslvrql 420

QY 421 GSL 423
 Db 421 gsl 423
 RESULT 3
 ID W93581 standard; Protein; 423 AA.
 AC W93581;
 XX
 XX 18-JUN-1999 (first entry)
 DE Human hAPO4-alpha protein.
 XX
 KW Tumour necrosis factor receptor; signal transducer molecule; TNF; APO4;
 KW developmental abnormality; gestational abnormality; prostate cancer;
 KW APO6; APO8; TNRL-1; TNRL-3; diagnosis; treatment; therapy; disease;
 KW cytoplasmic domain; immunogen; antibody preparation; breast carcinoma;
 KW apoptosis; human; APO4-alpha.
 XX
 XX Homo sapiens.
 XX
 PN WO9911791-A2.
 PD 11-MAR-1999.
 XX
 PF 04-SEP-1998; 98WO-US18393.
 XX
 PR 05-SEP-1997; 97US-0924634.
 XX
 XX (UNIW) UNIV WASHINGTON.
 PA
 PI Chaudhary PM;
 XX
 XX WPI; 1999-205191/17.
 DR N-PSDB; X23415.
 XX

New Tumor Necrosis Factor family receptor polypeptides and ligands -
 useful for diagnosis and treatment of prostate cancer and
 developmental or gestational abnormalities
 Claim 1; Fig 7C; 156pp; English.

This invention describes isolated Tumor Necrosis Factor (TNF) family
 receptor polypeptides: APO4, APO6, APO8 and APO9 or their active
 fragments, and isolated TNF related ligands 1 and 3 (TNRL1 and TNRL3) or
 their active fragments. APO4 is useful for diagnosing prostate cancer
 by determining levels of APO4 in an individual. Prostate cancer can also
 be treated using APO4 selective binding agents linked to a therapeutic
 moiety. APO4 polypeptides are also useful for identifying selective
 binding agents, useful in diagnosis/treatment of disease by binding of
 agents to the polypeptide/active fragment which is extracellular, or
 expressed on the cell surface. The binding is preferably performed in
 vivo. APO4 polypeptides/active fragments are also useful for screening
 for agonists and antagonists by binding and observing the change in APO4
 activity. Effective pharmacological agents useful in diagnosis or
 treatment of disease are also identified using APO4 polypeptides/active
 fragments and APO4 signal transducer molecules that specifically interact
 with a cytoplasmic domain of APO4 and detecting a change in level of APO4
 activity. The method is performed in vivo or in vitro. APO polypeptides
 are all useful as immunogens for preparing antibodies. APO4 is also
 useful for diagnosis/treatment of developmental or gestational
 abnormalities. APO8 was transfected to human breast carcinoma cell line
 MCF-7, and induced apoptosis.

Sequence 423 AA;

Query Match 98.9%; Score 2258; DB 20; Length 423;
 Best Local Similarity 98.6%; Pred. No. 1.5e-199;
 Matches 417; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 MALKVLEQEKTFFTLLVLLGYLSCKVTCTGDCRQEQFRDRSGNCPVPCNOGPGMELSK 60
 Db 1 malkvleqektfftlvllgylsckvtctesgdcrcqefdrsgncvpcncgpgmelsk 60
 QY 61 EGGFGYGEDAQCVTCRLHRFKEDWGFQCKPCLDCAVVNRFOKANCATSADAICGDCLPG 120
 Db 61 ecgfgygedaqcvaclhrfkedwgfqckpcldcavvnrfgkancsatsdaicgdcclpg 120
 QY 121 FYRKTLYGFQDMCEVPCGDDPPPEPHCASKVNLVKIATASSPRDTALAAVICSALAT 180
 Db 121 fyrktlygfdmcevcpgddpppephcaskvnlvkiatassprdtalaavicsalat 180
 QY 181 VLLALLILCVYCKRQFMEKKPSWLSRSDIOYNGSELSCLDROPOLHEYAHRAACQCRRD 240
 Db 181 vllallilcvyckrfmekkpswlsrsqdiqynetelscfarpqlheyahracqccrrd 240
 QY 241 SVQTGCPVRLPSCWCEBACSPNPATLGCVHSAASLAARNAGPAGEMVPTFFGSLTQSI 300
 Db 241 svqtgcpvrlpsscwbacspnpatlgcgvhsaaslaarnagpagemvptffgsltqsi 300
 QY 301 CGEFS DANPLMGNPMGDNISFCDSYPPELTGEDIHSLNPELESSTSLDSNSSQDLVGAV 360
 Db 301 cgefsdawnplmgpnmgdnisfcdsypelgtedihslnpelesstslsdsnssqdlvgav 360
 QY 361 PVQSHSENFTATDLRYNNTLVESASTQDALTMRSQLDOESGAIHPATQTSLOVRQL 420
 Db 361 pvqshsenftaatdlrynnltvlesastqtdaltmrsqldoesgaihpatsqlvqrql 420
 QY 421 GSL 423
 Db 421 gsl 423
 RESULT 4
 ID W98146 standard; Protein; 417 AA.
 XX
 AC W98146;
 XX
 DT 05-JUL-1999 (first entry)
 XX
 DE Human TRAIN-R.
 KW TRAIN-R; receptor; human; tumour necrosis factor receptor;
 KW agonist; antagonist; cancer; immunological disease; therapy;
 KW cytosolic.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Peptide 1..21 /note= "signal peptide"
 FT Protein 22..417 /note= "mature protein"
 FT Domain 26..173 /note= "extracellular domain"
 FT Domain 174..190 /note= "transmembrane domain"
 FT Domain 191..417 /note= "cytoplasmic domain"
 PN WO9913078-A1.
 XX
 PD 18-MAR-1999.
 XX
 PF 11-SEP-1998; 98WO-US19030.
 XX
 PR 06-MAY-1998; 98US-0084422.
 PR 12-SEP-1997; 97US-0058631.
 XX
 PA (BIOJ) BIOGEN INC.
 XX
 PI Hession C, Tschopp J;

XX WPI; 1999-229238/19.
 DR N-PSDB; X24978.
 XX
 PT New cysteine-rich tumor necrosis factor receptor
 PS
 PS Claim 2; Page 26; 30pp; English.
 XX
 CC The present sequence is a novel human cysteine-rich tumour
 CC necrosis factor receptor family member termed TRAIN-R that is
 CC expressed at low levels in every tissue and cell line tested thus
 CC far, with higher expression detected in heart, prostate, ovary,
 CC testis, peripheral blood lymphocytes, thyroid and adrenal gland.
 CC Cell death can be induced by administering an agent capable of
 CC inhibiting the binding of TRAIN-R to its ligand. A claimed method
 CC of treating, or reducing, the advancement, severity or effects of
 CC an immunological disease in a mammal comprises administering a
 CC pharmaceutical composition which comprises a TRAIN-R blocking agent,
 CC e.g. soluble TRAIN-R. TRAIN-R can be fused to an immunoglobulin to
 CC produce a fusion protein which may be targeted to various sites.
 CC It can be used in binding assays, and to identify antagonists and
 CC agonists. Anti-TRAIN-R antibodies can be used to reduce the
 CC severity of an immune response or to treat cancer. TRAIN-R
 CC blocking agents can also be used to reduce the severity or effects
 CC of an immunological disease (all claimed).
 XX
 SQ Sequence 417 AA;

Query Match 98.0%; Score 2237; DB 20; Length 417;
 Best Local Similarity 99.3%; Pred. No. 1.2e-197;
 Matches 412; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MALKVLEQEKTFLLVLLGLYSCKVCTGTGCRQEFRRDRSGNCVPCNQCQPGHLSK 60
 DB 1 malkvleqektftllvlllgylsckvtcesgdcrqgefrrdsgncvpcnqcpggmelsk 60
 QY 61 ECGFGYGEDAQVCTRLHREKEDWGFQKCKPCLDCAVNNRFKANCATSATSDAICGDLPG 120
 DB 61 ecgfygedaqvctrlhrfkedwgfqkcpcldcavnnrfkancatsatdaicgdlpg 120
 QY 121 FYRKTUFGQDMECVPCGDPDPPEPHCASKVNLKIASTASSPRDTALAAVICSALAT 180
 DB 121 fyrktlvgfdmecnvpcgdpdppephcaskvnlvkiastassprdtalaavicsalat 180
 QY 181 VLLALLILCVYCKRQPMKKPSLSRSDIOYNGSELSCLDRLPQLHEYAHRAACCCQRRD 240
 DB 181 vllallilcvyckrqpmekpslsrsdiqyngselscldrplqlheyahraccqrrd 240
 QY 241 SVQTCGPVRLPLSMCCCEACSPNPATLGCYVHSAASLQARNAGPAGMVPFTFGSLTQSI 300
 DB 241 svtcgvpvrlplsmcceeacspnpatlgcgvhsaaslgarnagpagemvptffgsltqsi 300
 QY 301 CGEFSDAWPLMQNPMGDNISFCDSPYELTGEDTHSLNPELESSTSLDSNSSQDLVGGAV 360
 DB 301 cgefsdawplmqnpgmgnisfcdsyelpeltgedthslnpelesstslsdsnsqdlvggav 360
 QY 361 PVQSHSENFATDLSRYNNLTVESASTQDALTMRSQLDQESGAIHPATQTSILQ 415
 DB 361 pvqshsenfataatdlsrynnltvesastqdaltrmsqldqesgaihpattqtsilq 415

RESULT 5
 W70386
 ID W70386 standard; Protein; 417 AA.
 AC W70386;
 XX
 XX 02-DEC-1998 (first entry)
 DE Amino acid sequence of human alpha-OAF065.
 XX Human; alpha-OAF065; stroma cell; antibody; inflammatory;

KW cytokine-mediated disease; rheumatism; ulcerative colitis.
 XX Homo sapiens.
 OS
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 223 /note= "encoded by AGA"
 FT Misc-difference 224 /note= "encoded by CCT"
 FT
 XX WO9838304-A1.
 PN
 XX
 XX 03-SEP-1998.
 PD
 XX
 XX 26-FEB-1998; 98WO-JP00799.
 PF
 XX
 XX 27-FEB-1997; 97JP-0043143.
 PR
 XX (ONOV) ONO PHARM CO LTD.
 PA
 XX Fukushima D, Konishi M, Tada H;
 PI
 XX WPI; 1998-481205/41.
 DR N-PSDB; V33361.
 XX
 XX Membrane polypeptide expressed by human stroma cells, and antibodies
 PT recognising it - for treatment of inflammatory and other
 PT cytokine-mediated diseases.
 PT
 XX Claim 1; Pages 28-30; 54pp; Japanese.
 PS
 XX This is the amino acid sequence of the human alpha-OAF065, used in
 CC the method of the invention. The process involves the use of peptides
 CC expressed by stroma cells, and its antibodies are used for in the
 CC prevention and treatment of inflammatory and other cytokine-mediated
 CC diseases such as rheumatism, ulcerative colitis.
 XX
 SQ Sequence 417 AA;

Query Match 97.7%; Score 2230; DB 19; Length 417;
 Best Local Similarity 99.5%; Pred. No. 5.4e-197;
 Matches 413; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 MALKVLEQEKTFLLVLLGLYSCKVCTGTGCRQEFRRDRSGNCVPCNQCQPGHLSK 60
 DB 1 malkvleqektftllvlllgylsckvtcetgcrqgefrrdsgncvpcnqcpggmelsk 60
 QY 61 ECGFGYGEDAQVCTRLHREKEDWGFQKCKPCLDCAVNNRFKANCATSATSDAICGDLPG 120
 DB 61 ecgfygedaqvctrlhrfkedwgfqkcpcldcavnnrfkancatsatdaicgdlpg 120
 QY 121 FYRKTUFGQDMECVPCGDPDPPEPHCASKVNLKIASTASSPRDTALAAVICSALAT 180
 DB 121 fyrktlvgfdmecnvpcgdpdppephcaskvnlvkiastassprdtalaavicsalat 180
 QY 181 VLLALLILCVYCKRQPMKKPSLSRSDIOYNGSELSCLDRLPQLHEYAHRAACCCQRRD 240
 DB 181 vllallilcvyckrqpmekpslsrsdiqyngselscldrplqlheyahraccqrrd 240
 QY 241 SVQTCGPVRLPLSMCCCEACSPNPATLGCYVHSAASLQARNAGPAGMVPFTFGSLTQSI 300
 DB 241 svtcgvpvrlplsmcceeacspnpatlgcgvhsaaslgarnagpagemvptffgsltqsi 300
 QY 301 CGEFSDAWPLMQNPMGDNISFCDSPYELTGEDTHSLNPELESSTSLDSNSSQDLVGGAV 360
 DB 301 cgefsdawplmqnpgmgnisfcdsyelpeltgedthslnpelesstslsdsnsqdlvggav 360
 QY 361 PVQSHSENFATDLSRYNNLTVESASTQDALTMRSQLDQESGAIHPATQTSILQ 415
 DB 361 pvqshsenfataatdlsrynnltvesastqdaltrmsqldqesgaihpattqtsilq 415

CC clone (see x59346). Homology to osteoprotegerin suggests that NTR-5
is involved in the regulation of bone mass, and may be useful for
CC regulating development, proliferation and death of osteoblast or
CC osteoclast cells or for regulating muscle metabolism, and that it
CC may be implicated in muscle diseases or disorders. A host-vector
CC system for production of NTR-5 is claimed. NTR-5 polypeptides can
CC be used as immunogens and in screening assays to identify NTR-5
CC ligands, agonists and antagonists. Polypeptides comprising the
CC extracellular domain of NTR-5 fused to an immunoglobulin constant
CC region, especially to a human immunoglobulin gamma-1 Fc region,
CC are claimed. The invention also provides for diagnostic and
CC therapeutic methods based on the interaction of NTR-5 and agents
CC that initiate signal transduction through binding to NTR-5.

XX Sequence 328 AA;

Query Match 67.7%; Score 1544.5; DB 20; Length 328;
Best Local Similarity 90.2%; Pred. No. 4.5e-134;
Matches 286; Conservative 4; Mismatches 14; Indels 13; Gaps 3;

QY 1 MALKVLEQEKTEFTLLVLGLYSCKVTCETGDCRQOEPRDRSGNVCVPCNQCGHWSLK 60
DB 1 malkvleqektftllvlglysckvtcesgdcrgqefdrsgnvcvpcnqcgpgmelsk 60
QY 61 ECGFGYGEDAQCVTCRLHREKEDWGFKCKPCLDCAVNNRFQKANGSATSDAICGDCPLG 120
DB 61 ecfgfygedaqvctrlhrfkedwgfgkcpcldcavnnrfqkangsatsdaicgdcplg 120
QY 121 FYRKTLLVGFQDMCEVPCGDPDPPEPHCASKVNLVKIASTASPRDTALAAVICSALAT 180
DB 121 fyrktllvlgfmdmcevpchgdpdppephcaskvnlvkiastasprdtalaavicsalat 180
QY 181 VLLALILCVYCKRQFMKKPSWSLSRSDIOYNGSELSCLDRPOLHEYAHRACCCRRD 240
DB 181 vllalilcvyckrgfmekppswslsrsgdiqngseiscldrpqlheyahraccrrd 240
QY 241 SVQTCGVRLLPSCMCEACSPNATLGGCVHSAASLQARNAGPAGEMVPTFFGSLTQSI 300
DB 241 svctcgvrllpsmcceacspnatlggcvhsaaslqarnagpagemvptffgsltsqi 300
QY 301 CGEFSDAWPLQNPMDG 317
DB 294 c-----wnpkstpllg 304

RESULT 8
Y06522
ID Y06522 standard; Protein; 214 AA.

XX Y06522;
XX Y06522;
XX 08-OCT-1999 (first entry)

XX Mouse STRIFE1 (Tango 127a) TNF receptor.

XX STRIFE1; Tango 127a; mouse; tumour necrosis factor receptor;
KW sepsis; circulatory collapse; toxic shock; infection;
KW immune disease; autoimmune disease; alcohol-induced hepatitis;
KW inflammation; graft versus host pathology; cancer; tumour;
KW cerebral malaria; multiple sclerosis; diagnosis; therapy.

XX Mus musculus.

XX Key Location/Qualifiers
FT Peptide 1..29
FT Protein /note= "signal peptide" 30..214
FT Protein /note= "mature protein" 34..72
FT Domain /note= "cysteine-rich domain" 75..114
FT Domain /note= "cysteine-rich domain"

FT Domain 169..193
FT /note= "transmembrane domain"
XX W09937818-A1.
XX 29-JUL-1999.
XX 27-JAN-1999; 99WO-US01679.
XX 27-JAN-1998; 98US-0014195.
XX (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
XX Busfield SJ;
XX WPI; 1999-458707/38.
XX N-PSDB; X87394.
XX New STRIFE1 and STRIFEII polypeptides, proteins and nucleic acid
XX molecules useful for modulating TNFR associated disorders
XX Claim 26; Fig 1A-B; 119pp; English.

XX The present sequence represents mouse STRIFE1 (also called Tango
127a or T127a), a novel member of the tumour necrosis factor
CC receptor (TNFR) superfamily. 2 Splice forms of murine STRIFE have
CC been identified, one that is predicted to be membrane-bound
CC (STRIFE1) and one that is secreted (STRIFE2, see Y06523). STRIFE
CC was identified as a TNFR homologue by a computer-based search of
CC EST databases. The invention provides STRIFE1 and STRIFE2
CC polynucleotides and polypeptides, fusion proteins, antigenic
CC peptides and antibodies. It also provides expression vectors,
CC host cells and transgenic animals, as well as diagnostic, screening
CC and therapeutic methods. STRIFE I and STRIFE II may play a role in
CC mediating inflammatory, immune and host defense functions and may
CC play a role in various neoplastic disease states. They may be
CC useful as targets for developing novel diagnostic and therapeutic
CC agents for TNF- and TNFR-associated disorders such as sepsis
CC syndrome, circulatory collapse and shock resulting from bacterial
CC infection, acute and chronic parasitic or infectious processes,
CC acute and chronic immune and autoimmune pathologies, alcohol-induced
CC hepatitis, chronic inflammatory pathologies, vascular inflammatory
CC pathologies, graft-versus-host pathology, malignant pathologies
CC involving TNF-secreting tumors, cerebral malaria and multiple
CC sclerosis.

XX Sequence 214 AA;

Query Match 42.8%; Score 977; DB 20; Length 214;
Best Local Similarity 84.6%; Pred. No. 4e-82;
Matches 176; Conservative 10; Mismatches 22; Indels 0; Gaps 0;

QY 1 MALKVLEQEKTEFTLLVLGLYSCKVTCETGDCRQOEPRDRSGNVCVPCNQCGHWSLK 60
DB 1 malkvleqektftllvlglysckvtcesgdcrgqefdrsgnvcvickqcgpgmelsk 60
QY 61 ECGFGYGEDAQCVTCRLHREKEDWGFKCKPCLDCAVNNRFQKANGSATSDAICGDCPLG 120
DB 61 ecfgfygedaqvctrlhrfkedwgfgkcpcldcavnnrfqkangsatsdavgdcplg 120
QY 121 FYRKTLLVGFQDMCEVPCGDPDPPEPHCASKVNLVKIASTASPRDTALAAVICSALAT 180
DB 121 fyrktllvlgfmdmcevpchgdpdppephcaskvnlvkiastasprdtalaavicsalat 180
QY 181 VLLALILCVYCKRQFMKKPSWSLSR 208
DB 181 vllalilcvyckrgfmekppswslrs 208

RESULT 9
W98145
ID W98145 standard; Protein; 214 AA.

CC W98146). Human TRAIN-R is expressed at low levels in every tissue
 CC and cell line tested thus far, with higher expression detected in
 CC heart, prostate, ovary, testis, peripheral blood lymphocytes,
 CC thyroid and adrenal gland. Cell death can be induced by
 CC administering an agent capable of inhibiting the binding of TRAIN-R
 CC to its ligand. A claimed method of treating, or reducing, the
 CC advancement, severity or effects of an immunological disease in a
 CC mammal comprises administering a pharmaceutical composition which
 CC comprises a TRAIN-R blocking agent, e.g. soluble TRAIN-R. TRAIN-R
 CC can be fused to an immunoglobulin to produce a fusion protein which
 CC may be targeted to various sites. It can be used in binding assays,
 CC and to identify antagonists and agonists. Anti-TRAIN-R antibodies
 CC can be used to reduce the severity of an immune response or to treat
 CC cancer. TRAIN-R blocking agents can also be used to reduce the
 CC severity or effects of an immunological disease (all claimed).
 XX
 SQ Sequence 150 AA;

Query Match 37.4%; Score 854; DB 20; Length 150;
 Best Local Similarity 99.3%; Pred. No. 5e-71;
 Matches 148; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MALKVLLDQKFTFFLLVLLGLYLSCKVTCETGDCRQQRQDRSGNCVPCNCGPGMELSK 60
 DB 1 malkvllleqektffllvllgylsckvtcesgdcrcqqrqefdrsgncvpcncgpgmelsk 60
 QY 61 ECGFGYGDAQCVCRLHREFKEDWGFCCKPCLDCAVNVNRFQKNCATSATSDAICGLPG 120
 DB 61 ecgfgygdaqcvcrlhfrkdwgfcckpckldcavvnrfqkncatsatsdaicgdcilpg 120
 QY 121 FYRKTGLVGFQDMECVPCGDPDPPEPHC 149
 DB 121 fyrktglvgfdmecnpcgdpdppephc 149

RESULT 13
 Y06399
 ID Y06399 standard; Protein; 160 AA.
 XX
 AC Y06399;
 XX
 DT 20-SEP-1999 (first entry)
 XX
 DE Mouse NTR-5 receptor.
 XX
 KW NTR-5; mouse; receptor; signal transduction; bone; muscle;
 KW diagnosis; therapy.
 XX
 OS Mus musculus.
 XX
 PN W09933967-A2.
 XX
 PD 08-JUL-1999.
 XX
 PF 28-DEC-1998; 98WO-US27688.
 XX
 PR 29-DEC-1997; 97US-0068925.
 XX
 PA (REGE-) REGENERON PHARM INC.
 XX
 PI Valenzuela DW;
 XX
 DR WPI: 1999-419102/35.
 DR N-PSDB; X59345.
 XX
 PT New mammalian receptor NTR-5 polypeptides
 XX
 PS Example 1; Page 19; 27pp; English.
 XX
 CC The present sequence represents a novel murine receptor, designated
 CC NTR-5, that shows homology to osteoprotegerin and to tumour necrosis
 CC factor receptor. The sequence was predicted from isolated cDNA

CC clones (see X59345). Human NTR-5 has also been identified (see
 CC Y06400). Homology to osteoprotegerin suggests that NTR-5 is
 CC involved in the regulation of bone mass, and may be useful for
 CC regulating development, proliferation and death of osteoblast or
 CC osteoclast cells or for regulating muscle metabolism, and that it
 CC may be implicated in muscle diseases or disorders. A host-vector
 CC system for production of NTR-5 is claimed. NTR-5 polypeptides can
 CC be used as immunogens and in screening assays to identify NTR-5
 CC ligands, agonists and antagonists. The invention also provides for
 CC diagnostic and therapeutic methods based on the interaction of
 CC NTR-5 and agents that initiate signal transduction through binding
 CC to NTR-5.
 XX
 SQ Sequence 160 AA;

Query Match 34.3%; Score 783; DB 20; Length 160;
 Best Local Similarity 91.6%; Pred. No. 1.9e-64;
 Matches 141; Conservative 4; Mismatches 9; Indels 0; Gaps 0;
 QY 55 GMELSKGCGYGGDAQCVCRLHREFKEDWGFCCKPCLDCAVNVNRFQKNCATSATSDAIC 114
 DB 1 gmelskcgfyggedagcvcprfrkdwgfcckpckldcavvnrfqkncatsdsv 60
 QY 115 GDCLPFGFYRKTKLVGFQDMECVPCGDPDPPEPHCASKVNLVKIATSSPRDTALAAVI 174
 DB 61 gdcilpgfyrktklvgfdmecnpcgdpdppephctskvnlvkiatssprdtalaavi 120
 QY 175 CSALATVLLALLILCVYCKRQFMKPKSWLSRS 208
 DB 121 csalatvllallilcvlyckrqfmekpkpsclips 154

RESULT 14
 Y06523
 ID Y06523 standard; Protein; 150 AA.
 XX
 AC Y06523;
 XX
 DT 08-OCT-1999 (first entry)
 XX
 DE Mouse STRIFE2 (Tango 127b) TNF receptor.
 XX
 KW STRIFE2; Tango 127b; mouse; tumour necrosis factor receptor;
 KW sepsis; circulatory collapse; toxic shock; infection;
 KW immune disease; autoimmune disease; alcohol-induced hepatitis;
 KW inflammation; graft versus host pathology; cancer; tumour;
 KW cerebral malaria; multiple sclerosis; diagnosis; therapy.
 XX
 OS Mus musculus.
 XX
 PH Key Location/Qualifiers
 FT Peptide 1..29
 FT /note= "signal peptide"
 FT Protein 30..150
 FT /note= "mature protein"
 FT Domain 34..72
 FT /note= "cysteine-rich domain"
 FT Domain 75..114
 FT /note= "cysteine-rich domain"
 XX
 PN W09937818-A1.
 XX
 PD 29-JUL-1999.
 XX
 PF 27-JAN-1999; 99WO-US01679.
 XX
 PR 27-JAN-1998; 98US-0014195.
 XX
 PA (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
 XX
 PI Busfield SJ;

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 16, 2001, 21:05:27 ; Search time 20.9 seconds
(without alignments)
363.437 Million cell updates/sec

Title: US-09-380-276A-8

Perfect score: 2283

Sequence: 1 MALKVLLLEQKFTFTLLVLL.....AIHPATQTSQVQRRLGSL 423

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 174772 seqs, 17957048 residues

Total number of hits satisfying chosen parameters: 174772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued_Patents_AA.*

1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep.*

2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*

3: /cgn2_6/ptodata/2/iaa/6_COMB.pep.*

4: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep.*

5: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	159	7.0	438	1	US-08-097-827-11
2	159	7.0	438	1	US-08-494-574-11
3	150	6.6	206	1	US-08-097-827-7
4	150	6.6	206	1	US-08-494-574-7
5	145	6.4	205	3	US-08-974-022-51
6	144	6.3	1104	2	US-08-327-832-5
7	144	6.3	1104	2	US-08-828-584-5
8	136	6.0	625	3	US-08-996-139-15
9	134	5.9	186	1	US-08-089-458B-6
10	133.5	5.8	2050	2	US-08-347-594A-2
11	132.5	5.8	197	2	US-08-505-606-1
12	131	5.7	139	2	US-08-219-237B-8
13	129	5.7	326	1	US-08-292-549-4
14	129	5.7	326	1	PCT-US91-02207-4
15	128.5	5.6	1170	1	US-08-313-288B-20
16	128	5.6	355	1	US-08-292-549-6
17	124.5	5.5	1111	3	US-08-317-450B-15
18	124.5	5.5	1111	3	US-08-800-593-15
19	124.5	5.5	1193	1	US-08-317-450B-13
20	124.5	5.5	1193	3	US-08-800-593-13
21	124.5	5.5	2813	3	US-08-896-449A-2
22	124.5	5.5	2813	3	US-09-132-652-2
23	123.5	5.4	1171	1	US-08-445-135-1
24	123.5	5.4	3075	2	US-08-460-309-5
25	123.5	5.4	3075	2	US-08-125-077-5
26	121.5	5.3	311	3	US-08-911-423-8
27	120	5.3	256	1	US-08-236-918A-6
28	120	5.3	256	4	PCT-US96-03965-2

29 117.5 5.1 1251 4 PCT-US95-02251-3 Sequence 3, Appli
30 117.5 5.1 1252 1 US-08-199-780-3 Sequence 3, Appli
31 117.5 5.1 1252 2 US-08-316-650-3 Sequence 3, Appli
32 117 5.1 255 1 US-08-236-918A-8 Sequence 8, Appli
33 117 5.1 255 2 US-08-816-605-9 Sequence 9, Appli
34 117 5.1 255 4 PCT-US96-03965-8 Sequence 8, Appli
35 116 5.1 417 3 US-08-815-469-2 Sequence 2, Appli
36 116 5.1 428 3 US-08-882-046-7 Sequence 7, Appli
37 116 5.1 1010 2 US-08-400-159-6 Sequence 6, Appli
38 116 5.1 1218 3 US-08-611-729A-6 Sequence 6, Appli
39 116 5.1 1218 3 US-08-882-046-2 Sequence 2, Appli
40 114.5 5.0 1253 3 US-08-479-722B-4 Sequence 4, Appli
41 114 5.0 280 3 US-08-974-022-46 Sequence 46, Appli
42 114 5.0 455 1 US-08-050-319B-25 Sequence 25, Appli
43 114 5.0 455 1 US-08-321-668-2 Sequence 2, Appli
44 114 5.0 455 1 US-08-837-941-2 Sequence 2, Appli
45 114 5.0 455 1 US-08-837-941-2

ALIGNMENTS

RESULT 1

US-08-097-827-11

; Sequence 11, Application US/08097827

; Patent No. 5457035

; GENERAL INFORMATION:

; APPLICANT: Baum, Peter

; APPLICANT: Goodwin, Ray

; APPLICANT: Fanslow, William

; APPLICANT: Gayle, Richard

; TITLE OF INVENTION: No. 5457035el Cytokine Which is a Ligand for

; TITLE OF INVENTION: OX40

; NUMBER OF SEQUENCES: 13

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Immunex Corporation

; STREET: 51 University Street

; CITY: Seattle

; STATE: WA

; COUNTRY: USA

; ZIP: 98101

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION NUMBER: US/08/097,827

; FILING DATE:

; CLASSIFICATION: 536

; ATTORNEY/AGENT INFORMATION:

; NAME: Perkins, Patricia A.

; REGISTRATION NUMBER: 34,693

; REFERENCE/DOCKET NUMBER: 2806

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 206-587-0730

; INFORMATION FOR SEQ ID NO: 11:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 438 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-097-827-11

Query Match

Best Local Similarity 7.0%; Score 159; DB 1; Length 438;

Matches 69; Conservative 31; Mismatches 93; Indels 58; Gaps 18;

QY 15 TLLVLLGVLSCVKTCTGCRQCFEDRSNG-CVPCNCGPGMELSKCEGFGYGEDAQCV 73

DB 9 TALLLLG-LTLGVTLRLNLCVKHTY--PSGHKC--CRCQPGHGMVNR--DHTRTLLCH 61

QY 74 TCRHFRKEDWGFKCKPCLDCAVAVNRFO-KANCSATSDAICGDCPLPGFYRKTKLVGFQD 132
 Db 62 PCETGFYNEAVNYDTCKQCTQCNRHSGSELKQNCPTPTQDTVC-RCRPGTQPR-----QD 114
 QY 133 -----MECVPCGDDPPPPYEP-----HCASKVNLVKIATASSPRDTALAIVIC---SALA 179
 Db 115 SGYKLGWDCVPC--PPGHFSPGNQACKPWTNCTLSGKQTRHPASDSDLAV-CEDRSLLA 171
 QY 180 TVLLALLILCVYCKRQFMEKKPSW---SLRSODIQVNGSELSCLDROPQLHEYAHRACCO 236
 Db 172 TLL-----WETQRTFRPTTVOSTVMPRTSELP--STPTLVE--PRSC-- 211
 QY 237 CRRDSVQTCGP 247
 Db 212 ---DKTHTCPP 219

RESULT 2
 US-08-494-574-11
 ; Sequence 11, Application US/08494574
 ; Patent No. 5783665
 ; GENERAL INFORMATION:
 ; APPLICANT: Baum, Peter
 ; APPLICANT: Goodwin, Ray
 ; APPLICANT: Fanslow, William
 ; APPLICANT: Gayle, Richard
 ; TITLE OF INVENTION: No. 5783665el Cytokine which is a Ligand for
 ; TITLE OF INVENTION: OX40
 ; NUMBER OF SEQUENCES: 13
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Immunex Corporation
 ; STREET: 51 University Street
 ; CITY: Seattle
 ; STATE: WA
 ; COUNTRY: USA
 ; ZIP: 98101
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; FILING DATE: 22-JUN-1995
 ; APPLICATION NUMBER: US/08/494,574
 ; CLASSIFICATION: 530
 ; PRIOR APPLICATION NUMBER: US/08/097,827
 ; FILING DATE: 23-JUL-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Perkins, Patricia A.
 ; REGISTRATION NUMBER: 34,693
 ; REFERENCE/DOCKET NUMBER: 2806
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 206-587-0730
 ; INFORMATION FOR SEQ ID NO: 11:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 438 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-494-574-11

Query Match 7.0%; Score 159; DB 1; Length 438;
 Best Local Similarity 27.5%; Pred. No. 8.2e-07;
 Matches 69; Conservative 31; Mismatches 93; Indels 58; Gaps 18;
 QY 15 TLVLVLLGYLSCKVTCETGDCRQEFRRDRSGN-CVPCNOCGPGMELSKCEGFGYGEDAQCV 73
 Db 9 TALLLLG-LTLGVYARLNCVKHTY--PSGKHC--CRECQPGHGMVNRG--DHTRTDLCH 61
 QY 74 TCRHFRKEDWGFKCKPCLDCAVAVNRFO-KANCSATSDAICGDCPLPGFYRKTKLVGFQD 132

Db 62 PCETGFYNEAVNYDTCKQCTQCNRHSGSELKQNCPTPTQDTVC-RCRPGTQPR-----QD 114
 QY 133 -----MECVPCGDDPPPPYEP-----HCASKVNLVKIATASSPRDTALAIVIC---SALA 179
 Db 115 SGYKLGWDCVPC--PPGHFSPGNQACKPWTNCTLSGKQTRHPASDSDLAV-CEDRSLLA 171
 QY 180 TVLLALLILCVYCKRQFMEKKPSW---SLRSODIQVNGSELSCLDROPQLHEYAHRACCO 236
 Db 172 TLL-----WETQRTFRPTTVOSTVMPRTSELP--STPTLVE--PRSC-- 211
 QY 237 CRRDSVQTCGP 247
 Db 212 ---DKTHTCPP 219

RESULT 3
 US-08-097-827-7
 ; Sequence 7, Application US/08097827
 ; Patent No. 5457035
 ; GENERAL INFORMATION:
 ; APPLICANT: Baum, Peter
 ; APPLICANT: Goodwin, Ray
 ; APPLICANT: Fanslow, William
 ; APPLICANT: Gayle, Richard
 ; TITLE OF INVENTION: No. 5457035el Cytokine which is a Ligand for
 ; TITLE OF INVENTION: OX40
 ; NUMBER OF SEQUENCES: 13
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Immunex Corporation
 ; STREET: 51 University Street
 ; CITY: Seattle
 ; STATE: WA
 ; COUNTRY: USA
 ; ZIP: 98101
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; FILING DATE: US/08/097,827
 ; CLASSIFICATION: 536
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Perkins, Patricia A.
 ; REGISTRATION NUMBER: 34,693
 ; REFERENCE/DOCKET NUMBER: 2806
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 206-587-0730
 ; INFORMATION FOR SEQ ID NO: 7:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 206 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-097-827-7

Query Match 6.6%; Score 150; DB 1; Length 206;
 Best Local Similarity 30.1%; Pred. No. 2e-06;
 Matches 55; Conservative 21; Mismatches 75; Indels 32; Gaps 13;

QY 15 TLVLVLLGYLSCKVTCETGDCRQEFRRDRSGN-CVPCNOCGPGMELSKCEGFGYGEDAQCV 73
 Db 9 TALLLLG-LTLGVYARLNCVKHTY--PSGKHC--CRECQPGHGMVNRG--DHTRTDLCH 61
 QY 74 TCRHFRKEDWGFKCKPCLDCAVAVNRFO-KANCSATSDAICGDCPLPGFYRKTKLVGFQD 132
 Db 62 PCETGFYNEAVNYDTCKQCTQCNRHSGSELKQNCPTPTQDTVC-RCRPGTQPR-----QD 114
 QY 133 -----MECVPCGDDPPPPYEP-----HCASKVNLVKIATASSPRDTALAIVIC---SALA 179
 Db 115 SGYKLGWDCVPC--PPGHFSPGNQACKPWTNCTLSGKQTRHPASDSDLAV-CEDRSLLA 171

;; TITLE OF INVENTION: Retroviral Expression Constructs Thereof

;; NUMBER OF SEQUENCES: 16

;; CORRESPONDENCE ADDRESS:

;; ADDRESSEE: Banner, Birch, McKie & Beckett

;; STREET: 1001 G Street, N.W.

;; CITY: Washington, D.C.

;; STATE: District of Columbia

;; COUNTRY: U.S.A.

;; ZIP: 20001

;; COMPUTER READABLE FORM:

;; MEDIUM TYPE: Floppy disk

;; COMPUTER: IBM PC compatible

;; OPERATING SYSTEM: PC-DOS/MS-DOS

;; SOFTWARE: Patent In Release #1.0, Version #1.25

;; CURRENT APPLICATION DATA:

;; APPLICATION NUMBER: US/08/327,832

;; FILING DATE:

;; CLASSIFICATION: 530

;; ATTORNEY/AGENT INFORMATION:

;; NAME: Posorske, Laurence H.

;; REGISTRATION NUMBER: 34,698

;; REFERENCE/DOCKET NUMBER: 1107.46362

;; TELECOMMUNICATION INFORMATION:

;; TELEPHONE: 20-2 508-9153

;; TELEFAX: 202 508-9299

;; INFORMATION FOR SEQ ID NO: 5:

;; SEQUENCE CHARACTERISTICS:

;; LENGTH: 1104 amino acids

;; TYPE: amino acid

;; TOPOLOGY: linear

;; MOLECULE TYPE: protein

;; US-08-327-832-5

Query Match 6.3%; Score 144; DB 2; Length 1104;

Best Local Similarity 18.8%; Pred. No. 7.4e-05;

Matches 110; Conservative 59; Mismatches 181; Indels 236; Gaps 27;

```
QY 24 SKVTCETGDCRQEFDRSGNVCPCNOCGPGMELSKGCG-----FCYGEDAQC-----72
DB 440 SCNLLCHPG-----PCPPCPAFMTKCEGRTHTVRCQAVSVHCSNPC 484
QY 73 ---VTCRLHREKEDWGQKCKPCLDCAVNRRQKANCATS-DAICGDCPLPGFYRKTCLV 128
DB 485 ENILNCGQHCAELCHGGCQPCQ--IILN--QVCYCGSTSRDLVCGTDV-----GKSD 534
QY 129 GFQDMEC-----VPCGD-----PPP-----PYEPHC--ASKVNLVKIASTASS 164
DB 535 GFGDFSLCTGCKDLKCGNHTCSQVCHPQCCQCPRLPOLVRCPCGQTPLSQLELGS 594
QY 165 PRDTALAAV-----IC-SALATVLLALLILC-----VIYCKRQFMKK- 201
DB 595 SRKTCMDPVPSCGKVCCKPLPGSLDFIHTCEKLCHEGDCGVPVSRVTSVSCRSFRTKEL 654
QY 202 PWSLRSQDI-----QYNGSELSCLDRPQ-----LH-----EYA 230
DB 655 PCTSLKSEDATEMCDKRCNKRKLCGRHKNCICCVDKHKPLNCGRLKRLCGLHRCCEPC 714
QY 231 HRACCO-CRRDSVQT-----CGPVRLLPMSCC-----EE 258
DB 715 HRGNCQTQWASFDLTCCHGASVIYPPVPCGTRPPECTQTCAVHECDHPVYHSHSEE 774
QY 259 ACS-----PNPATLGGCVHSAASI-----277
DB 775 KCPPTFTLTQKCMGKHEFRSNIPCHLVDSGLPFSATLPCGMHKCQRLCHKGLVD 834
QY 278 -----QAR-----NAGPAGEMYPTFFGSLTQSI 300
DB 835 PCKQPCTTPRADCGHPCMAPCHTSSPCVPTACKAKVELQCEGRRKEMVICSEASTYQR 894
QY 301 CGEFSDAWPLMQNPGDDNISCDSPYELTGEDIHSLNPELESSTLSDNSQDLYGGAV 360
DB 895 IAAISMASKITDQMLGGS-----VEISKLTITKKEVHOARLECEDECSALERKKR--LAEEF 948
```

QY 361 PVQSHSENFATAATDLRSYNNITLVESASTQDALTMRSQLDQSGAIL 406

DB 949 HISESDPENIRSSSGSKFSDSLKEDA--RKDLKFVSDVEKEMETLV 992

RESULT 7

US-08-828-584-5

;; Sequence 5, Application US/08828584

;; Patent No. 5908762

;; GENERAL INFORMATION:

;; APPLICANT: Ono, Santa J.

;; APPLICANT: Strominger, Jack L.

;; TITLE OF INVENTION: Transcription Factor Regulating MHC

;; TITLE OF INVENTION: Expression, cDNA and Genomic Clones Encoding Same and

;; TITLE OF INVENTION: Retroviral Expression Constructs Thereof

;; NUMBER OF SEQUENCES: 16

;; CORRESPONDENCE ADDRESS:

;; ADDRESSEE: Banner, Birch, McKie & Beckett

;; STREET: 1001 G Street, N.W.

;; CITY: Washington, D.C.

;; STATE: District of Columbia

;; COUNTRY: U.S.A.

;; ZIP: 20001

;; COMPUTER READABLE FORM:

;; MEDIUM TYPE: Floppy disk

;; COMPUTER: IBM PC compatible

;; OPERATING SYSTEM: PC-DOS/MS-DOS

;; SOFTWARE: Patent In Release #1.0, Version #1.25

;; CURRENT APPLICATION DATA:

;; APPLICATION NUMBER: US/08/828,584

;; FILING DATE:

;; CLASSIFICATION: 435

;; ATTORNEY/AGENT INFORMATION:

;; NAME: Posorske, Laurence H.

;; REGISTRATION NUMBER: 34,698

;; REFERENCE/DOCKET NUMBER: 1107.46362

;; TELECOMMUNICATION INFORMATION:

;; TELEPHONE: 20-2 508-9153

;; TELEFAX: 202 508-9299

;; INFORMATION FOR SEQ ID NO: 5:

;; SEQUENCE CHARACTERISTICS:

;; LENGTH: 1104 amino acids

;; TYPE: amino acid

;; TOPOLOGY: linear

;; MOLECULE TYPE: protein

;; US-08-828-584-5

Query Match 6.3%; Score 144; DB 2; Length 1104;

Best Local Similarity 18.8%; Pred. No. 7.4e-05;

Matches 110; Conservative 59; Mismatches 181; Indels 236; Gaps 27;

QY 24 SKVTCETGDCRQEFDRSGNVCPCNOCGPGMELSKGCG-----FCYGEDAQC-----72

DB 440 SCNLLCHPG-----PCPPCPAFMTKCEGRTHTVRCQAVSVHCSNPC 484

QY 73 ---VTCRLHREKEDWGQKCKPCLDCAVNRRQKANCATS-DAICGDCPLPGFYRKTCLV 128

DB 485 ENILNCGQHCAELCHGGCQPCQ--IILN--QVCYCGSTSRDLVCGTDV-----GKSD 534

QY 129 GFQDMEC-----VPCGD-----PPP-----PYEPHC--ASKVNLVKIASTASS 164

DB 535 GFGDFSLCTGCKDLKCGNHTCSQVCHPQCCQCPRLPOLVRCPCGQTPLSQLELGS 594

QY 165 PRDTALAAV-----IC-SALATVLLALLILC-----VIYCKRQFMKK- 201

DB 595 SRKTCMDPVPSCGKVCCKPLPGSLDFIHTCEKLCHEGDCGVPVSRVTSVSCRSFRTKEL 654

QY 202 PWSLRSQDI-----QYNGSELSCLDRPQ-----LH-----EYA 230

DB 655 PCTSLKSEDATEMCDKRCNKRKLCGRHKNCICCVDKHKPLNCGRLKRLCGLHRCCEPC 714

[illegible]

Query Match 6.0%; Score 136; DB 3; Length 625;

```
Best Local Similarity   22.28; Pred. No. 0.00019;
Matches 102; Conservative      51; Mismatches 171; Indels 136; Gaps 27;

QY    16  LLVLGLVLSCKVTCE-TGDCRQBEFRDRSGNCVPCNQCQGSMELSKCGFGYGEDAQOCT 74
       ||| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db    18  LCVLL--VPLQVTLQVTPCPTQERHYEHLGR-CSRCEPGKYLSSKC--TPTSDSVCCLP 71
       : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :

QY    75  CRLHRFKEDWGQ-KC---KPC-LDCAVV-----NRFOKANC SAT-----SDAIC---- 114
       : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db    72  CGPDEYLDTNNEEDKCLLHKVCDAGKALVAVDPGNHHTAPRRCACTAGYHWNSDCCCCRNN 131
       : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :

QY    115 GDCLPGFYRKTKLVGFQDMECVPC-----GDPPPY-----EPH----- 148
       : | | | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db    132 TECAPGGGAQHPLQNKDTVTCPLLGGFFSDVFSTDKCKPMTNCTLLGKLEAHOGTTES 191
       : | | | : | : | : | : | : | : | : | : | : | : | : | : | : | :

QY    149 --CASKNLVKIASTASSPRDTAAAVICSALATVLLALLILCIYICKROFMEKKPSWS 205
       : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db    192 DVCSSSMTLRBPKEAQAYLP SLI--VLLLFISVVVAAIFGVYKKGKALTANLWN 249
       : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :

QY    206 -LRSODIQYNSELSCLDRPOLHEYAHACC---OCRRDSVOTCGPVRLFLPMSCCEEACS 261
       : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db    250 WNDACSSLGNKKESSGDR-----CAGSHSATSQQEVCEGILL---MTR EKMV 296
       : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :

QY    262 PNPATLGGCVHSAS-----LQARNAGAGEWVP-----FTGS 295
       : | | | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db    297 PEDGAGVGCPYCAAGGPWAERYDRSRTFTLVSEVETQGBLSRKIPTDEYTD RPSQPSTGS 356
       : | | | : | : | : | : | : | : | : | : | : | : | : | : | : | :

QY    296 LTQSTCGFSDAWPLMQNPM---GGDNISFC-----DSYP ELT 330
       : | | | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db    357 LL--LIQGSKSIPFPQPLEVGENDSLSQCTGTTESTVDSGCDFT EPPSR TDSMP--V 412
       : | | | : | : | : | : | : | : | : | : | : | : | : | : | : | :

QY    331 GEDIHSLNPELESSTSL-----DSNSSQLVG-GAVPVQSH 365
       : | | | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db    413 SPEKH-LTFKETEGDSLCPWWVSSNSTDGYTGSGNT PGEDH 451
       : | | | : | : | : | : | : | : | : | : | : | : | : | : | : | :


RESULT          9
US-08-089-458B-6
; Sequence 6, Application US/08089458B
; Patent No. 5359039
; GENERAL INFORMATION:
; APPLICANT: Smith, Craig
; APPLICANT: Goodwin, Raymond
; TITLE OF INVENTION: Isolated Poxvirus A53R-Equivalent Tumor
; TITLE OF INVENTION: Necrosis Factor Antagonists
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patricia Anne Perkins, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: U.S.A.
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple Operating System 7.1
; SOFTWARE: Microsoft Word, Version #5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/089,458B
; FILING DATE: 07/09/93
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia A.
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2608
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; TELEX: 756822
; INFORMATION FOR SEQ ID NO.: 6:
;     SEQUENCE CHARACTERISTICS:
;         LENGTH: 186 amino acids
```


QY VVNRFQ-KANCSATSDATCGDCLPGFYRKTKLVGFQDMECVPCGDPFPPFYP-----HCAS 151

RESULT 14
PCT-US91-02207-4
Sequence 4, Application PC/TUS9102207
GENERAL INFORMATION:
APPLICANT: Smith, Craig A.
APPLICANT: Goodwin, Raymond G.
TITLE OF INVENTION: Isolated Viral Protein Cytokine Antagonists
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/02207
FILING DATE: 19910329
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Wight, Christopher L.
REGISTRATION NUMBER: 31,680
REFERENCE/DOCKET NUMBER: 2602
TELEPHONE: (206) 587-0430
TELEFAX: (206) 587-0606
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 326 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US91-02207-4

Query Match 5.7%; Score 129; DB 4; Length 326;
Best Local Similarity 24.1%; Pred. No. 0.00034;
Matches 49; Conservative 20; Mismatches 82; Indels 52; Gaps 12;
QY 14 FTLLVLLGLYLC-----KVTCTGDCRQOEFRDRSGNCVPCNQCGPMELSKCEGFGY 67
DB 2 FRULLLAVACVYGGAGYAGDRGKCRGNDY-EKDGLC--CTSCPPGYSASRLC--GPG 56
QY 68 EDACQVTCRLHREKEDWGF-QKCKPCLDCAVAVNRFOKANCATSATSDAICGDCLPGFY----122
DB 57 SDTVCSPCRNKTFTASTNHAPACVSCRGCTGHLSESQSCDKTRDVC-DCSAGNYCLLK 115
QY 123 -----RKTKL-VGF-----QDMECVPCGDDPPPY-----EPHCASKVNLY 156
DB 116 GQEGRCICAPKTKCPAGYVSGHTRGDVLCTKC-----PRYTVSDAVSSSTETCTSSFNVI 171
QY 157 KIASTASSPRDTALAIVCSALA 179
DB 172 SVEFNLYPVNDTS-----CTTTA 189

RESULT 15
US-08-313-288B-20
Sequence 20, Application US/08313288B
Patent No. 5750502
GENERAL INFORMATION:
APPLICANT: Jessell, Thomas M. and Avi Hu Klar
TITLE OF INVENTION: CLONING, EXPRESSION AND USES OF A
TITLE OF INVENTION: NOVEL SECRETED PROTEIN, F-SPONDIN
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas

CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/313,288B
FILING DATE: January 5, 1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 40028-A-PCT-US
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0526
TELEX:
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 1170 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-313-288B-20

Query Match 5.6%; Score 128.5; DB 1; Length 1170;
Best Local Similarity 21.1%; Pred. No. 0.0022;
Matches 87; Conservative 40; Mismatches 147; Indels 139; Gaps 24;
QY 26 KVTCTGDCRQOEFRDRSGNCVPCNQCGP-----MELSKCEGFGY-----66
DB 350 KVSCTPIMPCSNATVPD--GEC--CPRCWPDSADGWSWPSEWTSCTSCGNGIQGRKS 405
QY 67 -----GEDACQVTCRLH-----RFKEDWGFQCKPCLDCA-----VAVNRFOKANC 107
DB 406 CDSLNNRCEGSSVQTRTCHIQCCKRQDGGWSHSPSSCSVTGCGDVITRIL--CN 463
QY 108 ATSDAICGDCPLPGFYRKTLLV-----GF-----QDMECVPCG-----DPP 142
DB 464 SPSPQWNGKPCGEARETRKACKKDACPINGGWPSPWDICSVTCGGGVQKRSRLCINNPT 523
QY 143 PPY-EPHCASKVNLYKIASTASSPRDTALAIVCSALATVLLALLILCVYCKRQPMKK 201
DB 524 PQFGGKDCVGDVTENQICNKQDCPIDGCLSNPCFAG-----VKCTSY-----PD 567
QY 202 PSWSLRSDIQYNGSELSCLDRLPQ-----HEYAIRA-----CCQCRDVSQVT 244
DB 568 GSKKACGPPYSGNGIQCTVDDECKEVPDCAFNHNGHRCENTDPGYNCLPC-----620
QY 245 CGPVRLLPSM-----CCEACSP-NPATLG--CGVISAASLOARNAGP--AGEM 288
DB 621 --PPRTGSGQPGQGVHEHATANKQVCKPRNPTDGHDKNAKKNLYLGHYSOPMYRCEC 678
QY 289 VPTFFGSLTQSTICGEFS--DAMPLMNPMGGDNISF-----CDSYPELTGD 333
DB 679 KPGYAGN--GIICGEDTDLGGWP--NENLVANATYHCKKDKNCNPLNSGQED 728

Search completed: February 16, 2001, 21:05:30
Job time: 150 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 16, 2001, 21:06:39 ; Search time 31.47 Seconds
(without alignments)
912.678 Million cell updates/sec

Title: US-09-380-276a-8
Perfect score: 2283
Sequence: 1 MALKVLEQEKTFFTLLVLL.....AIHPATQTSLOVQRQLGSL 423

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 195891 seqs, 67900655 residues

Total number of hits satisfying chosen parameters: 195891

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	157	6.9	454	1 QOMST1	tumor necrosis fac
2	157	6.9	454	2 I57826	tumor necrosis fac
3	147	6.4	416	1 JN0006	nerve growth facto
4	147	6.4	1797	2 A55677	laminin beta-2 cha
5	146.5	6.4	1801	1 MMRIS	laminin beta-2 cha
6	145.5	6.4	435	2 I54182	tumor necrosis fac
7	145	6.4	271	2 S12783	OX40 antigen precu
8	144	6.3	272	2 I48700	gene ox40 protein
9	144	6.3	1104	2 I38869	transcription fact
10	141.5	6.2	461	1 GQRT11	tumor necrosis fac
11	140	6.1	425	1 A26431	nerve growth facto
12	134	5.9	1786	1 MMSB1	laminin beta-1 cha
13	133.5	5.8	2813	1 VWHU	von Willebrand fac
14	132.5	5.8	1170	2 A40558	thrombospondin 1 p
15	132	5.8	277	2 A60771	B-cell activation
16	130	5.7	1798	2 S33869	laminin beta-2 cha
17	129	5.7	326	1 GQVZML	t2 protein - myxom
18	128.5	5.6	1170	1 TSHUP1	thrombospondin 1 p
19	127	5.6	1650	2 S53457	dominant autoantig
20	127	5.6	1827	2 T34288	hypothetical prote
21	127	5.6	4660	2 T42737	gp330 protein prec
22	125.5	5.5	1548	2 S34583	serine proteinase
23	124.5	5.5	1111	2 B44018	laminin B2t chain
24	124.5	5.5	1193	2 A44018	laminin B2t chain
25	124.5	5.5	3712	2 S18253	laminin alpha-1 ch
26	124	5.4	349	2 D72175	G2R protein - vari
27	123	5.4	837	2 S43656	furin (EC 3.4.21.7
28	122.5	5.4	1680	2 A43434	furin (EC 3.4.21.7
29	122	5.3	1299	2 T43251	furin (EC 3.4.21.7

ALIGNMENTS

RESULT 1

QOMST1

tumor necrosis factor receptor 1 precursor - mouse
N:Alternate names: tumor necrosis factor receptor, 55K
C:Species: Mus musculus (house mouse)
C:Date: 30-Jun-1992 #sequence.revision 30-Jun-1992 #text_change 22-Jun-1999
C:Accession: A38634; B40254; S16677; S19021; I54532
R:Lewis, M.; Tartaglia, L.A.; Lee, A.; Bennett, G.L.; Rice, G.C.; Wong, G.H.W.; Chen, Proc. Natl. Acad. Sci. U.S.A. 88, 2830-2834, 1991
A:Title: Cloning and expression of cDNAs for two distinct murine tumor necrosis facto
A:Reference number: A38634; MUID:91187885
A:Accession: A38634
A:Molecule type: mRNA
A:Residues: 1-454 <LEW>
A:Cross-references: GB:M60468; NID:g199825; PIDN:AAA39751.1; PID:g199826
R:Goodwin, R.G.; Anderson, D.; Jerzy, R.; Davis, T.; Brannan, C.I.; Copeland, N.G.; J Mol. Cell. Biol. 11, 3020-3026, 1991
A:Title: Molecular cloning and expression of the type 1 and type 2 murine receptors f
A:Reference number: A40254; MUID:91246168
A:Accession: B40254
A:Molecule type: mRNA
A:Residues: 1-454 <G02>
A:Cross-references: GB:M60468; NID:g199825; PIDN:AAA39751.1; PID:g199826
R:Barrett, K.; Taylor-Fishwick, D.A.; Cope, A.P.; Kissoneghis, A.M.; Gray, P.W.; Fel Eur. J. Immunol. 21, 1649-1656, 1991
A:Title: Cloning, expression and cross-linking analysis of the murine p55 tumor necro
A:Reference number: S16677; MUID:91285014
A:Accession: S16677
A:Molecule type: mRNA
A:Residues: 1-454 <BAR>
A:Cross-references: EMBL:X59238; NID:g53578; PIDN:CAA41922.1; PID:g53579
R:Rothe, J.G.; Brockhaus, M.; Gentz, R.; Lesslauer, W. Immunogenetics 34, 338-340, 1991
A:Title: Molecular cloning and expression of the mouse Tnf receptor type b.
A:Reference number: S19021; MUID:92039815
A:Accession: S19021
A:Molecule type: mRNA
A:Residues: 1-454 <ROT>
A:Cross-references: EMBL:X57796; NID:g54848; PIDN:CAA40936.1; PID:g54849
R:Bebo, B.F. Immunogenetics 39, 450-451, 1994
A:Title: Nucleotide sequence of the TNF type I receptor from a mouse endothelioma cel
A:Reference number: I54532; MUID:94245292
A:Accession: I54532
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-454 <RES>
A:Cross-references: PIDN:AAA59361.1; PID:g430733
C:Comment: This protein is one of two distantly related receptors for both TNF-alpha
C:Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology
C:Keywords: duplication; glycoprotein; receptor; transmembrane protein
F:1-29/Domain: signal sequence #status predicted <SIG>

gene G4R protein -
laminin gamma 2 ch
notch4 - mouse
membrane glycoprot
hypothetical prote
t-cell antigen 4-1
hypothetical prote
laminin beta-1 cha
VLDL receptor prec
latent transformin
laminin alpha-1 ch
4-1BB - human
lymphocyte activat
gene shuttle craft
laminin beta-1 cha
hypothetical prote

F:30-454/Product: tumor necrosis factor receptor type 1 #status predicted <M>
F:30-212/Domain: extracellular #status predicted <EXT>
F:44-82/Domain: NGF receptor repeat homology <NG1>
F:84-126/Domain: NGF receptor repeat homology <NG2>
F:127-167/Domain: NGF receptor repeat homology <NG3>
F:168-204/Domain: NGF receptor repeat homology <NG4>
F:213-235/Domain: transmembrane #status predicted <MEM>
F:236-454/Domain: intracellular #status predicted <INT>
F:54,151,202/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 6.9%; Score 157; DB 1; Length 454;
Best Local Similarity 21.0%; Pred. No. 0.00021;
Matches 76; Conservative 42; Mismatches 140; Indels 104; Gaps 19;

QY 34 CROQEFDRSGNVCNQCPCGPHGELSKGCGFGYGEAQCVCYTCRLHRFKEDWGF-QKCKPC 92
DB 44 CPQGVHSHKNNISCTCKHKGTYLVSDCP-SPGRDTCRECEKGTFTTASQNYLROCLSC 102
QY 93 LDC-AVYNRFQKANCATSDAICG-----DCLPGFYRKTKL----- 127
DB 103 KTCRKEMSQVEISPCQADKDTVCCKENQFORYLSETHFQCVCDFCFNGTVPICKETQ 162
QY 128 -----VGF--QDMBCVPCGDPPIYPPEHCASKVNLVRIA-----STASSPRDTALAAV 173
DB 163 NTVCNCHAGFFLRESECVPCS-----HCKKNEECMKLCLPPPLANVTNPQDSGTAVL 214
QY 174 ICSALATVLLALLILCVYCKRQFMKKPSWLSRSODIQYNGSELSCLDPRPOLHEVAHRA 233
DB 215 L-----PLVILLGLLLSFIET--SLMCRYPW-----RPEVYSII--- 248
QY 234 CCOCRRDSV---OTCG-PVRLPLSMCCBEACSPNPATLGGCVHSAASLQARN----- 281
DB 249 ---C-RDPVPVKEEAKGKPLTPAPSPAFSTSGFNP-TLGFSTPGFSSPVSTPISPIFG 303
QY 282 -----AGPAGEMVPTFFGS--LTQSIG-----EFSDAWPLMNPNGGDNISFCDSYPPEL 329
DB 304 PSNWHFMPVSEVVPVTPQAGDPLLYSLCSVPAPTSVQKWEDSAHPQRPDNLAILYAVV 363
QY 330 TG 331
DB 364 DG 365

RESULT 2
I57826
tumor necrosis factor receptor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 23-Jul-1999
C:Accession: I57826
R:Rothe, J.G.; Bluethmann, H.; Gentz, R.; Lesslauer, W.; Steinmetz, M.
Mol. Immunol. 30, 165-176, 1993
A:Title: Genomic organization and promoter function of the murine tumor necrosis factor
A:Reference number: I57826; MUID:93156721
A:Status: preliminary
A:Molecule type: DNA
A:Cross-references: GB:M76656; NID:9202100; PIDN:AAA40465.1; PID:9202102
C:Gene: TNFR-2
A:Introns: 13/3; 65/1; 108/1; 158/1; 184/2; 210/1; 248/1; 257/3; 353/1
C:Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology
C:Keywords: cytokine receptor
F:44-82/Domain: NGF receptor repeat homology <NGF>

Query Match 6.9%; Score 157; DB 2; Length 454;
Best Local Similarity 21.0%; Pred. No. 0.00021;
Matches 76; Conservative 42; Mismatches 140; Indels 104; Gaps 19;

QY 34 CROQEFDRSGNVCNQCPCGPHGELSKGCGFGYGEAQCVCYTCRLHRFKEDWGF-QKCKPC 92
DB 44 CPQGVHSHKNNISCTCKHKGTYLVSDCP-SPGRDTCRECEKGTFTTASQNYLROCLSC 102
QY 93 LDC-AVYNRFQKANCATSDAICG-----DCLPGFYRKTKL----- 127
DB 103 KTCRKEMSQVEISPCQADKDTVCCKENQFORYLSETHFQCVCDFCFNGTVPICKETQ 162
QY 128 -----VGF--QDMBCVPCGDPPIYPPEHCASKVNLVRIA-----STASSPRDTALAAV 173
DB 163 NTVCNCHAGFFLRESECVPCS-----HCKKNEECMKLCLPPPLANVTNPQDSGTAVL 214
QY 174 ICSALATVLLALLILCVYCKRQFMKKPSWLSRSODIQYNGSELSCLDPRPOLHEVAHRA 233
DB 215 L-----PLVILLGLLLSFIET--SLMCRYPW-----RPEVYSII--- 248
QY 234 CCOCRRDSV---OTCG-PVRLPLSMCCBEACSPNPATLGGCVHSAASLQARN----- 281
DB 249 ---C-RDPVPVKEEAKGKPLTPAPSPAFSTSGFNP-TLGFSTPGFSSPVSTPISPIFG 303
QY 282 -----AGPAGEMVPTFFGS--LTQSIG-----EFSDAWPLMNPNGGDNISFCDSYPPEL 329
DB 304 PSNWHFMPVSEVVPVTPQAGDPLLYSLCSVPAPTSVQKWEDSAHPQRPDNLAILYAVV 363
QY 330 TG 331
DB 364 DG 365

DB 44 CPQGVHSHKNNISCTCKHKGTYLVSDCP-SPGRDTCRECEKGTFTTASQNYLROCLSC 102
QY 93 LDC-AVYNRFQKANCATSDAICG-----DCLPGFYRKTKL----- 127
DB 103 KTCRKEMSQVEISPCQADKDTVCCKENQFORYLSETHFQCVCDFCFNGTVPICKETQ 162
QY 128 -----VGF--QDMBCVPCGDPPIYPPEHCASKVNLVRIA-----STASSPRDTALAAV 173
DB 163 NTVCNCHAGFFLRESECVPCS-----HCKKNEECMKLCLPPPLANVTNPQDSGTAVL 214
QY 174 ICSALATVLLALLILCVYCKRQFMKKPSWLSRSODIQYNGSELSCLDPRPOLHEVAHRA 233
DB 215 L-----PLVILLGLLLSFIET--SLMCRYPW-----RPEVYSII--- 248
QY 234 CCOCRRDSV---OTCG-PVRLPLSMCCBEACSPNPATLGGCVHSAASLQARN----- 281
DB 249 ---C-RDPVPVKEEAKGKPLTPAPSPAFSTSGFNP-TLGFSTPGFSSPVSTPISPIFG 303
QY 282 -----AGPAGEMVPTFFGS--LTQSIG-----EFSDAWPLMNPNGGDNISFCDSYPPEL 329
DB 304 PSNWHFMPVSEVVPVTPQAGDPLLYSLCSVPAPTSVQKWEDSAHPQRPDNLAILYAVV 363
QY 330 TG 331
DB 364 DG 365

RESULT 3
JN0006
nerve growth factor receptor, low affinity precursor - chicken
N:Alternate names: NGF receptor
C:Species: Gallus gallus (chicken)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: JN0006; A60504
R:large, T.H.; Weskamp, G.; Helder, J.C.; Radeke, M.J.; Misko, T.P.; Shooter, E.M.; R
Neuron 2, 1123-1134, 1989
A:Title: Structure and developmental expression of the nerve growth factor receptor 1
A:Reference number: JN0006; MUID:90166579
A:Accession: JN0006
A:Molecule type: mRNA
A:Residues: 1-416 <LAR>
A:Experimental source: embryonic chick brain
R:Heuer, J.G.; Fatemie-Nainie, S.; Wheeler, E.F.; Bothwell, M.
Dev. Biol. 137, 287-304, 1990
A:Title: Structure and developmental expression of the chicken NGF receptor.
A:Reference number: A60504; MUID:90152140
A:Accession: A60504
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 21-35,'Y',37-172,'K',174-275,'S',277-395,'R',397-416 <HEU>
C:Comment: This receptor is found on sensory and sympathetic neurons, on neuroblastom
C:Comment: The cysteine-rich region of the extracellular domain may form part or all
C:Superfamily: nerve growth factor receptor; NGF receptor repeat homology
C:Keywords: duplication; glycoprotein; heterodimer; monomer; phosphoprotein; receptor
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-416/Product: nerve growth factor receptor #status predicted <WAT>
F:21-239/Domain: extracellular #status predicted <EXT>
F:24-57/Domain: NGF receptor repeat homology <NG1>
F:59-100/Domain: NGF receptor repeat homology <NG2>
F:101-139/Domain: NGF receptor repeat homology <NG3>
F:141-181/Domain: NGF receptor repeat homology <NG4>
F:189-237/Region: serine/threonine-rich
F:240-261/Domain: transmembrane #status predicted <MEM>
F:262-416/Domain: intracellular #status predicted <INT>
F:52/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 6.4%; Score 147; DB 1; Length 416;
Best Local Similarity 29.9%; Pred. No. 0.0011;
Matches 56; Conservative 17; Mismatches 82; Indels 32; Gaps 10;
QY 20 LGYLSCKVTCETGD-----CRQEFDRDR-SGNVCNQCPCGPHGELSKGCGFGY-----G 67

```
Db 82 VGLHSMAPCVESDDAVCAKAYGYFQDELGSCKECSIC-----EVGFLMFPCCRDS 133
Qy 68 EDAQCVCRLHREFEDWGFQKCKPCLDCAVV--NRFOKANGSATSDAICGLPCGFYRKT 125
Db 134 QUTCEECPEGTSEANF--VDFCLPTCTICEENVWVKECTASDAECRDLDHPRWTHHT 191
Qy 126 -KLGVFQDMECVPGDPPPPYPHPCASKVNLKIASTASSP---RDTA--LAAAVICSALA 179
Db 192 PSLAGSDSPE--PITRDPFNTFEGMATTIADIVTTVMGSSQPVVSRGTADNLIPVYCSILA 249
Qy 180 TVLIALL 186
Db 250 AVVVGIV 256

RESULT 4
A5677
laminin beta-2 chain precursor (version 1) - human
C:Species: Homo sapiens (man)
C:Date: 03-Mar-1995 #sequence_revision 03-Mar-1995 #text_change 17-Mar-1999
C:Accession: A5677
R:Wewer, U.M.; Gerecke, D.R.; Durkin, M.E.; Kurtz, K.S.; Mattei, M.G.; Champliaud, M.F.;
Genomics 24, 243-252, 1994
A:Title: Human beta2 chain of laminin (formerly S chain): cDNA cloning, chromosomal loca
A:Reference number: A5677; MUID:95213013
A:Accession: A5677
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-1797 <NEW>
A:Cross-references: GB:X79683
C:Genetics:
A:Gene: GDB:LAMB2
A:Cross-references: GDB:L32363; OMIM:150325
A:Map position: 3p21.3-3p21.2
C:Superfamily: laminin beta-1 chain; laminin-type EGF-like homology
C:Keywords: basement membrane; extracellular matrix; glycoprotein; heterotrimer
F:1-32/Domain: signal sequence #status predicted <SIG>
F:33-1797/Product: laminin beta-2 chain #status predicted <MAT>
F:283-344/Domain: laminin-type EGF-like homology <LE01>
F:347-407/Domain: laminin-type EGF-like homology <LE02>
F:410-467/Domain: laminin-type EGF-like homology <LE03>
F:470-519/Domain: laminin-type EGF-like homology <LE04>
F:522-552/Domain: laminin-type EGF-like homology #status atypical <LE05>
F:783-828/Domain: laminin-type EGF-like homology <LE06>
F:831-874/Domain: laminin-type EGF-like homology <LE07>
F:877-924/Domain: laminin-type EGF-like homology <LE08>
F:927-982/Domain: laminin-type EGF-like homology <LE09>
F:985-1034/Domain: laminin-type EGF-like homology <LE10>
F:1037-1091/Domain: laminin-type EGF-like homology <LE11>
F:1094-1139/Domain: laminin-type EGF-like homology <LE12>
F:1142-1186/Domain: laminin-type EGF-like homology <LE13>

Query Match 6.4%; Score 147; DB 2; Length 1797;
Best Local Similarity 22.4%; Pred. No. 0.0053;
Matches 88; Conservative 35; Mismatches 144; Indels 126; Gaps 24;

Qy 17 LVLLGYLSCKVTCETGDCRQOEFRDRSGNCV-----PCNQCGPMELSKCEGFGYV- 67
Db 775 LIYNGALPCQ--CNPQGSLSSECNPHGQCCLCKPGVWGRRCDCAPY-----YGFGP 825

Qy 68 -----EDAQCVCRLHFR-----KEDWGFQKCRKPCCL----- 93
Db 826 TGCQACQCSPRGALLSCLERTSGQL-CRTGAFGLRCDACQRGQNGFFSCRCPCVNGHAD 884
Qy 94 DCVAVNRFOKA--NC-SATSDAICGDCPLFGFYRKTKLGVFQDMECVPCGDDP-PPYEPHC 149
Db 885 EC---NTHTGACLGCRDLTGGEHCERCITAGPHGDRLP--YGAQCRPCPCPEGPGSQRHF 939
Qy 150 ASKVNVLKIASTASSPRTALAAVITCSALATVLLALLILCVIYKRFQME-KKP----- 202
Db 940 AT-----SCHQDEYSQOIVCHCRAGY---TGLRCEACAPGQFGDPSRPGACQLC 985
```

```
Qy 203 --SWSLSQDIQ-----YNGSELSCLE-----DRPOLHEYA-----HRACOCRRDS 241
Db 986 ECSGNIDPMDPADCPHGGQCLRLHHTGEPHCAHSKSGFGHQAARQSCHRCTCNLLGTN 1045
Qy 242 VQTC-----GPVRLPSM--CCBACASN--PATLGGCGVHSAASLQARNAGP- 284
Db 1046 PQQCPSPDQCHCDPSSGQCPLPNVQALAVDRCAPFNWLTSGHGCQPCACLPSEEGPT 1105
Qy 285 ----AGEMVP-TFFGSLTQSGSEFSDAWPLMQ 312
Db 1106 CNEFTGQCHPGAGFGGRTCSQCQLHMGDPGLQ 1138

RESULT 5
MMRTS
laminin beta-2 chain precursor - rat
N:Alternate names: laminin chain B3; S-laminin
C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 10-Dec-1999
C:Accession: S03539
R:Hunter, D.D.; Shah, V.; Merlie, J.P.; Sanes, J.R.
Nature 338, 229-234, 1989
A:Title: A laminin-like adhesive protein concentrated in the synaptic cleft of the ne
A:Reference number: S03539; MUID:89159410
A:Accession: S03539
A:Molecule type: mRNA
A:Residues: 1-1801 <HUN>
A:Cross-references: EMBL:X16563; NID:957250; PIDN:CAA34561.1; PID:957251
C:Complex: Laminins are trimers of an alpha-type, a beta-type, and a gamma-type lamin
C:Function:
A:Description: interact with cells and with other basement membrane proteins to promo
C:Superfamily: laminin beta-1 chain; laminin-type EGF-like homology
C:Keywords: basement membrane; calcium binding; cell binding; coiled coil; extracellu
F:1-35/Domain: signal sequence #status predicted <SIG>
F:36-1801/Product: laminin beta-2 chain #status predicted <MAT>
F:36-285/Domain: VI <DOM6>
F:286-555/Domain: V <DOM5>
F:286-347/Domain: laminin-type EGF-like homology <LE01>
F:350-410/Domain: laminin-type EGF-like homology <LE02>
F:413-470/Domain: laminin-type EGF-like homology <LE03>
F:473-522/Domain: laminin-type EGF-like homology <LE04>
F:525-555/Domain: laminin-type EGF-like homology #status atypical <LE05>
F:556-784/Domain: IV <DOM4>
F:786-831/Domain: laminin-type EGF-like homology <LE06>
F:788-1196/Domain: III <DOM3>
F:834-877/Domain: laminin-type EGF-like homology <LE07>
F:880-927/Domain: laminin-type EGF-like homology <LE08>
F:930-986/Domain: laminin-type EGF-like homology <LE09>
F:989-1038/Domain: laminin-type EGF-like homology <LE10>
F:1041-1095/Domain: laminin-type EGF-like homology <LE11>
F:1098-1143/Domain: laminin-type EGF-like homology <LE12>
F:1146-1190/Domain: laminin-type EGF-like homology <LE13>
F:1197-1412/Domain: II <DOM2>
F:1197-1412/Region: heptad repeats
F:1413-1445/Domain: alpha <ALP>
F:1446-1801/Region: heptad repeats
F:1446-1801/Domain: I <DOM1>
F:45-50/Disulfide bonds: #status predicted
F:251,371,1088,1252,1311,1351,1502/Binding site: carbohydrate (Asn) (covalent) #statu
F:1193,1196,1800/Disulfide bonds: interchain #status predicted

Query Match 6.4%; Score 146.5; DB 1; Length 1801;
Best Local Similarity 22.9%; Pred. No. 0.0057;
Matches 99; Conservative 33; Mismatches 146; Indels 155; Gaps 27;

Qy 17 LVLLGYLSCKVTCETGDCRQOEFRDRSGNCVPCNQCGPMELSKCE-----CFG--- 65
Db 778 LIYNGALPCQ--CDPQGSLSSECNPHGQC-----RCKFGV-VGRRCACATGYGFGPAG 830
Qy 66 -----YGEDAQCVTCRLHFR-----KEDWGFQKCRKPCLDCAVVRNF 101
```

```
Db 831 CQACQSPDQALSGALCEGTSGOCL-CRTGAFGLRCDHCQRGQWGFNCRPC-----VCNG 884
QY 102 QKANCATSDAI-----CGDCLPGFYRKTL-VGFQDMCEVPCGDDP-PPYEPH 148
Db 885 RADECDAGTACGLCRDYTGGEHCERCIAGFDGDLPLPYGGQ---CRPCECPGPGSRH 941
QY 149 CASKVNLVKTASTASSPRDTALAAVTSALATVLLALLLCVYCKRQFME-KKPSWSLR 207
Db 942 FAT-----SCHRDGYSQIVCHCRAGY---TGLRCEACAPGDFGDKSPKGGRCQ 987
QY 208 ----SQDIQ-----YNGSELSCLD-----RPLHEYA-----HRACCQCR 239
Db 988 LCSCSGNIDPTDGACDPHTGQCLRLHHTGPHGCHGKPGFPGHQAAROSCHRCTCNLLG 1047
QY 240 DSVOTC-----GPRVLLP---SMCCEACSPN--PATLGGCVHSAASLOARNA 282
Db 1048 TDQPCPSTDLCHCDPSTGOCPLPHVQGLSCDR-CAPFNWNTSRRGQCPACHPFSRAR 1106
QY 283 GP-----AGEMVPTFFGSLTQSGEFSDAWPLMQ-----NPMGGD----- 318
Db 1107 GPTCNEFTGQCHCHAG-----EGGRTCSQBELHWGDPGLQCRACDCDPRGIDKPCQHR 1160
QY 319 NISFCDSYPELTG 331
Db 1161 STGHCSCPGVSG 1173

RESULT 6
I54182
tumor necrosis factor receptor 2-related protein - human
C:Species: Homo sapiens (man)
C:Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 17-Mar-2000
C:Accession: I54182
R:Baens, M.; Chaffanet, M.; Cassiman, J.J.; Van den Berghe, H.; Marynen, P.
Genomics 16, 214-216, 1993
A:Title: Construction and evaluation of a hncDNA library of human l2p transcribed sequen
A:Reference number: I54182; MUID:93252381
A:Accession: I54182
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-435 <RES>
A:Cross-references: GB:I04270; NID:g339761; PIDN:AAA36757.1; PID:g339762
A:Gene: GDB:LTBR
A:Cross-references: GDB:I230195; OMIM:600979
A:Map position: 12p13.3-12p13.1
C:Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology

Query Match 6.4%; Score 145.5; DB 2; Length 435;
Best Local Similarity 21.4%; Pred. No. 0.0014;
Matches 73; Conservative 41; Mismatches 108; Indels 119; Gaps 19;

QY 16 LVLVLGYSCK-----VTCETGDCRQGE---FRDRSGNVCVPCNCGGPGMELSKGCGFG 65
Db 18 VLGLGFLAASQPQAVPPYASENQTRDQKEYEYEPQHRIC--CSRCPGTYVSARK--S 73
QY 66 YGEDAQCVTCLRHFRFEDMGF---QKCKPC-----LDCAVNRFQKANCATSATDAIC- 114
Db 74 RIRDTVCATCAENSYNEHWNLYICQLRCPDPMGLLEEIAFCTSKRKTKCRQCPQMFCA 133
QY 115 -----GDCLPGFYRKTK-LVGFQDMCEVPC-----GDP PPPPEPH--CAS 151
Db 134 AWALECTHCELLSDCPGTEAEKLDKGVGNHNCVCKAGHFQNTSSPARCQPHTRCEN 193
QY 152 KVNVLKTA-----STASSPRD-----TALAAVICSALATVLLALLILCVIY---- 192
Db 194 Q-GLVEAAPGTAQSDTTCKNPLEPLPPENSGTMLMLAVLLPLAFFLLATVFCINWKSHP 252
QY 193 --CKR--QFMKKP-----SNLSRSDIYQNGSELSCLDRPQLHEYAHRACCQCR 238
Db 253 SLCKRLGSLKRRPQEGGPNPVAGSW-----EPPKAHPYF----- 287
```

```
QY 239 RDSVQTCGPVRLLPSCMCCEACSPNPATLGGCVHSAASLQA 279
Db 288 PDLVQPLLPI-----SGDVSPVSTGLPAAVPLEA 316

RESULT 7
OX40 antigen precursor - rat
N:Alternate names: nerve growth factor receptor homolog
C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 05-Nov-1999
C:Accession: S12783; S08036
R:Mallett, S.; Fossum, S.; Barclay, A.N.
EMBO J. 9, 1063-1068, 1990
A:Title: Characterization of the MRC OX40 antigen of activated CD4 positive T lymphoc
A:Reference number: S12783; MUID:90214614
A:Accession: S12783
A:Molecule type: mRNA
A:Residues: 1-271 <MAL>
A:Cross-references: EMBL:X17037; NID:g57830; PIDN:CAA34897.1; PID:g57831
C:Superfamily: CD27 antigen; NGF receptor repeat homology
C:Keywords: growth factor receptor; transmembrane protein
F:1-15/Domain: signal sequence #status predicted <Sig>
F:20-271/Product: OX40 antigen #status predicted <MAT>
F:211-235/Domain: transmembrane #status predicted <TM>
```

```
Query Match 6.4%; Score 145; DB 2; Length 271;
Best Local Similarity 28.6%; Pred. No. 0.00094;
Matches 54; Conservative 23; Mismatches 76; Indels 36; Gaps 12;

QY 9 QEKTFETLLVLLGLYSCKVTCTGDCRQGEFRDR--SGN-CVPCNCGGPGMELSKGCGFG 65
Db 6 QQPTALLLGLSLGVTVKLC-----VKDTYPSGHKC--CRECQPGHGMVSR--D 52
QY 66 YGEDAQCVTCLRHFRFEDMGFQKCKPCLCAVVRFPQ-KANCATSATDAICGDCPLPGFYRK 124
Db 53 HTRDTVCHPCPEPGFYNEAVNYDFCKQCTQCNHRSGSELKQNTPTEDTVC-QCRPGTQPR 111
QY 125 TKLVGFQDMCEVPCGDP PPPPEP-----HCASKVNLV----KIATASSPRDTALAIVC- 175
Db 112 QSSSHKGLGVDCVPC--PPGHFSPGSNQACKPWTNCTLSGKQIRHPASNSLDT-----VCE 164
QY 176 --SALATVL 182
Db 165 DRSLLATLL 173
```

```
RESULT 8
I48700
gene ox40 protein - mouse
N:Alternate names: OX40 antigen
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 11-Jan-2000
C:Accession: I48700; I48334; S34377
R:Calderhead, D.M.; Buhlmann, J.E.; van den Eertwegh, A.J.; Claassen, E.; Noelle, R.J.
J. Immunol. 151, 5261-5271, 1993
A:Title: Cloning of mouse Ox40: a T cell activation marker that may mediate T-B cell
A:Reference number: I48700; MUID:94044750
A:Accession: I48700
A:Status: translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-272 <RES>
A:Cross-references: EMBL:X21674; NID:g312827; PIDN:CAA9772.1; PID:g312828
R:Birkeland, M.L.; Copeland, N.G.; Gilbert, D.J.; Jenkins, N.A.; Barclay, A.N.
Eur. J. Immunol. 25, 926-930, 1995
A:Title: Gene structure and chromosomal localization of the mouse homologue of rat OX
A:Reference number: I48334; MUID:95255413
A:Accession: I48334
A:Status: translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-14, 'G', 16-272 <RES>
A:Cross-references: EMBL:X85214; NID:g732818; PIDN:CAAS9476.1; PID:g732819
```


M62465; GB:M62466; GB:M62467; GB:M62468; GB:M62469; GB:M62470; NID:g511867; PIDN:AAA5061
R:Bornstein, P.; Alfli, D.; Devarayalu, S.; Framson, P.; Li, P.
J. Biol. Chem. 265, 16691-16698, 1990
A:Title: Characterization of the mouse thrombospondin gene and evaluation of the role of
A:Reference number: A37905; MUID:90375546
A:Accession: A37905
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-490 <BOR>
A:CROSS-references: GB:J05605; GB:J05606; NID:g201991; PIDN:AAA40431.1; PID:g554390
R:Laherty, C.D.; O'Rourke, K.; Wolf, F.W.; Katz, R.; Seldin, M.F.; Dixit, V.M.
J. Biol. Chem. 267, 3274-3281, 1992
A:Title: Characterization of mouse thrombospondin 2 sequence and expression during cell
A:Reference number: A42587; MUID:92147683
A:Accession: B42587
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-1152, P', 1154-1170 <LAH>
A:CROSS-references: GB:M87276
A:Note: sequence extracted from NCBI backbone (NCBIP:81501)
R:Chen, H.; Aeschlimann, D.; Nowlen, J.; Mosher, D.F.
FEBS Lett. 387, 36-41, 1996
A:Title: Expression and initial characterization of recombinant mouse thrombospondin 1 a
A:Reference number: S68787; MUID:96234006
A:Accession: S68787
A:Molecule type: protein
A:Residues: 19-26, 'X', 28-37 <CHE>
C:Complex: homotrimer, disulfide linked
C:Superfamily: thrombospondin 1; EGF homology; thrombospondin type 1 repeat homology; v
C:Keywords: calcium binding; glycoprotein; homotrimer
F:1-18/Domain: signal sequence #status predicted <SIG>
F:19-1170/Product: thrombospondin 1 #status predicted <MAT>
F:317-375/Domain: von Willebrand factor type C repeat homology <WMC>
F:378-429/Domain: thrombospondin type 1 repeat homology <PHR1>
F:434-490/Domain: thrombospondin type 1 repeat homology <THR2>
F:491-547/Domain: thrombospondin type 1 repeat homology <THR>
F:551-586/Domain: EGF homology <EGF>
F:248,360,708,1067/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 5.8%; Score 132.5; DB 2; Length 1170;
Best Local Similarity 21.0%; Pred. No. 0.04;
Matches 88; Conservative 39; Mismatches 141; Indels 151; Gaps 25;
Qy 26 KVTETGCRQOEFDRSGNCPVNCQCPG-----MELSKCCGFGY----- 66
Db 350 KVSCEPIMFCSNATVPD--GEC--CPRCHPSDSADGWSFSEWTSCTATCGNGIQORGRS 405
Qy 67 -----GEDACQVTCRLH-----RFKEDWGFKCKPCLDCA-----VNNRFQKAN-- 105
Db 406 CDSLNNRCGSSVQTRTCHIQCCKRFKQDGGWSHSPSSCSVTGCGDGVITRILCNRP 465
Qy 106 -----CSATSDAICGDCPLPGFYRKTKL 127
Db 466 SPQMGKPCGEARETKACKDADPINCNGWGPSPWDTCSTV-----CGG---GVQRRSRL 518
Qy 128 VGFQDMCEVCPGDPDPY-EPHCASKVNLVKIATSPRDTALAAVICSALATVLLALL 186
Db 519 -----CNNPTPQGGKDCVGVNTQVKNQKQDCPIDGLSNP-CFAGAK----- 561
Qy 187 ILCVYIKRQFMKPKPSLSLRSQDTQYNGSELSCILDRPQLHE-----YAHRAQCOCRR-D 240
Db 562 --CTSY-----PDGSNKGACACPPGYSNGIQCCKVDKVEVPDPCFNHNGEHRCKNTD 612
Qy 241 SVQTC--GPVRLLP-----MCCCEACSP-NPATLG---CGVHSAASLQARNAGP 284
Db 613 PGYNCLPCPPRFTGSPQFGRGVEHAMANKQVCKPRNPCTDGTDCNKNKAKNLYLGHYSDP 672
Qy 285 --AGEMVPTFFGSLQTSICGEFS--DAMPLMNPMPGDNISF-----CDSYPELTGED 333
Db 673 MYRCECKPGYAGN--GLICGEDTDLDGHP--NENLVCVANATYHCKKNCNPLNPSGQED 728

RESULT 15
A60771
B-cell activation protein CD40 precursor - human
N:Alternate names: B-cell surface antigen Bp50
C:Species: Homo sapiens (man)
C:Date: 03-Jun-1993 #sequence_revision 03-Feb-1994 #text_change 21-Jul-2000
C:Accession: S04460; A60771
R:Stamenkovic, I.; Clark, E.A.; Seed, B.
EMBO J. 8, 1403-1410, 1989
A:Title: A B-lymphocyte activation molecule related to the nerve growth factor recept
A:Reference number: S04460; MUID:89356608
A:Accession: S04460
A:Molecule type: mRNA
A:Residues: 1-277 <STA>
A:CROSS-references: EMBL:X60592; NID:g29850; PIDN:CAA43045.1; PID:g29851
R:Braesch-Andersen, S.; Paulie, S.; Koho, H.; Nika, H.; Aspenstroem, P.; Perlmann, P.
J. Immunol. 142, 562-567, 1989
A:Title: Biochemical characteristics and partial amino acid sequence of the receptor-
A:Reference number: A60771; MUID:89093941
A:Accession: A60771
A:Molecule type: protein
A:Residues: 21-50 <BRA>
A:Experimental source: Burkitt lymphoma cell line Raji
C:Genetics:
A:Gene: GDB:CD40
A:CROSS-references: GDB:215268; OMIM:109535
A:Map position: 20q12-20q13.2
C:Superfamily: CD27 antigen; NGF receptor repeat homology
C:Keywords: B-cell; glycoprotein; phosphoprotein; surface antigen; transmembrane prot
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-277/Product: B-cell activation protein CD40 #status experimental <MAT>
F:21-193/Domain: extracellular #status predicted <EXT>
F:194-215/Domain: transmembrane #status predicted <TM>
F:216-277/Domain: intracellular #status predicted <CYT>
F:153,180/Binding site: carbohydrate (Asn) (covalent) #status predicted
Query Match 5.8%; Score 132; DB 2; Length 277;
Best Local Similarity 24.6%; Pred. No. 0.0091;
Matches 52; Conservative 27; Mismatches 78; Indels 54; Gaps 11;
Qy 34 CRQOEFDRSGNCPVNCQCPGMELSKCCGFGYGEDACQVTCRLHFKEDWG-----F 86
Db 26 CREKQYLINS-QC--CSLCQPCQKLVSDC--TEFTETCLPCGSEFLDTWNRETHCHQH 80
Qy 87 QKCKPCLDCAVNRFQKANCATSDAIC-----GDCLPGFYRKTKL 127
Db 81 KYCDPNLGL-----RVQKGTSET-DTICTCEBGNHCTSEACESCVLHRSCTSPGFGVKQIA 135
Qy 128 VGFQDMCEVCP-----GDPPPPYE-----PHCASKVNLVKIAT-----ASSPRDTALAA 172
Db 136 TGVSDTICEPCVPVGFSSNVSSAFKCHPWTSCETKDLVVQQAQGTNKTVDVCGPQDRRLAL 195
Qy 173 VICSLATVLLALLILCVYIKRQFMKPKPS 203
Db 196 VWIPIFGILFAILLVLVLFIRK---VARKPT 223

Search completed: February 16, 2001, 21:06:44
Job time: 149 sec

THIS PAGE BLANK (USPTO)

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 16, 2001, 21:09:26 ; Search time 19.12 seconds
(without alignments)
714.456 Million cell updates/sec

Title: US-09-380-276A-8
Perfect score: 2283
Sequence: 1 MALKVLEQKFTFFLLVLL.....AIHPATQSLQVRQLGSL 423

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 88757 seqs, 32294092 residues

Total number of hits satisfying chosen parameters: 88757

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	157	6.9	454	1 TNRL_MOUSE	P25118 mus musculus
2	147	6.4	416	1 NGFR_HUMAN	P18519 gallus galli
3	146.5	6.4	1801	1 LMB2_RAT	P15800 rattus norv
4	145.5	6.4	435	1 TNRC_HUMAN	P36941 homo sapien
5	145	6.4	271	1 OX40_RAT	P15725 rattus norv
6	144	6.3	272	1 OX40_MOUSE	P47741 mus musculus
7	144	6.3	1104	1 NFX1_HUMAN	Q12986 homo sapien
8	141.5	6.2	461	1 TNRL_RAT	P22934 rattus norv
9	140	6.1	425	1 NGFR_RAT	P07174 rattus norv
10	137	6.0	1798	1 LMB2_HUMAN	P55268 homo sapien
11	134.5	5.9	415	1 TNRC_MOUSE	P50284 mus musculus
12	134	5.9	1786	1 LMB1_MOUSE	P02469 mus musculus
13	133.5	5.8	1799	1 LMB2_MOUSE	Q61292 mus musculus
14	133.5	5.8	2813	1 VWF_HUMAN	P04275 homo sapien
15	132.5	5.8	1170	1 TSP1_MOUSE	P35441 mus musculus
16	132	5.8	277	1 CD40_HUMAN	P25942 homo sapien
17	129	5.7	326	1 VTR_MVXVL	P29825 myxoma viru
18	128.5	5.6	1170	1 TSP1_HUMAN	P07996 homo sapien
19	127	5.6	4660	1 LRP2_RAT	P98158 rattus norv
20	126.5	5.5	471	1 TNRL_BOVIN	O19131 bos taurus
21	125.5	5.5	1173	1 TSP1_XENLA	P35448 xenopus lae
22	124.5	5.5	3712	1 LMA_DROME	Q00174 drosophila
23	122.5	5.4	1680	1 FUR2_DROME	P30432 drosophila
24	121	5.3	349	1 VC22_VARV	P34015 variola vir
25	121	5.3	1192	1 LMG2_MOUSE	Q61092 mus musculus
26	121	5.3	1964	1 NTC4_MOUSE	P31695 mus musculus
27	120.5	5.3	965	1 YNC3_YEAST	P53971 saccharomyc
28	120.5	5.3	2813	1 VWF_CANFA	Q28295 canis famil
29	120	5.3	256	1 L1BB_MOUSE	P20334 mus musculus
30	119.5	5.2	1193	1 LMG2_HUMAN	Q13753 homo sapien
31	119	5.2	1786	1 LMB1_HUMAN	P07942 homo sapien
32	118.5	5.2	863	1 LDVR_CHICK	P98165 gallus gall
33	118	5.2	1592	1 SORL_CHICK	Q98930 g sortilin-

RESULT 1

ID	TNRL_MOUSE	STANDARD;	PRT;	454 AA.
AC	P25118;			
DT	01-MAY-1992 (Rel. 22, Created)			
DT	01-MAY-1992 (Rel. 22, Last sequence update)			
DT	01-OCT-2000 (Rel. 40, Last annotation update)			
DE	TUMOR NECROSIS FACTOR RECEPTOR 1 PRECURSOR (P60) (TNF-R1) (TNF-RI) (P55).			
DE	TNFRSF1A OR TNFR1 OR TNFR-1.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
[1]	SEQUENCE FROM N.A.			
RP	MEDLINE-91187885; PubMed-1849278;			
RA	Lewis M., Tartaglia L.A., Lee A., Bennett G.L., Rice G.C.,			
RA	Wong G.H., Chen E.Y., Goeddel D.V.;			
RT	"Cloning and expression of cDNAs for two distinct murine tumor			
RT	necrosis factor receptors demonstrate one receptor is species			
RT	specific.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 88:2830-2834(1991).			
[2]	SEQUENCE FROM N.A.			
RP	MEDLINE-91246168; PubMed-1645445;			
RA	Goodwin R.G., Anderson D., Jerzy R., Davis T., Brannan C.I.,			
RA	Copeland N.G., Jenkins N.A., Smith C.A.;			
RT	"Molecular cloning and expression of the type 1 and type 2 murine			
RT	receptors for tumor necrosis factor.";			
RL	Mol. Cell. Biol. 11:3020-3026(1991).			
[3]	SEQUENCE FROM N.A.			
RP	MEDLINE-91285014; PubMed-1647956;			
RA	Barrett K., Taylor-Fishwick D.A., Cope A.P., Kissenerghis A.M.,			
RA	Gray P.W., Feldmann M., Foxwell B.M.J.;			
RT	"Cloning, expression and cross-linking analysis of the murine p55			
RT	tumor necrosis factor receptor.";			
RL	Eur. J. Immunol. 21:1649-1656(1991).			
[4]	SEQUENCE FROM N.A.			
RP	TISSUE-SPLEEN;			
RC	MEDLINE-92039815; PubMed-1657766;			
RA	Rothe J.G., Brockhaus M., Gentz R., Lesslauer W.;			
RT	"Molecular cloning and expression of the mouse Tnf receptor type b.";			
RL	Immunogenetics 34:338-340(1991).			
[5]	SEQUENCE FROM N.A.			
RP	MEDLINE-94245292; PubMed-8188324;			
RA	Bebo B.F., Linthicum D.S.;			
RT	"Nucleotide sequence of the TNF type I receptor from a mouse			
RT	endothelioma cell line.";			
RL	Immunogenetics 39:450-451(1994).			
[6]	SEQUENCE FROM N.A.			
RP	MEDLINE-93156721; PubMed-8381516;			
RA	Rothe J., Bluethmann H., Gentz R., Lesslauer W., Steinmetz M.;			

ALIGNMENTS

34	117.5	5.1	3075	1	LMAL_HUMAN	P25391 homo sapien
35	117	5.1	255	1	41BB_HUMAN	Q07011 homo sapien
36	116.5	5.1	1106	1	STC_DROME	P40798 drosophila
37	116	5.1	417	1	WSCI_HUMAN	Q93038 h wsl-1 pro
38	116	5.1	1790	1	LMB1_DROME	P11046 drosophila
39	114.5	5.0	1557	1	LMB1_CAEEL	Q18823 caenorhabdi
40	114	5.0	327	1	FASA_MOUSE	P25446 mus musculus
41	114	5.0	455	1	TNRL_HUMAN	P19438 homo sapien
42	113.5	5.0	427	1	NGFR_HUMAN	P08138 homo sapien
43	113	4.9	4753	1	LRP_CAEEL	Q04833 caenorhabdi
44	112.5	4.9	3635	1	LMA5_MOUSE	Q61001 mus musculus
45	112	4.9	461	1	TNRL_PIG	P50555 sus scrofa

RT "Genomic organization and promoter function of the murine tumor
 RL necrosis factor receptor beta gene.";
 CC Mol. Immunol. 30:165-175(1993).
 CC -1- FUNCTION: RECEPTOR FOR TNF-ALPHA. THE ADAPTOR MOLECULE FADD
 CC RECRUITS CASPASE-8 TO THE ACTIVATED RECEPTOR. THE RESULTING
 CC AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC)
 CC PERFORMS CASPASE-8 PROTEOLYTIC ACTIVATION WHICH INITIATES THE
 CC SUBSEQUENT CASCADE OF CASPASES (ASPARTATE-SPECIFIC CYSTEINE
 CC PROTEASES) MEDIATING APOPTOSIS (BY SIMILARITY).
 CC -1- SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFR1 LEADS TO
 CC HOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS
 CC PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY
 CC WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING
 CC PROTEINS SUCH AS TRAFs, RIP AND POSSIBLY FADD, ARE RECRUITED TO
 CC TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX
 CC ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND
 CC NF-KAPPA B SIGNALING (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
 CC -1- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: M60468; AAA39751.1; -
 CC EMBL: M59377; AAA40464.1; -
 CC EMBL: X59238; AAA41922.1; -
 CC EMBL: X57796; AAA40936.1; -
 CC EMBL: L26349; AAA59361.1; -
 CC EMBL: M76656; AAA40465.1; -
 CC EMBL: M88067; AAA40465.1; JOINED.
 CC EMBL: M76655; AAA40465.1; JOINED.
 CC PIR: A38634; GQMST1.
 CC PIR: S16677; S16677.
 CC PIR: S19021; S19021.
 CC HSP: P19438; LEXT.
 CC MGD: MGI:1314884; TNFRSF1A.
 CC INTERPRO: IPR000488; -
 CC INTERPRO: IPR001368; -
 CC PFAM: PF00020; TNFR_c6; 4.
 CC PFAM: PF00531; death; 1.
 CC PROSITE: PS00652; TNFR_NGFR_1; 3.
 CC PROSITE: PS00050; TNFR_NGFR_2; 3.
 CC PROSITE: PS50017; DEATH_DOMAIN; 1.
 CC Receptor; Transmembrane; Glycoprotein; Repeat; Signal; Apoptosis.
 FT SIGNAL 1 21 POTENTIAL.
 FT CHAIN 22 454 TUMOR NECROSIS FACTOR RECEPTOR 1.
 FT DOMAIN 22 212 EXTRACELLULAR (POTENTIAL).
 FT TRANSNEM 213 235 POTENTIAL.
 FT DOMAIN 236 454 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 43 196 4 X TNFR-CYS.
 FT REPEAT 43 82 TNFR-CYS 1.
 FT REPEAT 83 125 TNFR-CYS 2.
 FT REPEAT 126 166 TNFR-CYS 3.
 FT REPEAT 167 196 TNFR-CYS 4.
 FT DOMAIN 339 349 N-SMASE ACTIVATION DOMAIN (NSD).
 FT DOMAIN 356 441 DEATH DOMAIN.
 FT DISULFID 44 58 BY SIMILARITY.
 FT DISULFID 59 72 BY SIMILARITY.
 FT DISULFID 62 81 BY SIMILARITY.
 FT DISULFID 84 99 BY SIMILARITY.
 FT DISULFID 102 117 BY SIMILARITY.
 FT DISULFID 105 125 BY SIMILARITY.
 FT DISULFID 127 143 BY SIMILARITY.
 FT DISULFID 146 158 BY SIMILARITY.
 FT DISULFID 149 166 BY SIMILARITY.
 FT DISULFID 168 179 BY SIMILARITY.
 FT DISULFID 182 191 BY SIMILARITY.

FT DISULFID 185 195 BY SIMILARITY.
 FT CARBOHYD 54 54 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 151 151 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 202 202 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CONFLICT 394 394 R -> G (IN REF. 6).
 SQ SEQUENCE 454 AA; 50129 MW; 0710C2B8C3C2B6D9 CRC64;
 Query Match 6.9%; Score 157; DB 1; Length 454;
 Best Local Similarity 21.0%; Pred. No. 5.8e-05;
 Matches 76; Conservative 42; Mismatches 140; Indels 104; Gaps 19;
 QY 34 CROQEFDRSGNCPVQCQPGMELSKGEGYGEDAQCVTCRLHREKEDWGF-QKCKPC 92
 DB 44 CPOGKYVSHKNNISICCTKCHKGYLYSDCP-SPGRDVTVCRECEKGTFTASQNYLROCLSC 102
 QY 93 LDC-AVNVRFQKANCATSDAICG-----DCLPGFYRKTKL----- 127
 DB 103 KTCRKEMSOVEISPCQADKDTVCCKENOFQRYLSETHFQCVCDCSPCFNGTVTIPCKETQ 162
 QY 128 -----VGF--ODMECVCPGDPPEPHCASKVNLVITA-----STASSPRDTALAAY 173
 DB 163 NTVCNCHAGFFLRESECVPCS-----HCKNECMKLCCLPPPLANVTNPDSGTAVL 214
 QY 174 ICSALATVLLALILGVIYCKQFMKPSWLSRSDIQYNGSELSCLDROPQLHEYAHRA 233
 DB 215 L-----PLVILLGLCLLSFIFI--SLMCRYPRW-----RPEVYSII--- 248
 QY 234 CCOCRRDSV-----OTCG-PVRLPLSCCEACSPNATLGGVHSAASLOARN----- 281
 DB 249 ---C-RDPVPVKEEKAGKPLTPAPSPAFSTSGFNP-TLGFSTPGFSSPVSTPISPIFG 303
 QY 282 -----AGPAGEMVPTFFGS--LTQSTCG----EFSDANPLMONGMGGDNISFCDSYPEL 329
 DB 304 PSNWHFMPVSEVVPVTPQAGDPLLYESLCVSPAPTSVQKWEDESAHPORPDNADLILAYV 363
 QY 330 TG 331
 DB 364 DG 365
 RESULT 2
 NGFR_CHICK
 ID NGFR_CHICK STANDARD; PRT; 416 AA.
 AC P18519;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE LOW-AFFINITY NERVE GROWTH FACTOR RECEPTOR PRECURSOR (NGF RECEPTOR)
 DE (GP80-LNGFR) (P75 ICD).
 GN NGFR.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-BRAIN;
 RX MEDLINE-90166579; PubMed-2560385;
 RA Large T.H., Weskamp G., Helder J.C., Radeke M.J., Misko T.P.,
 RA Shooter E.M., Reichardt L.F.;
 RT "Structure and developmental expression of the nerve growth factor
 RL receptor in the chicken central nervous system.";
 RL Neuron 2:1123-1134(1989).
 RN [2]
 RP SEQUENCE OF 21-416 FROM N.A.
 RX MEDLINE-90152140; PubMed-2154393;
 RA Heuer J.G., Fatemie-Nainie S., Wheeler E.F., Bothwell M.;
 RT "Structure and developmental expression of the chicken NGF receptor.";
 RL Dev. Biol. 137:287-304(1990).
 CC -1- FUNCTION: LOW AFFINITY RECEPTOR WHICH CAN BIND TO NGF, BDNF,
 CC NT-3, AND NT-4.
 CC -1- SUBUNIT: NGF RECEPTOR CAN FORM A HOMODIMER THROUGH DISULFIDE

```

CC CC BOND FORMATION.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- PTM: N- AND O-GLYCOSYLATED AND IS PHOSPHORYLATED ON SERINE.
CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
CC -1- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
DR PIR: JN0006; JN0006.
DR HSP: A60504; A60504.
DR PIR: A60504; A60504.
DR INTERPRO: IPR001368; -.
DR PFAM: PF00020; TNFR_C6; 4.
DR PFAM: PF00531; death; 1.
DR PROSITE: PS00652; TNFR_NGFR_1; 3.
DR PROSITE: PS00500; TNFR_NGFR_2; 3.
DR PROSITE: PS00117; DEATH_DOMAIN; 1.
KW Receptor; Neurogenesis; Transmembrane; Glycoprotein; Repeat;
KW Phosphorylation; Signal.
FT SIGNAL 1 19
FT CHAIN 20 416
FT FT LOW-AFFINITY NERVE GROWTH FACTOR
FT FT RECEPTOR.
FT FT EXTRACELLULAR (POTENTIAL).
FT TRANSAMIN 29 239
FT DOMAIN 240 261
FT DOMAIN 262 416
FT DOMAIN 23 181
FT REPEAT 23 57
FT REPEAT 58 100
FT REPEAT 101 140
FT REPEAT 141 181
FT REPEAT 182 236
FT DOMAIN 188 236
FT DOMAIN 333 410
FT DISULFID 24 35
FT DISULFID 36 49
FT DISULFID 39 56
FT DISULFID 59 75
FT DISULFID 78 91
FT DISULFID 81 99
FT DISULFID 101 114
FT DISULFID 117 130
FT DISULFID 120 138
FT DISULFID 141 156
FT DISULFID 159 172
FT DISULFID 162 180
FT CARBOHYD 52 52
FT CONFLICT 36 36
FT CONFLICT 173 173
FT CONFLICT 276 276
FT CONFLICT 396 396
SQ SEQUENCE 416 AA; 44654 MW; 6BCEAAB54F4D2D56 CRC64;

Query Match
Best Local Similarity 29.9%; Pred. No. 0.00031;
Matches 56; Conservative 17; Mismatches 82; Indels 32; Gaps 10;

Qy 20 LGYLSKVTCTGQ-----CRQOEFRDR-SGNCVPCNCGPMELSKCGFGY-----G 67
Db 82 VGLHMSAPCVESDDAVRCAYGVQDELGSCKECSIC-----EVGFLMPFCRDS 133
Qy 68 EDAQCVCETLHRFKEDWGFQKCPCLDCAVV--NRFQKANCSDATCIGDCLPGFYRKT 125
Db 134 QTVCECEPGTFSDEANF--VDPCLPCTICBENEVMYKECTATSDACRDLHPRWTH 191
Qy 126 -KLVGQDMCEVCPCDPDPPEPHCAKSNLVKVIKASTASP---RDTA--LAAVICSALA 179
Db 192 PSLAGSDSPE--PITRDPENTEGMATTIADIVTTWVGSSQPVVSRGTADNLIPVCSILA 249
Qy 180 TVLLALL 186
Db 250 AVVWGLV 256

RESULT 3
LMB2_RAT

```

```

ID AC LMB2_RAT STANDARD; PRT; 1801 AA.
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE LAMININ BETA-2 CHAIN PRECURSOR (S-LAMININ) (LAMININ CHAIN B3).
GN LMB2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RX MEDLINE=89159410; PubMed=2922051;
RA Hunter D.D., Shah V., Merlie J.P., Sanes J.R.;
RT "A laminin-like adhesive protein concentrated in the synaptic cleft
of the neuromuscular junction.";
RL Nature 338:229-234(1989).
CC -1- FUNCTION: BINDING TO CELLS VIA A HIGH AFFINITY RECEPTOR, LAMININ
IS THOUGHT TO MEDIATE THE ATTACHMENT, MIGRATION, & ORGANIZATION OF
CELLS INTO TISSUES DURING EMBRYONIC DEVELOPMENT BY INTERACTING
WITH OTHER EXTRACELLULAR MATRIX COMPONENTS.
CC -1- SUBUNIT: LAMININ IS A COMPLEX GLYCOPROTEIN, CONSISTING OF THREE
DIFFERENT POLYPEPTIDE CHAINS (ALPHA, BETA, GAMMA), WHICH ARE BOUND
TO EACH OTHER BY DISULFIDE BONDS INTO A CROSS-SHAPED MOLECULE
COMPRISING ONE LONG & THREE SHORT ARMS WITH GLOBULES AT EACH END.
CC THE BETA-2 CHAIN IS A SUBUNIT OF LAMININ-3 (S-LAMININ), LAMININ-4
(S-MEROSIN), AND LAMININ-7 (KS-LAMININ).
CC -1- SUBCELLULAR LOCATION: EXTRACELLULAR.
CC -1- TISSUE SPECIFICITY: FOUND IN THE BASEMENT MEMBRANES (MAJOR
COMPONENT). S-LAMININ IS CONCENTRATED IN THE SYNAPTIC
CLEFT OF THE NEUROMUSCULAR JUNCTION.
CC -1- DOMAIN: THE ALPHA-HELICAL DOMAINS I AND II ARE THOUGHT TO INTERACT
WITH OTHER LAMININ CHAINS TO FORM A COILED COIL STRUCTURE.
CC -1- DOMAIN: DOMAINS VI AND IV ARE GLOBULAR.
CC -1- SIMILARITY: CONTAINS 1 LAMININ N-TERMINAL DOMAIN (DOMAIN VI).
CC -1- SIMILARITY: CONTAINS 12.5 LAMININ EGF-LIKE DOMAINS.
CC -1- SIMILARITY: CONTAINS 1 LAMININ DOMAIN IV.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL Outstation
at the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X16563; CAA34561.1; -.
DR PIR; S03539; MMRTS.
DR HSP; P02468; 1KLO.
DR INTERPRO: IPR000561; -.
DR INTERPRO: IPR001886; -.
DR INTERPRO: IPR002049; -.
DR PFAM; PF00053; laminin_EGF; 13.
DR PFAM; PF00055; laminin_Nterm; 1.
DR PRINTS; PR00011; EGF_LAMININ.
DR PROSITE; PS00022; EGF_1; 10.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01248; LAMININ_TYPE_EGF; 12.
DR Glycoprotein; Basement membrane; Extracellular matrix; Coiled coil;
KW Laminin EGF-like domain; Cell adhesion; Repeat; Signal.
FT SIGNAL 1 35
FT CHAIN 36 1801
FT DOMAIN 36 283
FT DOMAIN 286 555
FT FT LAMININ BETA-2 CHAIN.
FT FT LAMININ N-TERMINAL (DOMAIN VI).
FT FT 4.5 X LAMININ EGF-LIKE REPEATS (DOMAIN
V).
FT FT LAMININ EGF-LIKE 1.
FT FT LAMININ EGF-LIKE 2.
FT FT LAMININ EGF-LIKE 3.
FT FT LAMININ EGF-LIKE 4.
FT FT LAMININ EGF-LIKE 5 (INCOMPLETE).
FT FT LAMININ DOMAIN IV.
FT FT 8 X LAMININ EGF-LIKE REPEATS (DOMAIN
V).

```


modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

```
CC DE EMBL; L04270; AAA36757.1; -.
CC GN TFRS4 OR TXGPIL OR OX40.
CC OS Rattus norvegicus (Rat).
CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
CC RN [1]
CC RP SEQUENCE FROM N.A.
CC RC TISSUE=T-CELL;
CC RX MEDLINE=90214614; PubMed=2157591;
CC RA Mallett S., Fossum S., Barclay A.N.;
CC RT "Characterization of the MRC OX40 antigen of activated CD4 positive T
CC RL lymphocytes -- a molecule related to nerve growth factor receptor.";
CC EMBO J. 9:1063-1068(1990).
CC -!- FUNCTION: RECEPTOR FOR THE OX40L/GP34 CYTOKINE.
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -!- TISSUE SPECIFICITY: ACTIVATED T-CELLS.
CC -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
```

```
DE DR EMBL; X17037; CAA34897.1; -.
DE DR PIR; S08036; S08036.
DE DR PIR; S12783; S12783.
DE DR HSP; P25942; ICDP.
DE DR INTERPRO; IPR001368; -.
DE DR PFAM; PF00020; TNFR_C6; 3.
DE DR PROSITE; PS00652; TNFR_NGFR.1; 3.
DE DR PROSITE; PS00500; TNFR_NGFR.2; 2.
DE DR RECEPTOR; T-cell; Antigen; Glycoprotein; Transmembrane; Repeat;
DE KW Signal.
DE FT SIGNAL.
DE FT CHAIN 1 19
DE FT DOMAIN 20 271
DE FT DOMAIN 20 271
DE FT TRANSMEM 211 235
DE FT TRANSMEM 236 271
DE FT DOMAIN 25 164
DE FT DOMAIN 25 164
DE FT REPEAT 61 102
DE FT REPEAT 103 123
DE FT REPEAT 124 164
DE FT CARBOHYD 143 143
DE FT N-LINKED (GLCNAC...) (POTENTIAL).
DE SQ SEQUENCE 271 AA; 29895 MW; C06465136B16E821 CRC64;

Query Match 6.4%; Score 145.5; DB 1; Length 435;
Best Local Similarity 21.4%; Pred. No. 0.00042;
Matches 73; Conservative 41; Mismatches 108; Indels 119; Gaps 19;

QY 16 LVLVGLYSCK-----VTCGTGCRQF-----FDRSGNVCVPCNOCGPGMELSKCGFG 65
DB 18 VLGLGFLLAASQAPVPPYASENQCRCQKEYYEYFQHRIC--CSRCPPTGVYSKAC--S 73
QY 66 YGEDAQCVTCRLHREKEDWGF-----QKCKPC-----LDCAVNVNRFQKANCATSDAIC- 114
DB 74 RIRDIVCATCAENSNEHWNLYTICQLCRPCDPVGMGLEEIAPICTSKRTQCRQCPMCA 133
QY 115 -----GDCPLPGFYRKTR-LVGFQDMCVPC-----GDPPPPYPH--CAS 151
DB 134 AWALECTHCELLSDCPGTEAEALKEDEGVGNHNCVPCRGAGHFQNTSSPSARCPHTRCEN 193
QY 152 KYNLVKIA-----STASSPRD-----TALAAVTCSALATVLLALLILCVIY---- 192
DB 194 Q-GLVEAPAGTQAQSDTCKNPLEPLPEMPSGMTMLMLAVLLPLAFLLATVFCISWKSHP 252
QY 193 --CKR--QFMKKP-----SWSLRSDIQYNGSELSCLDRLPOLHEAHRAHCCQCR 238
DB 253 SLCKRLGSLKKRRPQEGNPNVAGSW-----EPKAPHYF----- 287
QY 239 RDSVQTGVRLLPSMCCCEASPNPATLGCVGHSAAISLQA 279
DB 288 PDLVQPLLP-----SGDVSPVSTGLPAAPVLEA 316

RESULT 5
OX40_RAT
ID OX40_RAT STANDARD; PRT; 271 AA.
AC P15725;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
```



```
QY 24 SKVCTGTGCRQGEFRDRSGNVCPCNQCQGMELSKCQ-----FGYGEDAQ----- 72
DB 440 SCNLLCHPG-----PCPCFAFTKTECGRTRHTVPCGAVSHVCNCP 484
QY 73 ---VTCRLHREFKDMGQKCPCLDCAVVRKFKANCATS-DAICGDCPLPGFYRKTKLV 128
DB 485 ENILNCQHQAELCHGCGQPCQ--IILN-QVCYCGSTSRDLVLCGTDV-----GKSD 534
QY 129 GFODMEC-----VPCGD-----PP-----PYEPHC--ASKVNLVKIATASS 164
DB 535 GFGDFCLTKCGKDLKCGNHTCSQVCHPQCCQPRLPQLVRCPCGQTLPSQLLELGS 594
QY 165 PROTALAAV-----IC-SALATVLLALLILC-----VIVCKRQFMKK- 201
DB 595 SRKTCMDPVSCGKVCCKPLPCGSLDFIHTCEKLCHEGDCGVPVSRVTSICRCSFRTEL 654
QY 202 PWSLRSODI-----QYNGSELSCDLRPQ-----LH---EYA 230
DB 655 PCTSLKSEDATFMDCKRCKKRLCGRHKCNIEICVDREHKCPLNCGRKLRCGLHRCCEPC 714
QY 231 HRACCO-CRDSVQT-----CGPVRLPSMCC-----EE 258
DB 715 HRGNCQTCWQASDELTCGASVIYPPVCGTRPPCTQTCARVHCDHPVYHSGHSEE 774
QY 259 ACS-----PNTATLGGVHSAASL----- 277
DB 775 KCPCTELTKQKWCHEFRSNIPCHLVDSGLPLCSATLPCGHHKQRLCHKGECLVDE 834
QY 278 -----QAR-----NAGPAGEWPTFFGSLTQSI 300
DB 835 PCKQCTTPRADCGHPCMACHTSSPCVPTACKAKVELQCEGRKRWKVCSEASSTYQR 894
QY 301 CGEFSDAWPLMOPMGDNISFCDSYFELTCEDIHSLNPELESSTLSDNSSQDLVGAV 360
DB 895 IAAISMASKITDMOLGGS-----VBIKLTKEVQHARLECDCECSALEKRKR--LAEAF 948
QY 361 PVQSHSENTAATDLSRYNLTVESATQDALTMRSQDQESGAI 406
DB 949 HISEDSPFNIRSSGSFSDSLKEDA--RKDLKFVSDVEKEMETLV 992
RESULT 8
TNRI_RAT
ID TNRI_RAT STANDARD; PRT; 461 AA.
AC P22934:
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DE 01-OCT-2000 (Rel. 40, Last annotation update)
DE TUMOR NECROSIS FACTOR RECEPTOR 1 PRECURSOR (P60) (TNF-RI) (TNF-RI) (P55).
GN TNFRSF1A OR TNFR1 OR TNFR-1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN [1]
RX MEDLINE-91090841; PubMed-1702293;
RA Himmeler A., Maurer-Fogy I., Kroenke M., Scheurich P., Pfizenmaier K.,
RA Lantz M., Olsson I., Hauptmann R., Stratowa C., Adolf G.R.;
RT "Molecular cloning and expression of human and rat tumor necrosis
RT factor receptor chain (p60) and its soluble derivative, tumor
RL necrosis factor-binding protein.";
RL DNA Cell Biol. 9:705-715(1990).
CC -1- FUNCTION: RECEPTOR FOR TNF-ALPHA. THE ADAPTOR MOLECULE FADD
CC RECRUITS CASPASE-8 TO THE ACTIVATED RECEPTOR. THE RESULTING
CC AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC)
CC PERFORMS CASPASE-8 PROTEOLYTIC ACTIVATION WHICH INITIATES THE
CC SUBSEQUENT CASCADE OF CASPASES (ASPARTATE-SPECIFIC CYSTEINE
CC PROTEASES) MEDIATING APOPTOSIS (BY SIMILARITY).
CC -1- SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFR1 LEADS TO
CC HOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS
CC PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY
```

```
CC WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING
CC PROTEINS SUCH AS TRAFs, RIP AND POSSIBLY FADD, ARE RECRUITED TO
CC TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX
CC ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND
CC NF-KAPPA B SIGNALING (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
CC -1- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
CC
CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; MG3122; AAA42256.1;
CC PIR; B36555; B36555.
CC HSP; P19438; ITNR.
CC INTERPRO: IPR000488;
CC INTERPRO: IPR001368;
CC PFAM; PF00020; TNFR_c6; 4.
CC PFAM; PF00531; death; 1.
CC PROSITE; PS00652; TNFR_NGFR_1; 3.
CC PROSITE; PS50050; TNFR_NGFR_2; 3.
CC PROSITE; PS50017; DEATH_DOMAIN; 1.
CC Receptor; Transmembrane; Glycoprotein; Repeat; Signal; Apoptosis.
FT SIGNAL 1 21
FT CHAIN 22 461
FT DOMAIN 22 211
FT TRANSMEM 212 234
FT DOMAIN 235 461
FT DOMAIN 43 196
FT REPEAT 43 82
FT REPEAT 83 125
FT REPEAT 126 166
FT REPEAT 167 196
FT REPEAT 344 354
FT DOMAIN 363 448
FT DISULFID 44 58
FT DISULFID 59 72
FT DISULFID 62 81
FT DISULFID 84 99
FT DISULFID 102 117
FT DISULFID 105 125
FT DISULFID 127 143
FT DISULFID 146 158
FT DISULFID 149 166
FT DISULFID 168 179
FT DISULFID 182 191
FT DISULFID 185 195
FT CARBOHYD 54 54
FT CARBOHYD 151 151
FT CARBOHYD 201 201
FT SEQUENCE 461 AA; 50969 MW; EB23C05450FBD202 CRC64;
QY 34 CROQEFDRSGNVCPCNQCQGMELSKCQGFYGEDAQCVTCRLHREFKDMGQKCPCL 93
DB 44 CPQKRYAHKPNKNSICCTKCHKGTYLVSDCP-SPQGETVCEVCDKGTFTASQ--NHVROCL 100
QY 94 DCAYVNR--FQK---ANGSATSDAICGDCPLPGFYRKTKLVGFGDMCEVPC----- 138
DB 101 SCKTCRMEFQVEISPCKADMDTVCGCKKNQFQRYLSETHFCQVDCSPCFNGTVPICKE 160
QY 139 -----GDPPEPYEPHCASKVNLVKI-----ASTASSPRDTAAAVICSALA 179
DB 161 KONTVCNCHAGFFLSGNECTPCS-HCKKNQCBMKLCLPPVANVTNPQDSGTAVLLPLVIF 219
```

Query Match 6.2%; Score 141.5; DB 1; Length 461;
Best Local Similarity 21.6%; Pred. No. 0.00092;
Matches 72; Conservative 37; Mismatches 113; Indels 111; Gaps 20;


```

RESULT 12
LMB1_MOUSE
AC P02469; STANDARD; PRT: 1786 AA.
DT 01-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1989 (Rel. 11, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE LAMININ BETA-1 CHAIN PRECURSOR (LAMININ B1 CHAIN).
GN LAMB1-1 OR LAMB-1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE-87147212; PubMed-3493487;
RA Sasaki M., Kato S., Kohno K., Martin G.R., Yamada Y.;
RT "Sequence of the cDNA encoding the laminin B1 chain reveals a
multidomain protein containing cysteine-rich repeats.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:935-939(1987).
[2]
RP SEQUENCE OF 1292-1786 FROM N.A.
RX MEDLINE-85051302; PubMed-6209134;
RA Barlow D.P., Green N.M., Kurkinen M., Hogan B.L.M.;
RT "Sequencing of laminin B chain cDNAs reveals C-terminal regions of
coiled-coil alpha-helix.";
RL EMBO J. 3:2355-2362(1984).
[3]
RP SEQUENCE OF 165-172; 539-547 AND 712-719.
RC STRAIN-BALB/C; TISSUE-ENDOTHELIAL CELLS;
RX MEDLINE-97363207; PubMed-9219532;
RA Frieser M., Noeckel H., Pausch F., Roeder C., Hahn A., Deutzmann R.,
RA Sorokin L.M.;
RT "Cloning of the mouse laminin alpha 4 cDNA. Expression in a subset of
endothelium.";
RL Eur. J. Biochem. 246:727-735(1997).
CC -1- FUNCTION: BINDING TO CELLS VIA A HIGH AFFINITY RECEPTOR. LAMININ
IS THOUGHT TO MEDIATE THE ATTACHMENT, MIGRATION, & ORGANIZATION OF
CELLS INTO TISSUES DURING EMBRYONIC DEVELOPMENT BY INTERACTING
WITH OTHER EXTRACELLULAR MATRIX COMPONENTS.
CC -1- SUBUNIT: LAMININ IS A COMPLEX GLYCOPROTEIN, CONSISTING OF THREE
DIFFERENT POLYPEPTIDE CHAINS (ALPHA, BETA, GAMMA), WHICH ARE BOUND
TO EACH OTHER BY DISULFIDE BONDS INTO A CROSS-SHAPED MOLECULE
COMPRISING ONE LONG & THREE SHORT ARMS WITH GLOBULES AT EACH END.
CC THE BETA-1 CHAIN IS A SUBUNIT OF LAMININ-1 (EHS LAMININ), LAMININ-
2 (MEROSIN), AND LAMININ-6 (K-LAMININ).
CC -1- SUBCELLULAR LOCATION: EXTRACELLULAR.
CC -1- TISSUE SPECIFICITY: FOUND IN THE BASEMENT MEMBRANES (MAJOR
COMPONENT).
CC -1- SIMILARITY: CONTAINS 1 LAMININ N-TERMINAL DOMAIN (DOMAIN VI).
CC -1- SIMILARITY: CONTAINS 12.5 LAMININ EGF-LIKE DOMAINS.
CC -1- SIMILARITY: CONTAINS 1 LAMININ DOMAIN IV.
-----
This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL Outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
-----
DR EMBL; M15525; AAA39407.1; ALT_INIT.
DR EMBL; X05212; CAA28839.1; -.
DR PIR; A26413; MMSB1.
DR HSP; P03069; I2IM.
DR MGD; MGI:96743; LAMB1-1.
DR INTERPRO; IPR000561; -.
DR INTERPRO; IPR001886; -.
DR INTERPRO; IPR002049; -.
DR PFW; PF00053; laminin_EGF; 13.
DR PFW; PF00055; laminin_Nterm; 1.
DR PRINTS; PR00011; EGF-LAMININ.

```

```

DR PROSITE; PS00022; EGF_1; 9.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01248; LAMININ_TYPE_EGF; 11.
KW Glycoprotein; Basement membrane; Extracellular matrix; Coiled coil;
KW Laminin EGF-like domain; Cell adhesion; Repeat; Signal.
FT SIGNAL 1 21
FT CHAIN 22 1786
FT DOMAIN 22 270
FT DOMAIN 271 540
FT DOMAIN 271 334
FT DOMAIN 335 397
FT DOMAIN 398 457
FT DOMAIN 458 509
FT DOMAIN 510 540
FT DOMAIN 541 772
FT DOMAIN 773 1178
FT DOMAIN 773 820
FT DOMAIN 821 866
FT DOMAIN 867 916
FT DOMAIN 917 975
FT DOMAIN 976 1027
FT DOMAIN 1028 1083
FT DOMAIN 1084 1131
FT DOMAIN 1132 1178
FT DOMAIN 1179 1397
FT DOMAIN 1398 1430
FT DOMAIN 1431 1786
FT DOMAIN 1216 1315
FT DOMAIN 1368 1388
FT DOMAIN 1448 1778
FT DISULFID 271 280
FT DISULFID 273 298
FT DISULFID 300 309
FT DISULFID 312 332
FT DISULFID 335 344
FT DISULFID 337 362
FT DISULFID 365 374
FT DISULFID 377 395
FT DISULFID 398 411
FT DISULFID 400 426
FT DISULFID 428 437
FT DISULFID 440 455
FT DISULFID 458 472
FT DISULFID 460 479
FT DISULFID 481 490
FT DISULFID 493 507
FT DISULFID 773 785
FT DISULFID 775 792
FT DISULFID 794 803
FT DISULFID 806 818
FT DISULFID 821 833
FT DISULFID 823 840
FT DISULFID 842 851
FT DISULFID 854 864
FT DISULFID 867 876
FT DISULFID 869 883
FT DISULFID 886 895
FT DISULFID 898 914
FT DISULFID 917 933
FT DISULFID 919 944
FT DISULFID 946 955
FT DISULFID 958 973
FT DISULFID 976 990
FT DISULFID 978 997
FT DISULFID 1000 1009
FT DISULFID 1012 1025
FT DISULFID 1084 1096
FT DISULFID 1086 1103
FT DISULFID 1105 1114
FT DISULFID 1117 1129
FT DISULFID 1132 1144

```



```

FT DISULFID 1134 1151 BY SIMILARITY.
FT DISULFID 1153 1162 BY SIMILARITY.
FT DISULFID 1165 1176 BY SIMILARITY.
FT DISULFID 1179 1179 INTERCHAIN (PROBABLE).
FT DISULFID 1182 1182 INTERCHAIN (PROBABLE).
FT DISULFID 1785 1785 INTERCHAIN (PROBABLE).
FT CARBOHYD 120 120 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 356 356 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 519 519 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 677 677 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1041 1041 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1195 1195 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1279 1279 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1336 1336 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1343 1343 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1487 1487 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1533 1533 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1542 1542 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1643 1643 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CONFLICT 1531 1534 SGNA -> MEMP (IN REF. 2).
FT CONFLICT 1749 1749 D -> N (IN REF. 2).
SQ SEQUENCE 1786 AA; 196904 MW; 846671B7BF41A474 CRC64;

Query Watch 5.9%; Score 134; DB 1; Length 1786;
Best Local Similarity 20.9%; Pred. No. 0.016;
Matches 84; Conservative 32; Mismatches 124; Indels 162; Gaps 24;

QY 21 GYLSKVTCTGDCROQFDRSGNCVP-----CNCQGGMELSKCEGFGYGED----- 69
DB 779 GSLSSVCDPNGGQCQ-----CRPNVVGRTCNRCAPGT-----FGFGNGCKPC 821
QY 70 -----ACQVTCRLHREK-----EDWGFQCKPC-----LDCAVVNR 100
DB 822 DCHLQGSASAFDAITGQCHFGIYARQCDRLPGYWGPPSCQCNCHALDCDVT- 880
QY 101 FQKANGSATSDAI-----CGDCLPGFYKTKLVGFQDMCVPCGDDPPPP-----YEPHCAS 151
DB 881 ---GECLSCQDYTTGHCNRCERLAGYV-GDPIIGSGD-HCRPCPCPDGPDGROFARSCYQ 935
QY 152 KVNVLKIASPTASSPRDTALAANVCISALATVLLALLILCVYCKRQPMKPKPSLSRSQDI 211
DB 936 DPTVLQLACVC-----DPGYTGSRCDD-----CASGFFGNPSDFGSGCQPC 976
QY 212 QYN-----GSELSCL-----DRPQLHEYAH-----RAC----- 234
DB 977 QCHNIDTTDPEACDRDTGRLCLKLYHTGDCQCLQCYGYGDALRQDCRKCVCNVLGTV 1036
QY 235 -----CQCRDVSQV-TGCPVRLPLPSMCCPEACSPNPATL-----GCGVHSAASLAQRN 281
DB 1037 KEHCNGSDCHDKATGQCSCLP-NVIGQNC--DRCAPNTWOLASGTGCGPCNCNA--AHS 1091
QY 282 AGPAGEWVPTFFGSLTQSGFESDAWPLMNQPMGDNISFC 323
DB 1092 FGPS-----CNEFTGQCQCPMG-FGGRTCSEC 1117

RESULT 13
LMB2_MOUSE
ID LMB2_MOUSE STANDARD; PRT: 1799 AA.
AC 061292; Q62182;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE LAMININ BETA-2 CHAIN PRECURSOR.
GN LAMB2 OR S-LAM OR LAMS.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129/J;
RX MEDLINE=96278760; PubMed=8662701;

```

```

RA Durkin M.E., Gautam M., Loechel S., Sanes J.R., Merlie J.P.,
RT Albrechtsen R., Wewer U.M.;
RT "Structural organization of the human and mouse laminin beta2 chain
RT genes, and alternative splicing at the 5' end of the human
RT transcript.;"
RT J. Biol. Chem. 271:13407-13416(1996).
RN [2]
RN SEQUENCE OF 348-428 FROM N.A.
RC TISSUE=LUNG;
RC MEDLINE=94319092; PubMed=8043959;
RX Aberdam D., Galliano M.F., Mattei M.-G., Ortonne J.P., Meneguzzi G.;
RA "S-laminin gene (Lams) maps to F1 band of mouse chromosome 9.;"
RT Mamm. Genome 5:393-394(1994).
RN [3]
RN FUNCTION.
RN STRAIN=129/J;
RC MEDLINE=95191550; PubMed=7885444;
RA Noakes P.G., Gautam M., Mudd J., Sanes J.R., Merlie J.P.;
RT "Aberrant differentiation of neuromuscular junctions in mice lacking
RT s-laminin/laminin beta 2.;"
RT Nature 374:258-262(1995).
CC -!- FUNCTION: BINDING TO CELLS VIA A HIGH AFFINITY RECEPTOR, LAMININ
CC IS THOUGHT TO MEDIATE THE ATTACHMENT, MIGRATION, & ORGANIZATION OF
CC CELLS WITH OTHER TISSUES DURING EMBRYONIC DEVELOPMENT BY INTERACTING
CC WITH OTHER EXTRACELLULAR MATRIX COMPONENTS.
CC -!- FUNCTION: LAMININ-3 (S-LAMININ) REGULATES THE FORMATION OF MOTOR
CC NERVE TERMINALS.
CC -!- SUBUNIT: LAMININ IS A COMPLEX GLYCOPROTEIN, CONSISTING OF THREE
CC DIFFERENT POLYPEPTIDE CHAINS (ALPHA, BETA, GAMMA), WHICH ARE BOUND
CC TO EACH OTHER BY DISULFIDE BONDS INTO A CROSS-SHAPED MOLECULE
CC COMPRISING ONE LONG AND THREE SHORT ARMS WITH GLOBULES AT EACH END.
CC THE BETA-2 CHAIN IS A SUBUNIT OF LAMININ-3 (S-LAMININ), LAMININ-4
CC (S-MEROSIN), AND LAMININ-7 (KS-LAMININ).
CC -!- SUBCELLULAR LOCATION: EXTRACELLULAR; FOUND IN THE BASEMENT
CC MEMBRANES (MAJOR COMPONENT).
CC -!- TISSUE SPECIFICITY: NEUROMUSCULAR SYNAPSE AND KIDNEY GLOMERULUS.
CC -!- DOMAIN: THE ALPHA-HELICAL DOMAINS I AND II ARE THOUGHT TO INTERACT
CC WITH OTHER LAMININ CHAINS TO FORM A COILED COIL STRUCTURE.
CC -!- DOMAIN: DOMAINS VI AND IV ARE GLOBULAR.
CC -!- SIMILARITY: CONTAINS 1 LAMININ N-TERMINAL DOMAIN (DOMAIN VI).
CC -!- SIMILARITY: CONTAINS 12.5 LAMININ EGF-LIKE DOMAINS.
CC -!- SIMILARITY: CONTAINS 1 LAMININ DOMAIN IV.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U43541; AAC53535.1;
CC EMBL; U42624; AAC53535.1; JOINED.
CC EMBL; X75928; CAAS3532.1;
CC HSP; P02468; IKLO.
CC MGD; MGI:99916; LAMB2.
CC INTERPRO; IPR000561;
CC INTERPRO; IPR001886;
CC INTERPRO; IPR002049;
CC PFAM; PF00053; laminin_EGF; 13.
CC PFAM; PF00055; laminin_Nterm; 1.
CC PRINTS; PR00011; EGFLAMININ.
CC PROSITE; PS00022; EGF_1; 10.
CC PROSITE; PS01186; EGF_2; 2.
CC PROSITE; PS01248; LAMININ_TYPE_EGF; 12.
CC Glycoprotein; Basement membrane; Extracellular matrix; Coiled coil;
KW Laminin EGF-like domain; Cell adhesion; Repeat; Signal.
FT SIGNAL 1 35 POTENTIAL.
FT CHAIN 36 1799 LAMININ BETA-2 CHAIN.
FT DOMAIN 36 283 LAMININ N-TERMINAL (DOMAIN VI).
FT DOMAIN 284 555 4.5 X LAMININ EGF-LIKE REPEATS (DOMAIN
FT DOMAIN 286 349 LAMININ EGF-LIKE 1.

```


Query Match 5.8%; Score 133.5; DB 1; Length 1799;
Best Local Similarity 20.1%; Pred. No. 0.017;
Matches 92; Conservative 40; Mismatches 121; Indels 205; Gaps 27;

Qy 17

LVLLGYLSCKVTCEFGDCRQQRDRSGNVCPCNOCGPGMELSKEC-----GFG--- 65

Db 776

LIYNGALPCQ--CDPQGLSSSECSPHGGQC-----RCKPGV-VGRRCDDVCATGYGFGPAG 828

Qy 66

-----YGEDAQCVTCRLHRF-----KEDWGFQKCKPCLDCAVVRNF 101

Db 829

COACQCPDGPALSALCEGTSGQC-PCRPAFGRLCDHCQGGQPGNCRPCV----- 879

Qy 102

QKANCATSDAI-----CGDCLPGFYRKTKL-VGFODMECVPGDPP 142

Db 880

-----CNGRADECDDTHTGACLGCRDYGGEHCERCIAGHGDPLPYGGO---CRPCPCPE 932

Qy 143

PPYEPHACKSVNLVKIASTASSPRDTALAAVICSALATVLLALLILCVYCKRPFM--- 198

Db 933

GPQSQRHFAT-----SCHRDGYSQQIVC-----HCRAGTYGLR 965

Qy 199

-----EKKP-----SWSLSRSDIQ-----YNGSELSCLD-----RP 224

Db 966

CEACAPGPGDPSKPGRCOLCECSGNIDPMDPADCDPHTGQCLRLHNTGPHGCKPK 1025

Qy 225

QLH-EYAHRAACCCRRDSVQTCGPVRLLPSC-----CE-----EA 259

Db 1026

GFHQAAQSQSCHRC-----TCNLLGTDPRRCPTDLCHCDPSTGQCPCPLHVQGLNCDH 1079

Qy 260

CSPN--PATLGGVHSAASLOARNAGP-----AGEMVPTFFGSLTQSGEFS 305

Db 1080

CAPNEFWNTSGRGQPCACHPSRARGPTCNFTGQCHCAG-----FGRTCSCEQELY 1133

Qy 306

DAWPLMQ-----NPMGGD-----NISFDSYPELTG 331

Db 1134

WGDPGLQCRACDPRGIDKPOCHRSTGHCSRCRPGVSG 1171

RESULT 14

VWF_HUMAN

ID VWF_HUMAN STANDARD; PRT; 2813 AA.

AC P04275;

DT 20-MAR-1987 (Rel. 04, Created)

DT 01-JUL-1993 (Rel. 26, Last sequence update)

DT 01-OCT-2000 (Rel. 40, Last annotation update)

DE VON WILLEBRAND FACTOR PRECURSOR (VWF).

GN F8VWF OR VWF.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE-90062044; PubMed-2584182;

RA Mancuso D.J., Tuley E.A., Westfield L.A., Morrall N.K.,

RA Shelton-Inloes B.B., Sorace J.M., Alevy Y.G., Sadler J.E.;

RT "Structure of the gene for human von Willebrand factor.;"

RL J. Biol. Chem. 264:19514-19527(1989).

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE-87016349; PubMed-3489923;

RA Bonthron D., Orr E.C., Mitsock L.M., Ginsburg D., Handin R.I.,

RA Orkin S.H.;

RT "Nucleotide sequence of pre-pro-von Willebrand factor cDNA.;"

RL Nucleic Acids Res. 14:7125-7128(1986).

RN [3]

RP SEQUENCE OF 1-120 FROM N.A., AND SEQUENCE OF 23-56.

RC TISSUE-UMBILICAL VEIN ENDOTHELIAL CELLS;

RX MEDLINE-87213253; PubMed-3495266;

RA Shelton-Inloes B.B., Broze G.J. Jr., Miletich J.P., Sadler J.E.;

RT "Evolution of human von Willebrand factor: cDNA sequence
RT polymorphisms, repeated domains, and relationship to von Willebrand
RT antigen II.";
RL Biochem. Biophys. Res. Commun. 144:657-665(1987).
RN [4]
RN
RP SEQUENCE OF 1-1400 FROM N.A.
RX MEDLINE=87004550; PubMed=3019665;
RA Verweij C.L., Diergaarde P.J., Hart M., Pannekoek H.;
RT "Full-length von Willebrand factor (vWF) cDNA encodes a highly
RT repetitive protein considerably larger than the mature vWF subunit.";
RL EMBO J. 5:1839-1847(1986).
RN [5]
RN
RN
RN
RA Verweij C.L., Diergaarde P.J., Hart M., Pannekoek H.;
RL EMBO J. 5:3074-3074(1986).
RN [6]
RN
RN
RX SEQUENCE OF 764-2813.
RX MEDLINE=86269895; PubMed=3524673;
RA Titani K., Kumar S., Takio K., Ericsson L.H., Wade R.D., Ashida K.,
RA Walsh K.A., Choek M.W., Sadler J.E., Fujikawa K.;
RT "Amino acid sequence of human von Willebrand factor.";
RL Biochemistry 23:3171-3184(1986).
RN [7]
RN
RN
RP SEQUENCE OF 781-1424 FROM N.A.
RX MEDLINE=86269894; PubMed=3488076;
RA Shelton-Inloes B.B., Titani K., Sadler J.E.;
RT "cDNA sequences for human von Willebrand factor reveal five types of
RT repeated domains and five possible protein sequence polymorphisms.";
RL Biochemistry 23:3164-3171(1986).
RN [8]
RN
RP SEQUENCE OF 764-873 AND 1289-2813 FROM N.A.
RX MEDLINE=86016708; PubMed=2864688;
RA Sadler J.E., Shelton-Inloes B.B., Sorace J.M., Harlan J.M.,
RA Titani K., Davie E.W.;
RT "Cloning and characterization of two cDNAs coding for human von
RT Willebrand factor.";
RL Proc. Natl. Acad. Sci. U.S.A. 82:6394-6398(1985).
RN [9]
RN
RN
RX SEQUENCE OF 990-1947 FROM N.A.
RX MEDLINE=91105089; PubMed=1988024;
RA Mancuso D.J., Tuley E.A., Westfield L.A., Lester-Mancuso T.L.,
RA Le Beau M.M., Sorace J.M., Sadler J.E.;
RT "Human von Willebrand factor gene and pseudogene: structural analysis
RT and differentiation by polymerase chain reaction.";
RL Biochemistry 30:253-269(1991).
RN [10]
RN
RP SEQUENCE OF 2731-2813 FROM N.A.
RX MEDLINE=85269603; PubMed=3875078;
RA Verweij C.L., de Vries C.J.M., Distel B., van Zonneveld A.-J.,
RA Geurts van Kessel A., van Mourik J.A., Pannekoek H.;
RT "Construction of cDNA coding for human von Willebrand factor using
RT antibody probes for colony-screening and mapping of the chromosomal
RT gene.";
RL Nucleic Acids Res. 13:4699-4717(1985).
RN [11]
RN
RP SEQUENCE OF 1-177 FROM N.A.
RX MEDLINE=88111704; PubMed=2828057;
RA Bonthron D., Orkin S.H.;
RT "The human von Willebrand factor gene. Structure of the 5' region.";
RL Eur. J. Biochem. 171:51-57(1988).
RN [12]
RN
RP SEQUENCE OF 2621-2813 FROM N.A.
RX MEDLINE=85244588; PubMed=3874428;
RA Ginsburg D., Handin R.I., Bonthron D.T., Donlon T.A., Bruns G.A.P.,
RA Latt S.A., Orkin S.H.;
RT "Human von Willebrand factor (vWF): isolation of complementary DNA
RT (cDNA) clones and chromosomal localization.";
RL Science 228:1401-1406(1985).
RN [13]
RN
RP SEQUENCE OF 2731-2813 FROM N.A.
RX MEDLINE=85201687; PubMed=3873280;
RA Lynch D.C., Zimmerman T.S., Collins C.J., Brown M., Morin M.J.,
RA Ling E.H., Livingston D.M.;

RT "Molecular cloning of cDNA for human von Willebrand factor:
RT authentication by a new method.";
RL Cell 41:49-56(1985).
RN [14]
RN
RP REVISIONS.
RA Lynch D.C.;
RL Submitted (JUL-1991) to the EMBL/GenBank/DBJ databases.
RN [15]
RN
RP SEQUENCE OF 2731-2813 FROM N.A.
RX MEDLINE=87260814; PubMed=3496594;
RA Collins C.J., Underdahl J.P., Levene R.B., Ravera C.P.,
RA Morin M.J., Dombalagian M.J., Ricca G., Livingston D.M.,
RA Lynch D.C.;
RT "Molecular cloning of the human gene for von Willebrand factor and
RT identification of the transcription initiation site.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:4393-4397(1987).
RN [16]
RN
RP DISULFIDE BONDS.
RX MEDLINE=88163465; PubMed=3502076;
RA Marti T., Rosselet S.J., Titani K., Walsh K.A.;
RT "Identification of disulfide-bridged substructures within human von
RT Willebrand factor.";
RL Biochemistry 26:8099-8109(1987).
RN [17]
RN
RP STRUCTURE OF CARBOHYDRATES.
RX MEDLINE=86274702; PubMed=3089784;
RA Samor B., Michalski J.C., Debray H., Mazurier C., Goudemand M.,
RA van Halbeek H., Vliegthart J.F.G., Montreuil J.;
RT "Primary structure of a new tetraantennary glycan of the N-
RT acetylglucosaminic type isolated from human factor VIII/von
RT Willebrand factor.";
RL Eur. J. Biochem. 158:295-298(1986).
RN [18]
RN
RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 1261-1468.
RX MEDLINE=98221174; PubMed=9553097;
RA Emsley J., Cruz M., Handin R., Liddington R.;
RT "Crystal structure of the von Willebrand factor A1 domain and
RT implications for the binding of platelet glycoprotein Ib.";
RL J. Biol. Chem. 273:10396-10401(1998).
RN [19]
RN
RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF 1685-1873.
RX MEDLINE=97472999; PubMed=9331419;
RA Huizinga E.G., Martijn van der Plas R., Kroon J., Sixma J.J., Gros P.;
RT "Crystal structure of the A3 domain of human von Willebrand factor:
RT implications for collagen binding.";
RL Structure 5:1147-1156(1997).
RN [20]
RN
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 1686-1872.
RX MEDLINE=97460108; PubMed=9312128;
RA Bienkowska J., Cruz M., Atiemo A., Handin R., Liddington R.;
RT "The von Willebrand factor A3 domain does not contain a metal ion-
RT dependent adhesion site motif.";
RL J. Biol. Chem. 272:25162-25167(1997).
RN [21]
RN
RP VARIANTS TRP-1597 AND ASP-1607.
RX MEDLINE=89264495; PubMed=2786201;
RA Ginsburg D., Konkle B.A., Gill J.C., Montgomery R.R.,
RA Bockenstedt P.L., Johnson T.A., Yang A.Y.;
RT "Molecular basis of human von Willebrand disease: analysis of
RT platelet von Willebrand factor mRNA.";
RL Proc. Natl. Acad. Sci. U.S.A. 86:3723-3727(1989).
RN [22]
RN
RP VARIANT THR-1628.
RX MEDLINE=91196734; PubMed=1673047;
RA Iannuzzi M.C., Hidaka N., Boehnke M., Bruck M.E., Hanna W.T.,
RA Collins F.S., Ginsburg D.;
RT "Analysis of the relationship of von Willebrand disease (vWD) and
RT hereditary hemorrhagic telangiectasia and identification of a
RT potential type IIA vWD mutation (Ile865 to Thr).";
RL Am. J. Hum. Genet. 48:757-763(1991).
RN [23]
RN
RP VARIANTS NORMANDY-2 AND NORMANDY-3.
RX MEDLINE=92001464; PubMed=1832934;

Gaucher C., Mercier B., Jorieux S., Oufkir D., Mazurier C.;
RT "Identification of two point mutations in the von Willebrand factor
RT gene of three families with the 'Normandy' variant of von Willebrand
RT disease.";

RN Br. J. Haematol. 78:506-514(1991). [24]

VARIANT CY5-1308.
RX MEDLINE=92104315; PubMed=1761120;
RA Donner M., Andersson A.-M., Kristofferson A.-C., Nilsson I.M.,
RA Dahlback B., Holmberg L.;
RT "An Arg545-->Cys545 substitution mutation of the von Willebrand
RT factor in type IIb von Willebrand's disease.";

RN Eur. J. Haematol. 47:342-345(1991). [25]
RNP VARIANTS TRP-1306; CYS-1308 AND PRO-1613.
RX MEDLINE=91185601; PubMed=2010538;
RA Randi A.M., Rabinowitz I., Mancuso D.J., Mannucci P.M., Sadler J.E.;
RT "Molecular basis of von Willebrand disease type IIb. Candidate
RT mutations cluster in one disulfide loop between proposed platelet
RT glycoprotein Ib binding sequences.";

RN J. Clin. Invest. 87:1220-1226(1991). [26]
RNP VARIANTS TRP-1306; CYS-1308; MET-1316; GLN-1341 AND HIS-1399.
RX MEDLINE=91185602; PubMed=1672694;
RA Cooney K.A., Nicholas W.C., Bruck M.E., Bahou W.F., Shapiro A.D.,
Query Match 5.8%; Score 133.5; DB 1; Length 2813;
Best Local Similarity 21.4%; Pred No. 0.029;
Matches 78; Conservative 38; Mismatches 107; Indels 141; Gaps 19;

QY 44 GNCVP---CNQCGRGMELSKCEGFGYGDAOCVTCRLHREKEDWGFKCKPCLCDCAVVNR 100
I::II I::II I::II I::II I::II I::II I::II I::II I::II I::II
Db GSCVPEEACTQC-----IGEDGV----QHQLFLEW-VPDHQPCQICTCLSG 2286

QY 101 FQRANCSA----TSDA-ICGDCLPGFRKYTKLVGFQDMEC-----VPCGDPPPPVEPHCAS 151
I::II I::II I::II I::II I::II I::II I::II I::II I::II I::II
Db -RKVNCTQPCTAKAPTGLGEVARLRQNADQCCPEYCVDPVSCDLPP---VPHGER 2342

QY 152 KVNVLKTASTASSPRDTALAAVICSA LATVLLALLLCVIYKRQFMKKFSWSLRSQDI 211
I::II I::II I::II I::II I::II I::II I::II I::II I::II I::II
Db -----GIQLPTNGE-----CRNF----- 2358

QY 212 QYNSELSCLDRPOLHEAHACQRRDSYOTCGPVRLPSM-----CCEE---ACSPNP 264
I::II I::II I::II I::II I::II I::II I::II I::II I::II I::II
Db -----TCACRKE-----ECKRVSPSCPPIRH-LPTLRKTQCCDEVCACNCVN 2400

QY 265 ATLCGGVHSASLARAGAPAGEVMPFFGSILTOSICGEFSDAWPL----- 310
I::II I::II I::II I::II I::II I::II I::II I::II I::II I::II
Db 2401 STVSCPLGYLASTATNDGC-----CTTTCLPKVCVHRSTIYPVGQFWBEGCDVCTCT 2454

QY 311 -MQPMGGDNISFCDSYP-----ELTGEDIHLINPELESSTSLDSSNQ 353
I::II I::II I::II I::II I::II I::II I::II I::II I::II I::II
Db 2455 DMEDAVMLRVAQCSOKPEDCSRSGFTYVLHGEGCCRCGLPSACEVVTGSPRGDSQSSW 2514

QY 354 DLVG 357
II
Db 2515 KS VG 2518

RESULT 15
TSPL_MOUSE ID TSPL_MOUSE STANDARD; PR T; 1170 AA.

AC P35441:
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE THROMBOSPONDIN 1 PRECURSOR.
GN THBS1 OR TSPL.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.

MEDLINE-92128941; PubMed-1774063;
Lawler J., Duquette M., Ferro P., Copeland N.G., Gilbert D.J.,
Jenkins N.A.,
"Characterization of the murine thrombospondin gene.";
Genomics 11:587-600(1991).
[2]
SEQUENCE FROM N.A.
MEDLINE-92147683; PubMed-1371115;
Laherty C.D., O'Rourke K., Wolf F.W., Katz R., Seldin M.F.,
Dixit V.M.,
"Characterization of mouse thrombospondin 2 sequence and expression
during cell growth and development.";
J. Biol. Chem. 267:3274-3281(1992).
[3]
SEQUENCE OF 1-490 FROM N.A.
MEDLINE-90375546; PubMed-2398070;
Bornstein P., Alfai D., Devarayalu S., Franson P., Li P.,
"Characterization of the mouse thrombospondin gene and evaluation of
the role of the first intron in human gene expression.";
J. Biol. Chem. 265:16591-16598(1990).
-!- FUNCTION: ADHESIVE GLYCOPROTEIN THAT MEDIATES CELL-TO-CELL AND
CELL-TO-MATRIX INTERACTIONS. CAN BIND TO FIBRINOGEN, FIBRONECTIN,
LAMININ AND TYPE V COLLAGEN.
-!- SUBUNIT: HOMOTRIMER, CROSS-LINKED BY DISULFIDE BONDS.
-!- SIMILARITY: BELONGS TO THE THROMBOSPONDIN FAMILY.
-!- SIMILARITY: CONTAINS 1 VMFC DOMAIN.
-!- SIMILARITY: CONTAINS 3 EGF-LIKE DOMAINS.
-!- SIMILARITY: CONTAINS 3 TYPE-1 TSP REPEATS AND 7 TYPE-3 TSP REPEATS
(WHICH BIND CALCIUM).

THIS SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation
at the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See <http://www.isb-sib.ch/announcement/>
or send an email to license@isb-sib.ch).

ENBL; M62470; AAA50611.1; -
ENBL; M62450; AAA50611.1; JOINED.
ENBL; M62451; AAA50611.1; JOINED.
ENBL; M62452; AAA50611.1; JOINED.
ENBL; M62453; AAA50611.1; JOINED.
ENBL; M62454; AAA50611.1; JOINED.
ENBL; M62455; AAA50611.1; JOINED.
ENBL; M62456; AAA50611.1; JOINED.
ENBL; M62457; AAA50611.1; JOINED.
ENBL; M62458; AAA50611.1; JOINED.
ENBL; M62459; AAA50611.1; JOINED.
ENBL; M62460; AAA50611.1; JOINED.
ENBL; M62461; AAA50611.1; JOINED.
ENBL; M62462; AAA50611.1; JOINED.
ENBL; M62463; AAA50611.1; JOINED.
ENBL; M62464; AAA50611.1; JOINED.
ENBL; M62465; AAA50611.1; JOINED.
ENBL; M62466; AAA50611.1; JOINED.
ENBL; M62467; AAA50611.1; JOINED.
ENBL; M62468; AAA50611.1; JOINED.
ENBL; M62469; AAA50611.1; JOINED.
ENBL; M87276; AAA53063.1; -
ENBL; J05606; AAA40431.1; -
ENBL; J05605; AAA40431.1; JOINED.
PIR; A40558; A40558.
PIR; B42587; B42587.
PIR; A37905; A37905.
HSSP; P35555; IEMO.
MGD; MGI:98737; THBS1.
INTERPRO: IPR000561; -
INTERPRO: IPR000884; -
INTERPRO: IPR001007; -
PFAM; PF00008; EGF; 2.
PFAM; PF00090; tsp_1; 3.
PFAM; PF00093; vwc; 1.

